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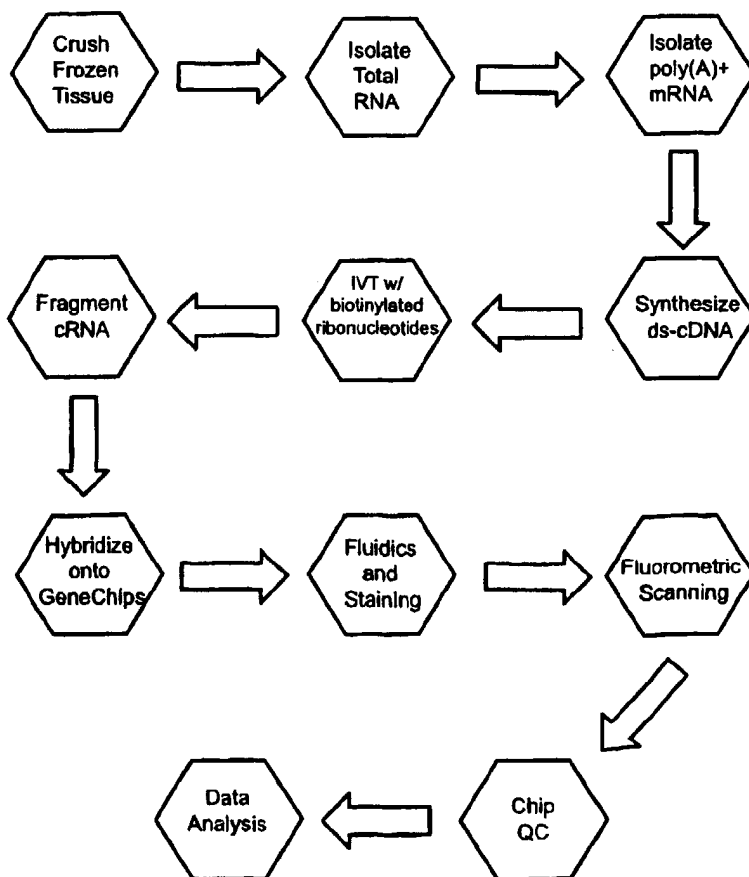
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(54) Title: GENE EXPRESSION PROFILES IN LIVER CANCER



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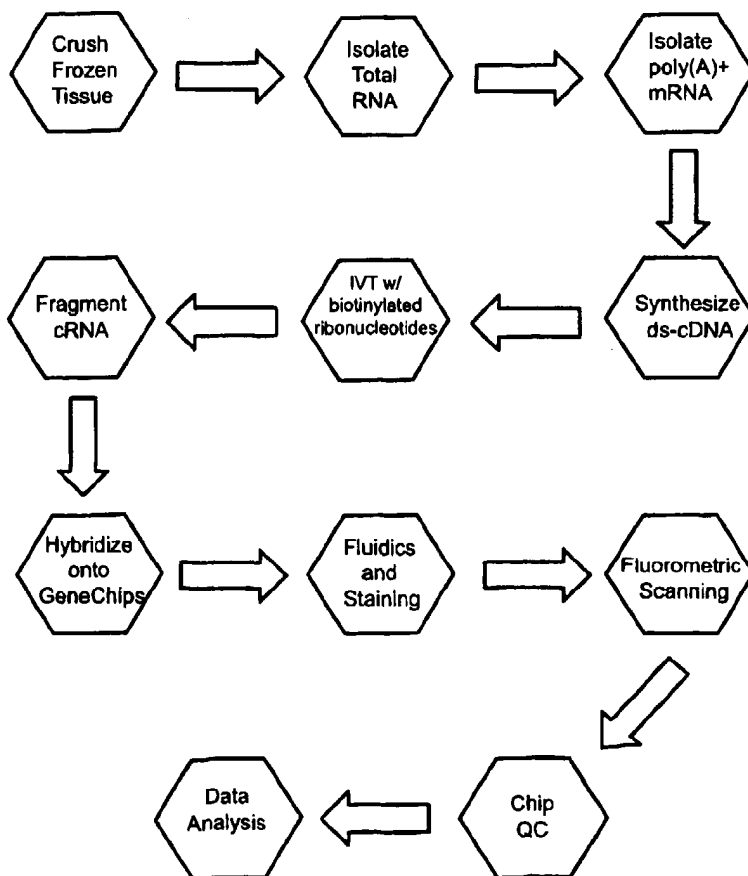
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GENE EXPRESSION PROFILES IN LIVER CANCER

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RELATED APPLICATIONS

This application is related to U.S. Provisional Application 60/211,379, filed on June 14, 2000, and is related to U.S. Provisional Application 60/237,054, filed October 2, 2000, and is related to U.S. Application 09/880,107, filed June 14, 2001, each of which is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Primary hepatocellular carcinoma (HCC) is a widespread cancer throughout the world, especially prevalent where the incidence of chronic hepatitis B (HBV) and hepatitis C (HCV) viral infections are endemic (Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57; Idilman *et al.*, (1998) *J. Viral. Hepat.* 5, 110-117; Di Bisceglie *et al.*, (1998) *Hepatol.* 28, 1161-1165; Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Sheu, (1997) *J. Gastroenterol. Hepatol.* 12, S309-313). Hepatocellular carcinomas are very malignant tumors that generally offer a poor prognosis, dependent on the size of the tumor, the effect on normal liver functions, and the involvement of metastases. They are best treated by surgical resection, when the tumors are diagnosed at a stage where this is a viable possibility, but the recurrence rate for these cancers remains high (Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Schafer & Sorrell, (1999) *Lancet* 353, 1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57; Sitzman, (1995) *World. J. Surg.* 19, 790-794; DiCarlo, (1995) *Hepato-Gastroenterol.* 42, 222-259; Tanaka *et al.*, (1996) *Hepato-Gastroenterol.* 43, 1172-1181; El-Assal *et al.*, (1997) *Surgery* 122, 571-577).

Numerous risk factors for the development of HCC have been identified: cirrhosis, HBV or HCV infection, being male, alcohol-related liver disease, exposure to aflatoxins, vinyl chloride and radioactive thorium dioxide, cigarette smoking, ingestion of inorganic arsenic, the use of oral contraceptives and anabolic steroids, iron accumulation, and various inherited metabolic disorders (hemochromatosis, glycogen storage disease, porphyria,

tyrosinemia, α -1-antitrypsin deficiency) (Di Bisceglie *et al.*, (1998) *Hepatology* 28, 1161-1165; Chen *et al.*, (1997) *J. Gastroenterol. Hepatology* 12, S294-308; Schafer & Sorrell (1999) *Lancet* 353, 1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57; Idilman *et al.*, (1998) *J. Viral. Hepat.* 5, 110-117; Johnson, (1997) *Hepato-Gastroenterol.* 44, 307-312).

5 In addition to liver tumors attributed to hepatocellular carcinoma, there are liver tumors that arise as metastases from primary tumors in other parts of the body. These tumors most often metastasize from the gastrointestinal organs, primarily the colon and rectum, but it is possible for metastatic liver cancers to occur from primary cancers throughout the body (Sitzman, (1990) *Hepatic Neoplasia*, in Bayless (editor) *Current*
10 *Therapy in Gastroenterology and Liver Disease*, Marcel Dekker; Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57). These cancers can be treated using the routine therapies such as chemotherapy, radiotherapy, surgical resection, liver transplantation, chemoembolization, cryosurgery, or a combination of therapies (Sitzman 1990, Groen 1999).

 The characterization of genes that are differentially expressed in tumorigenesis is an
15 important step in identifying those that are intimately involved in the details of a cell's transformation from normal to cancerous. Little is known about the molecular changes that take place in the liver during the course of tumor progression. While changes in the expression level of individual genes has been reported, for example, galectin-3 (Hsu *et al.*, (1999) *Int. J. Cancer* 81: 519-526; Iurisci *et al.*, (2000) *Clin. Cancer Res.* 6: 1389-1393;
20 Nakamura *et al.*, (1999) *Int. J. Oncol.* 15: 143-148) and pancreatic secretory trypsin inhibitor (PTSI, Ohmachi *et al.*, (1994) *Int. J. Cancer* 55: 728-734) the investigation of the global changes in gene expression which occur in liver have not been documented. The identification of genes that are expressed in tumor tissue at differing levels, but not expressed at any level in normal liver tissue will be very valuable for monitoring tumor
25 progression. The identification of genes and ESTs that are expressed in both types of tumors, *i. e.*, primary hepatocellular carcinomas as well as metastatic tumors of a different origin, and not in normal liver cells would be extremely valuable for the diagnosis of liver cancer. Thus there exists a need in the art for the identification of new genes and ESTs to serve as molecular markers to monitor the onset and development of liver cancer. These
30 and other needs are met by the present invention.

SUMMARY OF THE INVENTION

The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

The invention includes methods of diagnosing the presence or absence of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. In some preferred embodiments, the method may include detecting the expression level of one or more genes selected from a group consisting Tetraspan NET-6 protein; collagen, type V, alpha; and glypican 3.

The invention also includes methods of detecting the progression of liver cancer and/or differentiating nonmetastatic from metastatic disease. For instance, methods of the invention include detecting the progression of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with liver cancer, comprising administering a pharmaceutical composition to the patient and preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising liver cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 3-9. In other preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In another aspect, the present invention provides a method of treating a patient with liver cancer, comprising administering to the patient a pharmaceutical composition, wherein

the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising liver cancer cells. In some preferred embodiments, one or more
5 genes may be selected from a group consisting of the genes listed in Tables 3-5.

In one aspect, the present invention provides a method of diagnosing hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma. In some preferred embodiments, one or more
10 genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In another aspect, the present invention provides a method of detecting the progression of hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.
15 In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention also provides materials and methods for monitoring the treatment of a patient with a hepatocellular carcinoma. The present invention provides a method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising
20 administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both. In some preferred embodiments, the method may include detecting the
25 level of expression of one or more genes from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In a related aspect, the present invention provides a method of treating a patient with hepatocellular carcinoma, comprising administering to the patient a pharmaceutical
30 composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells and comparing the patient expression profile to a

gene expression profile from an untreated cell population comprising hepatocellular carcinoma cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

5 The present invention provides a method of diagnosing a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

10 The present invention provides a method of detecting the progression of a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

15 In a related aspect, the present invention provides a method of monitoring the treatment of a patient with a metastatic liver tumor, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression
20 profile from a cell population comprising metastatic liver tumor cells or to both. In some preferred embodiments, the method of the present invention may include detecting the expression level of one or more genes selected from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

25 In some preferred embodiments, the present invention provides a method of treating a patient with a metastatic liver tumor, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells and comparing the patient expression profile
30 to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The invention also includes methods of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

The invention further includes methods of screening for an agent capable of modulating the onset or progression of liver cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

Any of the methods of the invention described above may include the detection of at least 2 genes from the tables. Preferred methods may detect all or nearly all of the genes in the tables. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 as well as solid supports comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes computer systems comprising a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9; and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal liver tissue and malignant tissue (metastatic and nonmetastatic) and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue or cell to the level of

expression of the gene in the database. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

BRIEF DESCRIPTION OF THE DRAWINGS

5 Figure 1 is a flow chart showing a schematic representation of the experimental protocol.

Figures 2A-2C are graphs of the number of genes present in all samples as a function of the number of samples for the second sample set.

10 DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.*, through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often
15 characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, (1991) *Cell*, 64, 313-326; Weinberg, (1991) *Science*, 254, 1138-1146).
20 Thus, changes in the expression levels of particular genes (*e.g.*, oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often
25 such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue samples from normal liver, metastatic malignant liver and hepatocellular carcinoma to identify the global changes in gene expression associated with liver cancer. The protocol used is schematically represented in
30 Figure 1. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Definitions

In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interests of clarity and consistency of interpretation, the
5 definitions of certain terms and phrases are provided.

The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, *i.e.*, normal versus cancerous. As used herein, the phrase "detecting the level of expression" includes methods that quantitate expression levels as well as methods that determine
10 whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under
15 stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe
20 nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target
25 nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the
30 average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that

where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e.g., probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

The term "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, U, C or T) or modified bases (7-

deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

5 The term “stringent conditions” refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are
10 selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotide). Stringent
15 conditions may also be achieved with the addition of destabilizing agents such as formamide.

The “percentage of sequence identity” or “sequence identity” is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may
20 optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical monomer unit (*e.g.*, nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched
25 positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity may be determined by **BLAST** (Basic Local Alignment
30 Search Tool) analysis using the algorithm employed by the programs **blastp**, **blastn**, **blastx**, **tblastn** and **tblastx** (Karin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are

tailored for sequence similarity searching. The approach used by the **BLAST** program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a
5 discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.*, (1994) *Nature Genet.* 6, 119-129) which is fully incorporated by reference. The search parameters for **histogram**, **descriptions**, **alignments**, **expect** (*i.e.*, the statistical significance threshold for reporting matches against database sequences), **cutoff**, **matrix** and **filter** are at the default settings. The default scoring matrix used by **blastp**, **blastx**, **tblastn**, and **tblastx**
10 is the **BLOSUM62** matrix (Henikoff *et al.*, (1992) *Proc. Natl. Acad. Sci. USA* 89, 10915-10919, fully incorporated by reference). Four **blastn** parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent **Blastp** parameter settings were Q=9;
15 R=2; wink=1; and gapw=32. A **Bestfit** comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

20 *Uses for the Liver Cancer Markers as Diagnostics*

As described herein, the genes and gene expression information provided in Tables 3-9 may be used as diagnostic markers for the prediction or identification of the malignant state of the liver tissue. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described herein or by any other method known to
25 those skilled in the art, and the expression levels from a gene or genes from the Tables, in particular the genes in Tables 3-5, may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Expression profiles generated from the tissue or other sample that substantially resemble an expression profile from normal or diseased liver tissue may be used, for instance, to aid in
30 disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Monitoring Disease Progression

As described above, the genes and gene expression information provided in Tables 3-9 may also be used as markers for the monitoring of disease progression, for instance, the development of liver cancer. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described above, and the expression levels in the sample from a gene or genes from or 3-9 may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Drug Screening

According to the present invention, the genes identified in Tables 3-9 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, a liver cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of drugs' effects by looking at the number of markers affected by different drugs and comparing them. More specific drugs will affect fewer transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agents action. Agents can be rationally

selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats

The genes identified as being differentially expressed in liver cancer may be used in a variety of nucleic acid detection assays to detect or quantitate the expression level of a gene or multiple genes in a given sample. Any hybridization assay format may be used, including solution-based and solid support-based assay formats, for example, traditional Northern blotting. Other suitable assay formats that may be used for detecting gene expression levels include, but are not limited to, nuclease protection, RT-PCR and differential display methods. These methods are useful for some embodiments of the invention; however, methods and assays of the invention are most efficiently designed with array or chip hybridization-based methods for detecting the expression of a large number of genes. Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

Assays to monitor the expression of a marker or markers as defined in Tables 3-9 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least two genes from Tables

3-9 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the 3' or 5' regulatory regions of a gene in Tables 3-9 and any assayable fusion partner may be prepared. Numerous
5 assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, (1990) Anal. Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents
10 which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of one or more genes identified in Tables 3-9. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under
15 appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be
20 expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, derived from liver tissue. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector)
25 construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further
30 comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media
5 comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed
10 by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

15 Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein(s) encoded by the genes in Tables 3-9. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell
20 population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell
25 line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation
30 of genes within a population. However, it may be preferable to use polyA⁺ RNA as a source, as it can be used with less processing steps.

The sequences of the expression marker genes are in the public databases. Tables 3-9 provide the Affymetrix gene ID and GenBank accession number for each marker identified. The nucleotide sequence for each marker has been provided in electronic format with this application and these sequences are incorporated herein by reference as are
5 equivalent and related sequences present in the public databases.

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10,
10 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

Probe design

One of skill in the art will appreciate that an enormous number of array designs are
15 suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be
20 oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from
25 natural sources or amplified from natural sources using natural nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high
30 density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label
5 intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized
10 that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they
15 are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control
20 probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the β -actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are
25 oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent
30 conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a

probe is a twenty-mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross
5 hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect
10 match and the mismatch probe ($I_{(PM)} - I_{(MM)}$) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the
15 methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, Tijssen, (1993)
20 (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

25 Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid,
30 or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports

Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc.

5 Such wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined
10 location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, about 2, 10, 100, 1000 to 10,000; 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.

15 Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.*, (1996) Nat. Biotechnol. 14, 1675-1680; McGall *et al.*, (1996) Proc. Nat. Acad. Sci. USA 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays
20 may also contain oligonucleotides that are complementary or hybridize to at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or or more the genes described herein.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical
25 coupling, and mechanically directed coupling (see Pirrung *et al.*, (1992) U.S. Patent No. 5,143, 854; Fodor *et al.*, (1998) U.S. Patent No. 5,800,992; Chee *et al.*, (1998) 5,837,832.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane
30 reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5'

photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been
5 synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor *et al.*, (1993). WO
10 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

15

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart *et al.*, (1999) WO 99/32660).
20 The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids.

Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid
25 duplexes (*e.g.*, DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary.

Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may
30 be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6× SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*,

1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25× SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be
5 evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest
10 stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides
15 adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of
20 means well known to those of skill in the art (see Lockhart *et al.*, (1999) WO 99/32660).

Databases

The present invention includes relational databases containing sequence information, for instance for the genes of Tables 3-9, as well as gene expression information in various
25 liver tissue samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database.
30 Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom *et al.*, (1999) U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 3-9, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

5 Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client-server environments, database servers and networks
10 are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

15 The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 3-9 comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of
20 expression of a gene or genes in Tables 3-9 from a sample to the expression levels found in tissue from normal liver, malignant liver or hepatocellular carcinoma. Such methods may also be used in the drug or agent screening assays as described below.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the
25 compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

30 Example 1: Tissue Sample Acquisition and Preparation

Figure 1 outlines the experimental protocol used. Liver tissue samples were excised and snap frozen in liquid nitrogen. The clinical data for each of the samples included in this

study are outlined in Table 1. The sample set was composed of eight samples of normal liver tissue (N1-N8), five samples of metastatic adenocarcinoma arising from rectum (designated M1 and M3) and colon (M2, M4 and M5) tissues and six samples of primary hepatocellular carcinomas. Samples were named according to type of tissue:

- 5 HCC=hepatocellular carcinoma, M=metastatic, N=normal. Table 1 includes the TNM classification (the American Joint Committee on Cancer's system of classifying cancers) of the tissues used as samples where T refers to the extent of the primary tumor, N refers to the absence or presence and extent of regional lymph node metastasis, and M refers to the absence or presence of distant metastasis. Numbers following T, N, and M refer to the size
10 of the primary tumor and the amount of vascular invasion, where 0=no evidence of tumor, lymph node involvement or metastasis, 4=multiple tumors involved, and x=cannot be assessed. Histopathologic grade (Table 1) is a qualitative assessment of differentiation of a tumor, where G1=most differentiated and G4=undifferentiated. Clinical stage (Table 1) characterizes the anatomic extent of disease in the patient from whom the sample was taken,
15 where I and II are early stages, III and IV are late stages.

- With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was
20 200-500 µg. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 µl, an ethanol precipitation step was required to bring the concentration to 1 µg/µl. Using 1-5 µg of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7-(dT₂₄) oligonucleotide. The cDNA was then phenol-chloroform
25 extracted and ethanol precipitated to a final concentration of 1 µg/µl.

- From 2 µg of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5×
30 fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55 µg of fragmented cRNA was hybridized on the human Hu35k set and the

HuGeneFL array for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between.

5 Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1.0).

10

Example 2: Gene Expression Analysis

All samples were prepared as described and hybridized onto the Affymetrix HuGeneFL array and the Human Hu35k set of arrays. Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly
15 matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the
20 perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average
25 difference was figured using the average differences of each individual sample within the set. The median average difference must be greater than 150 to assure that the expression level is well above the background noise of the hybridization. For the purposes of this study, only the genes and ESTs with a median average difference greater than 150 have been further studied in detail.

30 The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently

absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature.

Example 3: Gene Expression Analysis of Normal Liver Tissue

The gene expression patterns and Gene Signature were individually determined for each sample set: eight samples with normal liver pathology, six samples whose pathology indicated the primary malignancy to be hepatocellular carcinoma, and five samples whose primary colorectal adenocarcinoma had metastasized to the liver. The Gene Signatures obtained for the normal sample set is shown in Figure 2A, the metastatic liver cancer set in Figure 2B and the hepatocellular carcinoma set in Figure 2C.

The Gene Signature considers the present and absent genes alone, and does not take into consideration those that have been called marginal. Table 2 shows the numbers of present genes, called the positive Gene Signature, and the number of absent genes, called the negative Gene Signature, for each of the three sets of samples.

The Gene Signature is the set of genes that are commonly present or commonly absent in N-1 samples of a given sample set. The positive Gene Signature for the normal liver tissues contains 6,213 genes and ESTs. This same set of normal samples did not show any detectable level of expression of 24,900 genes. Many of the genes and ESTs in this positive Gene Signature are housekeeping genes or structural genes that are not only expressed in the liver, but are ubiquitously expressed in tissues throughout the body. Within

this positive Gene Signature are also those genes whose expression is specifically restricted to normal liver tissue and those genes required for the liver to function at its normal capacities. It is the group of genes unique to the liver whose expression levels are most likely to change during tumorigenesis. Whether up-regulated or down-regulated or turned
5 completely on or turned completely off, the changes in expression of these vital genes very likely contributes to the drastic changes in liver function caused by the transformation of normal liver cells into cancerous cells.

Example 4: Gene Expression Analysis of Malignant Liver Tissue

10 There are 8,479 genes and ESTs in the positive Gene Signature for the HCC tumors, and a total of 23,233 genes and ESTs are included in the negative Gene Signature of the HCC samples. This negative Gene Signature includes all the genes that have been completely turned off during tumorigenesis, as well as those genes that are not usually expressed in liver tissue. These results include a number of genes and ESTs that are not
15 regularly expressed in liver tissues, but through the process of tumor production, their expression patterns have been dramatically altered from no detectable level of expression to some significant level of expression in comparison with the normal liver.

The colorectal metastases in the liver commonly express 5,102 genes and ESTs, and do not show expression of 30,455 additional genes and ESTs. As with the negative Gene
20 Signature for the HCC sample set, the genes included in this data set are generally not expressed in liver tissue, whether tumor or normal tissue. The 5,102 in the sample set of metastatic tumors also identify those genes with expression levels that have been changed from off to on as a result of tumor formation.

Example 5: Analysis of Gene Expression Profiles

A differential comparison of the genes and ESTs expressed in the normals and the two different types of liver tumors identifies a subset of the genes included in the positive Gene Signatures that are uniquely expressed in each sample set. This Gene Signature
Differential highlights genes whose expression profiles have most dramatically changed in
30 the transformation from normal to diseased liver cells. The parameters for these analyses were set to accommodate variation in expression of one of eight normal samples and one of the six HCC samples or one of the 5 metastatic tumor samples, such that the genes

categorized as unique to normal were called present by the software in seven of eight (87%) normal liver samples and were also called absent in five of six HCC (83%) or four of five (80%) metastatic liver tumor. Conversely, the genes categorized as unique to each set of tumors as compared to the normal livers were called present in five of six HCC (83%) or
5 four of five (80%) metastatic tumor samples and absent in seven of eight normal livers (87%).

The Gene Signature Differential comparing the normal livers to those with metastatic tumors identified a total of 903 sequences expressed only in normal liver tissue. The number of genes or ESTs that meet the median average difference minimum of 150 is
10 449, of which 289 are genes and the number of ESTs is 160. The remaining ESTs and genes may be indistinguishable from the background noise of the hybridization. The same comparison of normals versus metastatic tumors demonstrates that in the metastatic tumor samples there are 296 uniquely expressed sequences. Those that meet the median average difference minimum requirement are 83 genes and 72 ESTs. Those genes and ESTs
15 expressed in metastatic and not in normal liver tissue are shown in Table 9A and those present in normal liver tissue and not metastatic tissue Table 9B. Numerous genes with differing expression levels in metastatic liver tumor tissue compared to normal tissue were identified. The fifteen genes whose expression level was most different in metastatic as compared to normal tissue are shown in Table 4. Those with the most increased expression
20 are in Table 4A and those with the most decreased expression are in Table 4B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05 . Only the characterized genes
25 have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) in Table 4 denotes those genes that were also identified in the Gene Signature differential between metastatic liver carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 6. Table 6A contains those genes and ESTs whose expression level increased in metastatic tissue
30 relative to normal tissue and Table 6B contains those genes and ESTs whose expression level decreased.

The Gene Signature Differential between the normal liver samples and the HCC

samples identifies a total of 47 unique expressers in the normals, 23 with an median average difference of 150 ,13 of which are named gene and 10 of which are ESTs. When comparing the expression of the HCC samples with the normal livers, there are 243 genes and ESTs only expressed in the HCC samples.

5 Those genes and ESTs expressed in HCC and not in normal liver tissue are shown in Table 8A and those present in normal liver tissue and not HCC tissue in Table 8B. Numerous genes with differing expression levels in HCC compared to normal tissue were identified. The fifteen genes whose expression level was most different in HCC as compared to normal tissue are shown in Table 3. Those with the most increased expression
10 are in Table 3A and those with the most decreased expression are in Table 3B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05. Only the characterized genes
15 have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) denotes those genes that were also identified in the Gene Signature differential between hepatocellular carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 7. Table 7A contains those genes and ESTs whose expression level increased in hepatocellular carcinoma tissue
20 relative to normal tissue and Table 7B contains those genes and ESTs whose expression level decreased.

 Analysis of sample set identified 24 ESTs and 42 genes that are expressed in both metastatic liver tumors and hepatocellular carcinomas, but not in normal liver tissues. The fifteen genes with the most increase in expression level in both types of cancer are shown in
25 Table 5. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. The mean expression value for HCC and metastatic carcinomas was greater than 250, and included only those genes that showed a fold change greater than 3 with significant p values for both sets of tumors. No detectable level of expression was found in the normal liver tissues for these genes. Only the
30 characterized genes have been listed; the ESTs with similar fold changes that are unique to the tumors are not presented here.

Differential gene expression patterns between normal liver samples and

hepatocellular carcinomas and between normal livers and metastatic liver tumors were examined. Genes uniquely expressed by each of the groups individually were identified, as well as those genes that are commonly expressed among liver tumors, whether primary hepatocellular carcinomas or metastatic liver tumors.

5

Example 6: Association of Liver Cancer with Specific Gene Expression

The present inventors have closely examined a number of the tumor-expressing genes to determine if their expression patterns correlate with previous reports published in the literature, and to define a logical relationship between the gene and
10 hepatocarcinogenesis. A number of genes that have previously been associated with either liver cancer or other types of cancers were identified, as well as numerous genes that have not been linked to cancers in any previous studies.

842 genes and ESTs that are up-regulated in hepatocellular carcinomas were identified when compared with normal liver tissue. One such gene is PTTG1, pituitary
15 tumor-transforming gene 1, or securin, an oncogene that inhibits sister chromatid separation during anaphase. Normal tissues show little or no PTTG1 expression, but high levels of expression have been associated with various tumors, including liver tumors, and carcinoma cell lines. Overexpression in NIH3T3 cells resulted in transformation, and these cells caused the formation of tumors when injected into mice. The mechanism by which this
20 tumorigenic activity takes place is postulated to be through the missegregation of sister chromatids, resulting in aneuploidy and, therefore, genetic instability. Our data further support this overexpression of PTTG1 in hepatocellular carcinoma, with a fold change of 10.7 ($P=0.00052$), and no detectable level of expression in normal tissues, as identified by the differential comparison of the consensus patterns of gene expression of these two sample
25 sets.

Galectin 3, LGALS3, one of a family of beta-galactoside-binding animal lectins, is significantly overexpressed both in primary hepatocellular carcinoma and metastatic liver carcinomas with fold changes of 6.8 ($P=0.00103$) and 27.1 ($P=0.00001$), respectively. Expression of LGALS3 has been associated with tumor growth, progression, and metastasis,
30 as well as cell-cell and cell-matrix interactions and inflammatory processes. Although expression studies by Hsu *et al.* revealed no detectable level of galectin-3 in normal liver cells, samples from patients with hepatocellular carcinoma revealed considerable levels of

LGALS3 expression. The abnormal expression of this lectin may be an early event in the process of transformation of normal cells to tumor cells, or it may impart an increased capacity for these tumor cells to survive and proliferate. Consistent with the reports by Iurisci *et al* and Nakamura *et al*, an increased expression level was found in both types of tumor, but higher concentrations of galectin-3 were observed in liver metastases from colorectal tumors than in the primary HCC tumors.

Another gene that is overexpressed in both hepatocellular carcinoma and metastatic colorectal adenocarcinomas with fold changes of 12.2 ($P=0.00169$) and 58.0 ($P=0.00063$), respectively, is solute carrier family 2, member 3, or glucose transporter 3 (GLUT3). It is one of a family of transmembrane proteins that function as facilitative glucose transporters, which has a unique specificity for brain and neuronal tissues. Glucose uptake and metabolism are known to be increased in carcinoma cells compared to normal cells. Glucose transporter expression may be elevated in response to the increase in glucose utilization seen in actively proliferating cells, like those of tumors. Conversely, the high levels of glucose transporter expression may be responsible for the enhanced influx of glucose into the tumor cells. Various reports have indicated increased expression of one or more of the family of glucose transporters in malignancies, including those of the brain, esophagus, colon, pancreas, liver, breast, lung, bladder, ovary, testis, skin, head and neck, kidney, and gastric tumors. Kurata *et al.* (Jpn J Cancer Res 1999 Nov;90(11):1238-43) specifically report that metastatic liver carcinomas have even higher levels of GLUT3 expression than primary tumors. Consistent with previous studies, the current data confirm the significant overexpression of GLUT3 both in primary liver cancer, hepatocellular carcinoma, and in tumors that have metastasized from the colon and rectum.

One of the significantly underexpressed genes identified by comparing the expression profiles of hepatocellular carcinomas and metastatic liver tumors with that of normal liver tissue is metallothionein 1L. The expression level in HCC is 26.9 fold lower than that of normal ($P=0.00999$), and in metastatic colorectal adenocarcinomas it is down-regulated 66.5 fold ($P=0.00415$). Metallothioneins are heavy metal binding proteins that are involved in detoxification of metals, zinc and copper metabolism cellular adaptation mechanisms, and may be involved in regulating apoptosis. Colorectal adenocarcinoma that has metastasized to the liver has been specifically reported to express less metallothionein than normal liver tissue. Comparison of the consensus patterns of gene expression between

metastatic liver samples and normal liver samples show no significant level of MT1L expression in the tumors. Furthermore, additional work has determined that human hepatocellular carcinomas contain much lower levels of metallothioneins than normal liver tissue, and that this decrease correlates with the degree of differentiation and concentrations of copper and zinc in the cells. By comparing the expression profiles of hepatocellular carcinoma and normal liver tissue, this significant reduction in MT1L expression in HCC was confirmed.

A number of enzymes belonging to the family of cytochrome P450s are drastically underexpressed in the two sets of liver tumors in comparison with the normal liver tissue. For example, expression of CYP2A6 is decreased in HCC with a fold change of 14.2 ($P=0.0307$), and in metastatic tumors with a fold change of 69.9 ($P=0$). CYP8B1 is down-regulated 19.3 fold ($P=0.00807$) in HCC and 65.1 fold ($P=0.0039$) in liver metastases. In addition to these commonly down-regulated cytochrome P450s, in HCC samples CYP2B is underexpressed 17.9 fold ($P=0.01469$), and in the metastatic liver tumors CYP2C9 and CYP2A7 are underexpressed 84.7 fold ($P=0.00327$) and 72.0 fold ($P=0$), respectively. Several of these genes are also identified by the differential comparison between expression profiles of tumor and normal, confirming the significant decrease in expression in tumor tissues. Many of these P450 enzymes are critical players in the metabolism of carcinogens, drugs, and other chemical compounds, that are expressed in normal liver.

In addition to genes that are underexpressed in metastatic adenocarcinomas in the liver, more than 1000 genes and ESTs that are overexpressed specifically in these tumors were identified. Two of the most highly up-regulated are claudin 4, also known as clostridium perfringens enterotoxin receptor 1 (fold change 84.4, $P=0$) and occludin (fold change 43.1, $P=0$). Both of these genes are tight junction proteins, responsible for the formation and maintenance of continuous seals around epithelial cells to form a physical barrier that blocks the free passage of water and solutes through the paracellular space. More specifically, claudin-4 is one member of a family of transmembrane proteins that comprise tight junction strands, and occludin is a cell adhesion molecule (Morita *et al.*, (1999) Proc. Natl. Acad. Sci. U.S.A. 96: 511-516). Claudins likely function as paracellular channels, regulating the flow of ions and solutes into and out of the paracellular space (Simon *et al.*, (1999) Science 235: 103-106; Wong & Goodenough (1999) Science 285: 62; Anderson & Van Itallie (1999) Curr. Biol. 9: R922-924). Tight junction proteins also

contribute to the regulation of the cellular processes of cell growth and differentiation (Matter & Balda (1999) *Int. Rev. Cytol.* 186: 117-146). Permeability of tight junctions has been associated with tumor formation, where a breakdown in the barrier function of tight junctions allows an increase in the cellular permeability. This breakdown then opens the tight junction barrier, permitting invasion by tumor cells (Zak *et al.*, (2000) *Pflugers Arch.* 440: 179-183; Mullin (1997) *J. Exp. Zool.* 279: 484-489). It has been reported that tight junctions of colon tumors leak more than do the tight junctions of normal colon (Soler *et al.*, (1999) *Carcinogenesis* 20: 1425-1431). A complete loss of tight junction function and a loss of cell-cell contact growth control was seen in cells that had been transfected with oncogenic Raf-1, and expression levels of occludin and another claudin are lower in these cells (Li & Mrsny (2000) *J. Cell Biol.* 148: 791-800). Occludin expression has been up-regulated *in vitro* by the addition of various fatty acids that have anti-cancer effects, decreasing the paracellular permeability (Jiang *et al.*, (1998) *Biochem. Biophys. Res. Commun.* 244: 414-420). The extreme down-regulation of occludin and claudin-4 in metastatic liver tumors is strongly supported by the reports of tight junction breakdown in tumor tissues.

The present study identified 93 significantly up-regulated genes in both primary HCC and metastatic liver tumors that were not found to have any detectable level of expression in the normal samples. Serine protease inhibitor, Kazal type I (SPINK1), also called pancreatic secretory trypsin inhibitor (PSTI) or tumor-associated trypsin inhibitor (TATI), is one such gene. It is highly expressed in the cells of normal pancreas and in the mucosa of the gastrointestinal tract where it offers protection from proteolytic breakdown. A marked increase in expression is seen in various pancreatic diseases and in tumors of different tissues, including gastric carcinomas, colorectal cancers, and other neoplastic tissues. This increase is presumably due to the elevated expression of trypsin in the tumors, and not related to amplification or rearrangements within the gene. SPINK1 is also considered a valuable marker for a number of solid tumors. A drastic elevation of SPINK1 in the blood of patients with hepatocellular carcinoma has been seen (see Ohmachi *et al.*). Furthermore, it has been suggested that the level of expression correlates with the extent of tumor, such that this heightened expression level could be indicative of HCC under certain conditions. In keeping with this report of overexpression in these tumors, the present expression data show the levels of expression of this gene in HCC samples to be 28.9 times

higher than normal ($P=0.00003$), and in metastatic liver tumors the expression level is 9.8 times higher than normal ($P=0.03697$).

Midkine is one of a family of heparin-binding growth factors, inducible by retinoic acid, and is actively involved in cell-cell interactions and angiogenesis. The expression
5 pattern of midkine is highly restricted in normal adult tissues, and no expression has been reported in normal adult liver, although its expression is required during embryogenesis for normal development. However, it is expressed in moderate to high levels in many tumors, including Wilm's tumors of the kidney, stomach, colon, pancreas, lung, esophagus, breast, and liver tumors. The present data confirm these reports, showing a significant
10 overexpression of midkine in hepatocellular carcinoma samples (fold change 9.9, $P=0.02104$) and in liver metastases (fold change 10.4, $P=0.01818$), but no noticeable expression in normal liver.

Stathmin, leukemia-associated phosphoprotein 18, is a phosphoprotein whose expression pattern and phosphorylation status are controlled by extracellular signals
15 responsible for the regulation of the processes of cell proliferation and differentiation. It is also involved in the regulation of cell division via the destabilization of microtubules. When comparing expression levels between non-malignant tissues and malignant tissues, the tumors generally show a significant up-regulation of this phosphoprotein, specifically lymphomas, leukemias, breast and prostate tumors. One reason proposed for this elevated
20 expression in cancer cells is the dissimilarity in the rates of cell proliferation and states of differentiation between normal and tumor cells. In both HCC samples and metastatic adenocarcinomas, significant up-regulation of stathmin, 9.4 fold in HCC ($P=0.00015$) and 4.8 fold in metastatic tumors ($P=0.00514$) was seen.

Both the genes and ESTs described here will provide valuable information for the
25 identification of new drug targets against liver carcinomas, and that information may be extended for use in the study of carcinogenesis in other tissues.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following
30 claims. All cited patents, applications and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1. Clinical Information for Hepatocellular Carcinoma, Metastatic Liver Tumor, and Normal Liver Samples Included in this Study

| Sample | Pathology | Primary Tumor | Age | Gender | Race | TNM Classification | Histopathologic Grade | Clinical Stage |
|--------|---------------------------|---------------|-----|--------|-----------|--------------------|-----------------------|------------------|
| HCC1 | Hepatocellular Carcinoma | Liver | 64 | Male | Caucasian | T3,Nx,Mx | G2 | stage III |
| HCC2 | Hepatocellular Carcinoma | Liver | 27 | Female | Caucasian | T3,N0,Mx | G1 | stage III |
| HCC3 | Hepatocellular Carcinoma | Liver | 78 | Female | Caucasian | T4,Nx,Mx | G2 | stage III |
| HCC4 | Hepatocellular Carcinoma | Liver | 43 | Male | Asian | T4,N1,Mx | G2 | stage IV |
| HCC5 | Hepatocellular Carcinoma | Liver | 51 | Male | Caucasian | T4,N0,Mx | G2 | stage IV |
| HCC6 | Hepatocellular Carcinoma | Liver | 57 | Male | Caucasian | unavailable | G2 | stage III |
| M1 | Metastatic Adenocarcinoma | Rectum | 61 | Female | Caucasian | Tx,Nx,M1 | G3 | stage IV; Duke D |
| M2 | Metastatic Adenocarcinoma | Colon | 54 | Male | Caucasian | unavailable | G2 | stage IV; Duke D |
| M3 | Metastatic Adenocarcinoma | Rectum | 50 | Female | Caucasian | Tx,Nx,M1 | G2 | stage IV; Duke D |
| M4 | Metastatic Adenocarcinoma | Colon | 60 | Male | Caucasian | Tx,Nx,M1 | G2 | stage IV; Duke D |
| M5 | Metastatic Adenocarcinoma | Colon | 57 | Male | Caucasian | Tx,Nx,M1 | G2 | stage IV; Duke D |
| N1 | Normal liver | | 54 | Female | Caucasian | | | |
| N2 | Normal liver | | 55 | Female | Caucasian | | | |
| N3 | Normal liver | | 58 | Male | Caucasian | | | |
| N4 | Normal liver | | 44 | Female | Caucasian | | | |
| N5 | Normal liver | | 40 | Female | Caucasian | | | |
| N6 | Normal liver | | 72 | Female | Caucasian | | | |
| N7 | Normal liver | | 48 | Female | Unknown | | | |
| N8 | Normal liver | | 55 | Female | Caucasian | | | |

Table 2. Summary of Genes and ESTs Expressed in HCC, Metastatic Liver Tumors, and Normal Livers

| | Fingerprint of Gene Expression | | |
|--|--|-----------------------|---------------|
| | Hepatocellular Carcinoma | Colorectal Metastases | Normal Livers |
| I. Fingerprint of Gene Expression | Genes and ESTs commonly expressed in sample set | 8479 | 6213 |
| | Genes and ESTs commonly unexpressed in sample set | 23233 | 24900 |
| II. Fold Change | Genes and ESTs overexpressed in tumors (fold change >3 and $p < 0.05$) | 1044 | |
| | Number of Genes | 603 | |
| | Number of ESTs | 441 | |
| | Genes and ESTs underexpressed in tumors (fold change >3 and $p < 0.05$) | 1867 | |
| | Number of Genes | 1016 | |
| | Number of ESTs | 851 | |
| III. Differential Comparison between Normal and Tumor Expression | Genes and ESTs turned ON in tumors | 296 | |
| | Genes and ESTs with expression level above threshold in tumor | 155 | |
| | Number of Genes | 83 | |
| | Number of ESTs | 72 | |
| | Genes and ESTs turned OFF in tumors | 903 | |
| | Genes and ESTs with expression level above threshold in normal | 449 | |
| | Number of Genes | 289 | |
| | Number of ESTs | 160 | |

Table 3A. Top fifteen genes overexpressed in hepatocellular carcinoma.

| Genbank | Seq ID | Unigene Cluster | Gene Name | Fold Change | Pvalue |
|----------|--------|-----------------|---|-------------|---------|
| AA055896 | 135 | Hs.146428 | collagen, type V, alpha 1 | 10.9* | 0.00907 |
| AA156187 | 339 | Hs.81634 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | 9.4 | 0.02007 |
| AA428172 | 986 | Hs.8546 | Notch (Drosophila) homolog 3 | 9.6* | 0.00195 |
| AA430032 | 1009 | Hs.252587 | pituitary tumor-transforming 1 | 10.7* | 0.00052 |
| AA505133 | 1417 | Hs.279905 | solute carrier family 2 (facilitated glucose transporter), member 3 | 12.2 | 0.00169 |
| AA610116 | 1499 | Hs.102737 | tetraspan NET-6 protein | 16.4 | 0.00249 |
| AA620881 | 1510 | Hs.21858 | trinucleotide repeat containing 3 | 9.5 | 0.00062 |
| D31094 | 1639 | Hs.109798 | G8 protein | 9.4 | 0.0048 |
| D51276 | 1678 | Hs.81915 | leukemia-associated phosphoprotein p18 (stathmin) | 9.4 | 0.00015 |
| J03464 | 2094 | Hs.179573 | collagen, type I, alpha 2 | 10.4 | 0.00979 |
| M94250 | 2426 | Hs.82045 | midkine (neurite growth-promoting factor 2) | 9.9* | 0.02104 |
| N33920 | 2493 | Hs.44532 | diubiquitin | 50.3 | 0 |
| W45320 | 3523 | Hs.228059 | KRAB-associated protein 1 | 10.1* | 0.00002 |
| Y00705 | 3850 | Hs.181286 | serine protease inhibitor, Kazal type 1 | 28.9 | 0.00003 |
| Z37987 | 3882 | Hs.119651 | glypican 3 | 10.7 | 0.02304 |

Table 3B. Top fifteen genes underexpressed in hepatocellular carcinoma.

| Genbank | Seq ID | Unigene Cluster | Gene Name | Fold Change | Pvalue |
|----------|--------|-----------------|---|-------------|---------|
| AA007395 | 17 | Hs.1219 | alcohol dehydrogenase 4 (class II), pi polypeptide | 37.8 | 0.00939 |
| AA010605 | 26 | Hs.2899 | 4-hydroxyphenylpyruvate dioxygenase | 25.5 | 0.00855 |
| AA448002 | 1113 | Hs.23759 | putative type II membrane protein | 14.1* | 0 |
| H58692 | 1960 | Hs.9520 | formyltetrahydrofolate dehydrogenase | 20.2 | 0.00485 |
| H80901 | 2005 | Hs.272576 | ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) | 18.6 | 0 |
| H81070 | 2006 | Hs.8765 | RNA helicase-related protein | 39.6 | 0.00002 |
| K03192 | 2127 | Hs.183584 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 14.2 | 0.0307 |
| M29873 | 2318 | Hs.1360 | cytochrome P450, subfamily IIB (phenobarbital-inducible) | 17.9 | 0.01469 |
| N80129 | 2703 | Hs.94360 | metallothionein 1L | 26.9 | 0.00999 |
| R97419 | 3004 | Hs.35718 | cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), polypeptide 1 | 19.3 | 0.00807 |
| T48075 | 3130 | Hs.251577 | hemoglobin, alpha 1 | 35.8 | 0.00471 |
| T67931 | 3184 | Hs.7645 | fibrinogen, B beta polypeptide | 17.3 | 0.00128 |
| T95813 | 3262 | Hs.137476 | KIAA1051 protein | 20.4 | 0.01361 |
| U56814 | 3393 | Hs.88646 | deoxyribonuclease I-like 3 | 17.7 | 0.00007 |
| W88946 | 3639 | Hs.18508 | putative glycine-N-acyltransferase | 25.3 | 0.00221 |

Table 4A. Top fifteen genes overexpressed in metastatic carcinomas of the liver.

| Genbank | Seq ID | Unigene Cluster | Gene Name | Fold Change | Pvalue |
|---------------|--------|-----------------|---|-------------|---------|
| AA100719 | 212 | Hs.73848 | Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | 50.9* | 0.00081 |
| AA156243 | 340 | Hs.154737 | Serine protease, umbilical endothelium | 41.4* | 0.00139 |
| AA335191 | 741 | Hs.173724 | Creatine kinase, brain | 47.4* | 0.00419 |
| AA421562 | 934 | Hs.91011 | Anterior gradient 2 (Xenopus leavis) homolog | 56.3* | 0.0041 |
| AA427468 | 973 | Hs.5372 | Claudin 4 | 84.4* | 0 |
| AA429009 | 994 | Hs.233950 | Serine protease inhibitor, Kunitz type 1 | 30.0* | 0.00001 |
| AA610116 | 1499 | Hs.102737 | Tetraspan NET-6 protein | 33.7 | 0.00171 |
| H58873 | 1961 | Hs.169902 | Solute carrier family 2 (facilitated glucose transporter), member 3 | 58.0* | 0.00063 |
| H94471 | 2042 | Hs.171952 | Occludin | 43.1 | 0 |
| H95233 | 2048 | Hs.31439 | Serine protease inhibitor, Kunitz type, 2 | 47.1 | 0 |
| HG2788-HT2896 | | Hs.27258 | Calycalin binding protein | 33.2 | 0 |
| M29540 | 2317 | Hs.220529 | Carcinoembryonic antigen-related cell adhesion molecule 5 | 36.6* | 0.0116 |
| M35252 | 2343 | Hs.84072 | Transmembrane 4 superfamily member 3 | 39.1 | 0 |
| N92934 | 2725 | Hs.17409 | Cysteine-rich protein 1 (intestinal) | 35.5 | 0.002 |
| X93036 | 3830 | Hs.92323 | FXD domain-containing ion transport regulator 3 | 42.4* | 0.00167 |

Table 4B. Top fifteen genes underexpressed in metastatic carcinoma of the liver.

| Genbank | Seq ID | Unigene Cluster | Gene Name | Fold Change | Pvalue |
|----------|--------|-----------------|---|-------------|---------|
| AA256367 | 579 | Hs.107966 | Paraoxonase 3 | 70.3 | 0.00192 |
| H58692 | 1960 | Hs.9520 | Formyltetrahydrofolate dehydrogenase | 81.4* | 0 |
| K03192 | 2127 | Hs.183584 | Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 69.9* | 0 |
| L16883 | 2166 | Hs.167529 | Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 | 84.7 | 0.00327 |
| M15656 | 2268 | Hs.234234 | Aldolase B, fructose-bisphosphate | 96.7* | 0 |
| M16594 | 2272 | Hs.89552 | glutathione S-transferase A2 | 73.2* | 0 |
| M81349 | 2405 | Hs.1955 | Serum amyloid A4, constitutive | 76.2 | 0.00015 |
| N53031 | 2556 | Hs.89691 | UDP glycosyltransferase 2 family, polypeptide B4 | 97.6 | 0.00022 |
| N54417 | 2567 | Hs.90765 | Fibrinogen, A alpha polypeptide | 99.3 | 0.00001 |
| R43174 | 2848 | Hs.1898 | Paraoxonase 1 | 74.0* | 0.00038 |
| R49459 | 2882 | Hs.63758 | Transferrin receptor 2 | 85.6 | 0.00048 |
| T48039 | 3129 | Hs.2351 | Protein C (inactivator of coagulation factors Va and VIIIa) | 84.4 | 0.00112 |
| T59148 | 3158 | Hs.50966 | Carbamoyl-phosphate synthetase 1, mitochondrial | 88.9* | 0 |
| U22029 | 3327 | Hs.250615 | Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 | 72.0* | 0 |
| X55283 | 3734 | Hs.1259 | Asialoglycoprotein receptor 2 | 85 | 0.00084 |

Table 5. Top fifteen genes expressed in both hepatocellular carcinomas and metastatic liver tumors ad not in normal livers.

| Genbank | Seq ID | Unigene Cluster | Gene Name | HCC Fold Change | HCC p value | Metastatics Fold Change | Metastatic p value |
|----------|--------|-----------------|---|--------------------|----------------|-------------------------------|-----------------------|
| AA055896 | 135 | Hs.146428 | collagen, type V, alpha 1 | 10.9 | 0.00907 | 18.2 | 0.00146 |
| AA204927 | 425 | Hs.77899 | tropomyosin 1 (alpha) | 6.1 | 0.0014 | 7.1 | 0.00074 |
| AA335191 | 741 | Hs.173724 | creatine kinase, brain | 6.5 | 0.01462 | 47.4 | 0.00419 |
| AA429472 | 997 | Hs.236522 | DKFZP434P106 protein | 8.8 | 0.00063 | 8.3 | 0.00208 |
| AA434418 | 1036 | Hs.72172 | KIAA1115 protein | 6.8 | 0.0032 | 5.1 | 0.00498 |
| AA452724 | 1149 | Hs.166468 | programmed cell death 5 | 7.7 | 0.00085 | 7.2 | 0.00908 |
| AA610116 | 1499 | Hs.102737 | tetraspan NET-6 protein | 16.4 | 0.00249 | 33.7 | 0.00171 |
| AA620881 | 1510 | Hs.21858 | trinucleotide repeat containing 3 | 9.5 | 0.00062 | 8.7 | 0.00735 |
| D26129 | 1635 | Hs.78224 | ribonuclease, RNase A family, 1 (pancreatic) | 6.9 | 0.00008 | 5.7 | 0.03827 |
| D31094 | 1639 | Hs.109798 | G8 protein | 9.4 | 0.0048 | 4.4 | 0.04845 |
| D51276 | 1678 | Hs.81915 | leukemia-associated phosphoprotein p18 (stathmin) | 9.4 | 0.00015 | 4.8 | 0.00514 |
| H27188 | 1908 | Hs.9930 | collagen-binding protein 2 (collagen 2) | 5.8 | 0.01826 | 4.2 | 0.02073 |
| J03464 | 2094 | Hs.179573 | collagen, type I, alpha 2 | 10.4 | 0.00979 | 9.8 | 0.00028 |
| M94250 | 2426 | Hs.82045 | midkine (neurite growth-promoting factor 2) | 9.9 | 0.02104 | 10.4 | 0.01818 |
| Y00705 | 3850 | Hs.181286 | serine protease inhibitor, Kazal type 1 | 28.9 | 0.00003 | 9.8 | 0.03697 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA001409_i_at | AA001409 | 1 | EST | 3.35 | up | 0.04092 |
| rc_AA001504_f_at | AA001504 | 2 | EST | 9.98 | up | 0.00336 |
| rc_AA007158_f_at | AA007158 | 15 | EST | 3.05 | up | 0.01964 |
| rc_AA007160_at | AA007160 | 16 | EST | 6 | up | 0.01035 |
| rc_AA010065_s_at | AA010065 | 22 | CDC28 protein kinase 2 | 6.25 | up | 0.02752 |
| rc_AA011134_at | AA011134 | 29 | EST | 28.79 | up | 0.00602 |
| rc_AA011383_at | AA011383 | 31 | EST | 5.17 | up | 0.00008 |
| rc_AA025166_s_at | AA025166 | 50 | fusion, derived from t(12;16) malignant liposarcoma | 3.71 | up | 0.0052 |
| rc_AA025277_at | AA025277 | 51 | EST | 4.56 | up | 0.03136 |
| rc_AA026030_at | AA026030 | 53 | EST | 11.01 | up | 0.01649 |
| rc_AA026092_at | AA026092 | 54 | EST | 3.83 | up | 0.04596 |
| rc_AA026150_at | AA026150 | 55 | EST | 5.14 | up | 0.01072 |
| rc_AA026356_at | AA026356 | 57 | EST | 4.1 | up | 0.00133 |
| rc_AA027946_at | AA027946 | 60 | EST | 3.22 | up | 0.00098 |
| rc_AA028103_at | AA028103 | 61 | EST | 3.52 | up | 0.01142 |
| rc_AA028132_s_at | AA028132 | 62 | EST | 6.25 | up | 0.00646 |
| rc_AA029215_at | AA029215 | 64 | adaptor-related protein complex 2, beta 1 subunit | 3.65 | up | 0.00037 |
| rc_AA029356_at | AA029356 | 66 | EST | 3.68 | up | 0.01545 |
| rc_AA033790_f_at | AA033790 | 74 | apolipoprotein D | 4.21 | up | 0.03247 |
| rc_AA034378_f_at | AA034378 | 77 | endogenous retroviral protease | 4.01 | up | 0.00974 |
| rc_AA034499_s_at | AA034499 | 78 | zinc finger protein 198 | 3.7 | up | 0.02143 |
| rc_AA040465_at | AA040465 | 95 | EST | 3.25 | up | 0.00146 |
| rc_AA043959_at | AA043959 | 101 | tropomyosin 4 | 8.54 | up | 0.00222 |
| rc_AA053007_f_at | AA053007 | 123 | putative receptor protein | 6.76 | up | 0.00061 |
| rc_AA053033_at | AA053033 | 124 | EST | 7.83 | up | 0.00379 |
| rc_AA053102_s_at | AA053102 | 125 | cadherin 17, LI cadherin (liver-intestine) | 26.63 | up | 0.01745 |
| rc_AA053248_i_at | AA053248 | 126 | EST | 7.01 | up | 0.00003 |
| rc_AA053248_f_at | AA053248 | 126 | EST | 6.16 | up | 0.00191 |
| rc_AA053424_at | AA053424 | 127 | EST | 8.76 | up | 0.01775 |
| rc_AA053660_at | AA053660 | 128 | EST | 15.98 | up | 0.00003 |
| rc_AA055805_s_at | AA055805 | 132 | EST | 42.83 | up | 0.00142 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA055811_s_at | AA055811 | 133 | glycoprotein A33 (transmembrane) | 6.86 | up | 0.02152 |
| rc_AA055896_at | AA055896 | 135 | collagen, type V, alpha 1 | 18.16 | up | 0.00146 |
| AA056361_at | AA056361 | 140 | integral membrane protein 2C | 3.53 | up | 0.02983 |
| rc_AA062721_at | AA062721 | 146 | nuclear factor (erythroid-derived 2)-like 1 | 6.2 | up | 0.00024 |
| rc_AA070206_at | AA070206 | 155 | EST | 4.26 | up | 0.00018 |
| rc_AA070827_at | AA070827 | 157 | EST | 4.41 | up | 0.01902 |
| rc_AA074514_at | AA074514 | 160 | EST | 7.69 | up | 0 |
| rc_AA075299_at | AA075299 | 164 | EST | 34.27 | up | 0.00002 |
| rc_AA075580_f_at | AA075580 | 165 | EST | 4.98 | up | 0.02083 |
| rc_AA075722_at | AA075722 | 166 | nuclear transport factor 2 (placental protein 15) | 4.14 | up | 0.00374 |
| AA078862_s_at | AA078862 | 173 | EST | 6.52 | up | 0.00025 |
| rc_AA084901_at | AA084901 | 181 | ribosomal protein S6 kinase, 70kD, polypeptide 2 | 9.13 | up | 0.00003 |
| rc_AA084921_f_at | AA084921 | 182 | ribosomal protein S10 | 3.29 | up | 0.04872 |
| | | | kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody 1A4)) | | | |
| rc_AA086232_f_at | AA086232 | 186 | | 5.14 | up | 0.01916 |
| AA093497_s_at | AA093497 | 199 | DEK oncogene (DNA binding) | 5.6 | up | 0.02551 |
| AA094517_at | AA094517 | 202 | EST | 3.52 | up | 0.04805 |
| AA094752_at | AA094752 | 203 | hypothetical 43.2 Kd protein | 4.47 | up | 0.00243 |
| rc_AA099404_s_at | AA099404 | 208 | EST | 29.07 | up | 0 |
| | | | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | | | |
| rc_AA100719_s_at | AA100719 | 212 | | 50.88 | up | 0.00081 |
| rc_AA101551_at | AA101551 | 216 | EST | 24.78 | up | 0 |
| rc_AA113149_s_at | AA113149 | 226 | tumor suppressing subtransferable candidate 3 | 10.58 | up | 0.00543 |
| | | | transmembrane 4 superfamily member (tetraspan NET-7) | | | |
| rc_AA113303_at | AA113303 | 227 | | 3.73 | up | 0.00084 |
| rc_AA116036_at | AA116036 | 233 | chromosome 20 open reading frame 1 | 8.81 | up | 0.00133 |
| rc_AA121315_at | AA121315 | 237 | KIAA1077 protein | 4.86 | up | 0.02438 |
| rc_AA122386_at | AA122386 | 239 | collagen, type V, alpha 2 | 4.28 | up | 0.005 |
| rc_AA126044_at | AA126044 | 245 | EST | 11.23 | up | 0.00041 |
| rc_AA126429_at | AA126429 | 247 | peroxisomal farnesylated protein | 3.23 | up | 0.00478 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA126459_s_at | AA126459 | 248 | DKFZP566B023 protein | 3.69 | up | 0.00352 |
| rc_AA126719_at | AA126719 | 250 | EST | 5.31 | up | 0.00026 |
| AA127712_at | AA127712 | 255 | EST | 6.59 | up | 0.03706 |
| rc_AA127851_at | AA127851 | 257 | EST | 3.23 | up | 0.01943 |
| rc_AA128407_at | AA128407 | 259 | EST | 3.78 | up | 0.01081 |
| rc_AA128561_at | AA128561 | 261 | collagen, type XVII, alpha 1 | 6.09 | up | 0.0433 |
| rc_AA131084_at | AA131084 | 265 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 | 4.74 | up | 0.00427 |
| rc_AA131162_s_at | AA131162 | 266 | EST | 4.68 | up | 0.00042 |
| rc_AA131584_at | AA131584 | 268 | DKFZP564O0463 protein | 6.83 | up | 0.00025 |
| rc_AA131894_at | AA131894 | 269 | EST | 3.76 | up | 0.00384 |
| rc_AA131919_at | AA131919 | 270 | putative type II membrane protein | 15.36 | up | 0.00027 |
| rc_AA132032_s_at | AA132032 | 271 | trinucleotide repeat containing 1 | 4.19 | up | 0.00295 |
| rc_AA132554_at | AA132554 | 273 | EST | 4.96 | up | 0.02076 |
| rc_AA132983_at | AA132983 | 274 | DKFZP586G1517 protein | 3.31 | up | 0.01155 |
| rc_AA132986_at | AA132986 | 275 | EST | 9.72 | up | 0.00552 |
| rc_AA133590_at | AA133590 | 282 | EST | 3.23 | up | 0.03565 |
| rc_AA133936_at | AA133936 | 284 | EST | 9.19 | up | 0.00088 |
| rc_AA134052_s_at | AA134052 | 285 | Rab geranylgeranyltransferase, alpha subunit | 3.54 | up | 0.03062 |
| rc_AA134158_s_at | AA134158 | 287 | EST | 3.42 | up | 0.0277 |
| rc_AA134968_at | AA134968 | 289 | EST | 12.11 | up | 0.00079 |
| rc_AA134985_at | AA134985 | 290 | EST | 12.11 | up | 0.00318 |
| rc_AA135407_f_at | AA135407 | 292 | endogenous retroviral protease | 3.64 | up | 0.01086 |
| rc_AA135871_at | AA135871 | 294 | EST | 3.39 | up | 0.01544 |
| rc_AA135894_at | AA135894 | 295 | retinoic acid induced 3 | 14.27 | up | 0.00558 |
| rc_AA136547_at | AA136547 | 302 | EST | 3.51 | up | 0.00308 |
| rc_AA143493_at | AA143493 | 310 | pleckstrin 2 (mouse) homolog | 4.58 | up | 0.01037 |
| rc_AA143763_at | AA143763 | 311 | EST | 18.09 | up | 0.00347 |
| rc_AA146619_at | AA146619 | 312 | EST | 4.87 | up | 0.00863 |
| rc_AA147084_at | AA147084 | 314 | proliferation-associated 2G4, 38kD | 4.4 | up | 0.0045 |
| rc_AA147439_s_at | AA147439 | 315 | EST | 5.01 | up | 0.00336 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA148885_at | AA148885 | 320 | minichromosome maintenance deficient (S. cerevisiae) 4 | 6.39 | up | 0.0125 |
| rc_AA148977_at | AA148977 | 322 | EST | 3.64 | up | 0.02911 |
| rc_AA149889_at | AA149889 | 326 | neighbor of A-kinase anchoring protein 95 | 3.34 | up | 0.02054 |
| rc_AA150053_at | AA150053 | 327 | EST | 3.71 | up | 0.00102 |
| rc_AA151182_at | AA151182 | 332 | EST | 3.51 | up | 0.00043 |
| rc_AA151428_s_at | AA151428 | 335 | matrix metalloproteinase 23B | 7.15 | up | 0.00056 |
| rc_AA151778_at | AA151778 | 338 | claudin 7 | 5.77 | up | 0.00002 |
| rc_AA156187_at | AA156187 | 339 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | 23.24 | up | 0.00006 |
| rc_AA156243_at | AA156243 | 340 | serine protease, umbilical endothelium | 41.44 | up | 0.00139 |
| rc_AA156450_at | AA156450 | 342 | EST | 3.33 | up | 0.00587 |
| rc_AA157818_f_at | AA157818 | 349 | endogenous retroviral protease | 25.99 | up | 0.00153 |
| rc_AA158234_at | AA158234 | 351 | EST | 17.04 | up | 0.00711 |
| rc_AA158795_at | AA158795 | 352 | EST | 3.07 | up | 0.00057 |
| rc_AA159525_at | AA159525 | 354 | EST | 49.39 | up | 0.00062 |
| rc_AA161043_at | AA161043 | 356 | tetraspan 1 | 18.8 | up | 0.00015 |
| rc_AA161292_s_at | AA161292 | 357 | interferon, alpha-inducible protein 27 | 13.84 | up | 0.00004 |
| rc_AA164252_f_at | AA164252 | 358 | VEGF nerve growth factor inducible | 3.41 | up | 0.00154 |
| rc_AA169837_at | AA169837 | 364 | NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) | 3.17 | up | 0.03038 |
| rc_AA171760_at | AA171760 | 367 | (NADH-coenzyme Q reductase) | 17.86 | up | 0 |
| rc_AA171939_at | AA171939 | 368 | EST | 4.67 | up | 0.00104 |
| rc_AA172076_at | AA172076 | 369 | EST | 3.06 | up | 0.00326 |
| rc_AA173430_at | AA173430 | 371 | EST | 4.32 | up | 0.04362 |
| rc_AA179298_at | AA179298 | 378 | stomatatin-like protein 2 | 3.72 | up | 0.00299 |
| rc_AA179787_at | AA179787 | 380 | polyglutamine binding protein 1 | 6.44 | up | 0.00206 |
| rc_AA179845_at | AA179845 | 381 | EST | 5.77 | up | 0.01414 |
| rc_AA181600_at | AA181600 | 384 | EST | 5.38 | up | 0.03316 |
| rc_AA182001_i_at | AA182001 | 386 | EST | 3.56 | up | 0.00945 |
| rc_AA187938_at | AA187938 | 391 | EST | 3.86 | up | 0.00512 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA188378_i_at | AA188378 | 392 | EST | 9.56 | up | 0.00271 |
| rc_AA188378_f_at | AA188378 | 392 | EST | 5.54 | up | 0.01359 |
| rc_AA189015_at | AA189015 | 394 | EST | 5.27 | up | 0.00004 |
| rc_AA191708_at | AA191708 | 400 | EST | 3.87 | up | 0.01904 |
| rc_AA192755_at | AA192755 | 401 | EST | 3.13 | up | 0.00442 |
| rc_AA194237_at | AA194237 | 408 | EST | 3.13 | up | 0.00212 |
| rc_AA194724_at | AA194724 | 409 | endonuclease G | 3.09 | up | 0.04011 |
| rc_AA196790_at | AA196790 | 421 | EST | 7.64 | up | 0.00287 |
| rc_AA204927_at | AA204927 | 425 | tropomyosin 1 (alpha) | 7.09 | up | 0.00074 |
| rc_AA211483_at | AA211483 | 435 | EST | 44.07 | up | 0.00175 |
| rc_AA211851_f_at | AA211851 | 436 | EST | 3.66 | up | 0.00789 |
| rc_AA213696_at | AA213696 | 437 | poly(A)-binding protein, cytoplasmic 1 | 24.65 | up | 0.00001 |
| AA215299_s_at | AA215299 | 439 | U6 snRNA-associated Sm-like protein LSm7 | 15.84 | up | 0.00001 |
| rc_AA215468_s_at | AA215468 | 441 | ADP-ribosylation factor-related protein 1 | 3.9 | up | 0.04549 |
| rc_AA218663_at | AA218663 | 444 | acid-inducible phosphoprotein | 3.26 | up | 0.03537 |
| AA224502_at | AA224502 | 451 | EST | 4.12 | up | 0.00694 |
| rc_AA226932_at | AA226932 | 453 | DKFZP564F0923 protein | 6.84 | up | 0.00405 |
| rc_AA227560_at | AA227560 | 458 | EST | 12.81 | up | 0.01693 |
| rc_AA227926_at | AA227926 | 460 | EST | 6.81 | up | 0.01701 |
| rc_AA233886_s_at | AA233886 | 475 | D site of albumin promoter (albumin D-box) binding protein | 3.38 | up | 0.0218 |
| rc_AA233959_i_at | AA233959 | 477 | EST | 19.69 | up | 0.00101 |
| rc_AA234096_at | AA234096 | 479 | EST | 23.72 | up | 0.00018 |
| rc_AA234362_at | AA234362 | 481 | EST | 3.89 | up | 0.03524 |
| rc_AA235707_at | AA235707 | 500 | EST | 9.17 | up | 0.00005 |
| rc_AA236037_at | AA236037 | 506 | EST | 5.74 | up | 0.0091 |
| rc_AA236533_s_at | AA236533 | 514 | ecotropic viral integration site 1 | 4.01 | up | 0.02882 |
| rc_AA236714_f_at | AA236714 | 516 | nuclear mitotic apparatus protein 1 | 4.35 | up | 0.00083 |
| rc_AA237017_at | AA237017 | 521 | KIAA1068 protein | 3.52 | up | 0.00976 |
| rc_AA243133_at | AA243133 | 525 | serine/threonine kinase 15 | 7.73 | up | 0.04328 |
| rc_AA243173_at | AA243173 | 526 | EST | 8.75 | up | 0.00003 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| AA249819_s_at | AA249819 | 535 | EST | 5.09 | up | 0.00136 |
| rc_AA251230_at | AA251230 | 540 | EST | 4.75 | up | 0.00054 |
| rc_AA251299_s_at | AA251299 | 541 | KIAA0014 gene product | 16.86 | up | 0.00046 |
| rc_AA251909_at | AA251909 | 549 | EST | 3.35 | up | 0.03937 |
| rc_AA252994_at | AA252994 | 557 | apoptosis inhibitor 4 (survivin) | 3.55 | up | 0.00075 |
| rc_AA253011_f_at | AA253011 | 558 | KIAA0713 protein | 4.73 | up | 0.01944 |
| AA253330_s_at | AA253330 | 562 | adaptor-related protein complex 1, gamma 1 subunit | 3.87 | up | 0.00708 |
| rc_AA253473_at | AA253473 | 567 | EST | 15.23 | up | 0.00171 |
| rc_AA256273_at | AA256273 | 577 | EST | 4.13 | up | 0.03874 |
| rc_AA256642_at | AA256642 | 582 | EST | 11.17 | up | 0.00035 |
| rc_AA258482_s_at | AA258482 | 596 | zinc finger protein | 3.17 | up | 0.04606 |
| rc_AA261907_at | AA261907 | 603 | DKFZP566E144 protein | 4.54 | up | 0.02289 |
| rc_AA262477_at | AA262477 | 608 | ribonuclease H1, large subunit | 4.87 | up | 0.00005 |
| rc_AA262887_at | AA262887 | 610 | EST | 5.4 | up | 0.04719 |
| rc_AA262943_at | AA262943 | 611 | EST | 13.42 | up | 0.00234 |
| rc_AA262969_f_at | AA262969 | 613 | ferritin, heavy polypeptide 1 | 4.49 | up | 0.00013 |
| AA263044_s_at | AA263044 | 615 | H2A histone family, member Y | 4.13 | up | 0.00024 |
| rc_AA278817_at | AA278817 | 618 | EST | 4.22 | up | 0.00061 |
| rc_AA278838_s_at | AA278838 | 620 | EST | 3 | up | 0.02832 |
| rc_AA279177_at | AA279177 | 624 | lymphocyte antigen 75 | 6.05 | up | 0.01821 |
| rc_AA279840_at | AA279840 | 632 | titin-cap (telethonin) | 5.58 | up | 0.01253 |
| rc_AA280283_s_at | AA280283 | 637 | EST | 4.99 | up | 0.02644 |
| rc_AA280734_i_at | AA280734 | 639 | KIAA0618 gene product | 9.64 | up | 0.00003 |
| rc_AA280928_at | AA280928 | 642 | EST | 3.27 | up | 0.04625 |
| rc_AA282149_s_at | AA282149 | 654 | huntingtin interacting protein-1-related | 4.19 | up | 0.00091 |
| rc_AA282247_at | AA282247 | 657 | EST | 8 | up | 0.00014 |
| rc_AA283085_s_at | AA283085 | 667 | EST | 4.93 | up | 0.00382 |
| rc_AA284879_at | AA284879 | 679 | EST | 24.68 | up | 0.00001 |
| rc_AA284945_at | AA284945 | 680 | EST | 5.98 | up | 0.00026 |
| rc_AA287022_s_at | AA287022 | 685 | thymidine kinase 1, soluble | 4.51 | up | 0.02582 |
| rc_AA287347_at | AA287347 | 687 | EST | 5.47 | up | 0.00034 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA287393_at | AA287393 | 688 | EST | 5.68 | up | 0.00062 |
| rc_AA290674_s_at | AA290674 | 692 | eukaryotic translation initiation factor 4E binding protein 1 | 11.59 | up | 0.00036 |
| rc_AA291137_at | AA291137 | 694 | EST | 5.21 | up | 0.00685 |
| rc_AA291139_at | AA291139 | 695 | EST | 8.69 | up | 0.04573 |
| rc_AA291168_at | AA291168 | 696 | EST | 40.67 | up | 0.00065 |
| AA291456_s_at | AA291456 | 700 | EST | 3.96 | up | 0.03633 |
| rc_AA291659_at | AA291659 | 702 | EST | 3.83 | up | 0.01934 |
| rc_AA292379_at | AA292379 | 708 | EST | 6.04 | up | 0.00568 |
| rc_AA292659_at | AA292659 | 710 | EST | 3.48 | up | 0.00037 |
| rc_AA292765_at | AA292765 | 712 | ZW10 interactor | 7.14 | up | 0.02623 |
| rc_AA292788_s_at | AA292788 | 714 | EST | 7.69 | up | 0.00967 |
| rc_AA292931_at | AA292931 | 715 | EST | 3.97 | up | 0.00067 |
| rc_AA293719_at | AA293719 | 720 | EST | 4.69 | up | 0.02181 |
| AA295819_s_at | AA295819 | 722 | EST | 8 | up | 0.01793 |
| AA298786_at | AA298786 | 727 | EST | 4.65 | up | 0.02821 |
| AA306121_at | AA306121 | 729 | EST | 4.85 | up | 0.00381 |
| AA307748_s_at | AA307748 | 730 | EST | 3.7 | up | 0.00001 |
| AA320369_s_at | AA320369 | 735 | chromosome 19 open reading frame 3 | 4.33 | up | 0.00554 |
| AA328993_s_at | AA328993 | 738 | EST | 3.66 | up | 0.00146 |
| rc_AA331393_at | AA331393 | 739 | EST | 16.73 | up | 0.00848 |
| rc_AA335091_at | AA335091 | 740 | EST | 5.28 | up | 0.0009 |
| rc_AA335191_f_at | AA335191 | 741 | creatine kinase, brain | 47.35 | up | 0.00419 |
| rc_AA338729_at | AA338729 | 743 | EST | 3.33 | up | 0.00046 |
| rc_AA338889_f_at | AA338889 | 745 | actin related protein 2/3 complex, subunit 4 (20 kD) | 10.77 | up | 0.03782 |
| AA364267_at | AA364267 | 762 | EST | 5.01 | up | 0.00255 |
| rc_AA370163_at | AA370163 | 766 | EST | 3.34 | up | 0.00643 |
| rc_AA372018_at | AA372018 | 768 | EST | 14.3 | up | 0.00178 |
| AA372630_s_at | AA372630 | 769 | differentially expressed in hematopoietic lineages | 25.49 | up | 0.01743 |
| AA384184_s_at | AA384184 | 774 | DKFZP586B0519 protein | 3.38 | up | 0.01209 |
| rc_AA394121_at | AA394121 | 778 | laminin receptor 1 (67kD, ribosomal protein SA) | 23.78 | up | 0.00099 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA397906_at | AA397906 | 782 | DKFZP434I216 protein | 3.2 | up | 0.00138 |
| rc_AA397916_f_at | AA397916 | 784 | EST | 3.27 | up | 0.02895 |
| rc_AA398205_at | AA398205 | 789 | EST | 4.17 | up | 0.00004 |
| rc_AA398761_s_at | AA398761 | 799 | EST | 3.43 | up | 0.00726 |
| rc_AA398908_at | AA398908 | 801 | EST | 38.69 | up | 0.01089 |
| rc_AA399226_at | AA399226 | 803 | tight junction protein 3 (zona occludens 3) | 3.59 | up | 0.02002 |
| rc_AA400271_at | AA400271 | 814 | EST | 3.51 | up | 0.00742 |
| rc_AA401958_at | AA401958 | 832 | EST | 3.62 | up | 0.01232 |
| rc_AA402495_at | AA402495 | 838 | EST | 4.91 | up | 0.00235 |
| AA402937_at | AA402937 | 843 | EST | 3.11 | up | 0.00182 |
| rc_AA402968_at | AA402968 | 844 | EST | 3.1 | up | 0.00453 |
| rc_AA403159_at | AA403159 | 845 | Ste-20 related kinase | 7.33 | up | 0.00187 |
| rc_AA404338_at | AA404338 | 849 | EST | 10.9 | up | 0.00668 |
| rc_AA405310_at | AA405310 | 856 | EST | 3.23 | up | 0.00138 |
| rc_AA405460_at | AA405460 | 857 | EST | 4.02 | up | 0.03492 |
| rc_AA405715_at | AA405715 | 862 | hypothetical protein | 4.68 | up | 0.00898 |
| rc_AA405791_at | AA405791 | 864 | EST | 21.22 | up | 0 |
| rc_AA406145_f_at | AA406145 | 870 | EST | 6.71 | up | 0.00047 |
| rc_AA406218_at | AA406218 | 872 | EST | 4.88 | up | 0.02194 |
| rc_AA406385_at | AA406385 | 876 | DKFZP564B0769 protein | 3.21 | up | 0.00724 |
| rc_AA406542_at | AA406542 | 878 | EST | 8.27 | up | 0.00724 |
| rc_AA410469_at | AA410469 | 883 | EST | 6.3 | up | 0.00103 |
| rc_AA410508_at | AA410508 | 885 | EST | 16.04 | up | 0.02635 |
| rc_AA410962_s_at | AA410962 | 887 | peroxisome proliferative activated receptor, delta | 3.45 | up | 0.04574 |
| rc_AA410972_at | AA410972 | 888 | EST | 3.12 | up | 0.00023 |
| rc_AA411502_at | AA411502 | 889 | EST | 16.42 | up | 0.00241 |
| rc_AA411685_at | AA411685 | 890 | EST | 3.83 | up | 0.00417 |
| rc_AA411813_at | AA411813 | 893 | postmeiotic segregation increased 2-like 11 | 6.76 | up | 0.03499 |
| rc_AA412301_at | AA412301 | 899 | EST | 4.57 | up | 0.00026 |
| rc_AA412403_at | AA412403 | 900 | EST | 3.09 | up | 0.00047 |
| rc_AA412405_s_at | AA412405 | 901 | EST | 13.82 | up | 0.01021 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA412720_at | AA412720 | 905 | EST | 3.6 | up | 0.01396 |
| rc_AA416963_at | AA416963 | 911 | EST | 3.69 | up | 0.03956 |
| rc_AA416973_at | AA416973 | 913 | EST | 3.61 | up | 0.0091 |
| rc_AA419217_at | AA419217 | 923 | DKFZP586E1422 protein | 6.77 | up | 0.00045 |
| rc_AA421562_at | AA421562 | 934 | anterior gradient 2 (Xenopus laevis) homolog | 56.3 | up | 0.0041 |
| rc_AA421638_at | AA421638 | 935 | EST | 3.05 | up | 0.00487 |
| rc_AA422049_at | AA422049 | 937 | EST | 3.38 | up | 0.0067 |
| rc_AA422086_at | AA422086 | 938 | EST | 10.71 | up | 0.03418 |
| rc_AA422150_at | AA422150 | 939 | cytochrome P540 family member predicted from ESTs | 17.14 | up | 0.00108 |
| rc_AA424029_at | AA424029 | 943 | EST | 8.68 | up | 0.00081 |
| rc_AA424487_at | AA424487 | 945 | EST | 38.41 | up | 0.00002 |
| rc_AA424881_at | AA424881 | 949 | EST | 6.3 | up | 0.00556 |
| rc_AA425279_at | AA425279 | 951 | quiescin Q6 | 6.15 | up | 0.00083 |
| rc_AA425401_at | AA425401 | 954 | serine/threonine kinase 24 (Ste20, yeast homolog) | 3.22 | up | 0.00625 |
| rc_AA425852_s_at | AA425852 | 958 | EST | 7.78 | up | 0.00239 |
| rc_AA425852_i_at | AA425852 | 958 | EST | 4.8 | up | 0.03874 |
| rc_AA426447_at | AA426447 | 965 | EST | 4.23 | up | 0.0309 |
| rc_AA426521_at | AA426521 | 967 | Sjogren's syndrome nuclear autoantigen 1 | 3.47 | up | 0.01161 |
| rc_AA427442_at | AA427442 | 971 | guanine nucleotide regulatory factor | 3.43 | up | 0.01547 |
| AA427468_s_at | AA427468 | 973 | claudin 4 | 84.43 | up | 0 |
| rc_AA427636_at | AA427636 | 976 | EST | 19.23 | up | 0.00145 |
| rc_AA427825_at | AA427825 | 981 | EST | 3.32 | up | 0.01615 |
| rc_aa427925_s_at | AA427925 | 982 | EST | 3.23 | up | 0.01806 |
| rc_AA427946_at | AA427946 | 983 | dynein, axonemal, light polypeptide 4 | 3.01 | up | 0.00001 |
| AA428172_f_at | AA428172 | 986 | Notch (Drosophila) homolog 3 | 9.53 | up | 0.02562 |
| rc_AA428964_at | AA428964 | 993 | kalikrein 10 | 21.83 | up | 0.02324 |
| rc_AA429009_at | AA429009 | 994 | serine protease inhibitor, Kunitz type 1 | 30.04 | up | 0.00001 |
| rc_AA429470_at | AA429470 | 996 | EST | 3.67 | up | 0.00782 |
| rc_AA429472_at | AA429472 | 997 | DKFZP434P106 protein | 8.27 | up | 0.00208 |
| rc_AA429636_at | AA429636 | 1001 | hexokinase 2 | 10.43 | up | 0.00597 |
| AA429825_at | AA429825 | 1003 | DKFZP566B023 protein | 6.63 | up | 0.00032 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA429890_s_at | AA429890 | 1004 | cisplatin resistance associated | 12.51 | up | 0.00053 |
| rc_AA430032_at | AA430032 | 1009 | pituitary tumor-transforming 1 | 16.87 | up | 0.00659 |
| rc_AA430048_at | AA430048 | 1012 | KIAA0160 protein | 6.27 | up | 0.00631 |
| rc_AA430674_at | AA430674 | 1018 | EST | 15.11 | up | 0.00293 |
| rc_AA431719_at | AA431719 | 1025 | EST | 4.25 | up | 0.00015 |
| rc_AA431776_at | AA431776 | 1027 | EST | 3.24 | up | 0.01814 |
| rc_AA431873_at | AA431873 | 1028 | EST | 4.03 | up | 0.00785 |
| rc_AA432162_at | AA432162 | 1029 | DKFZP586B2022 protein | 3.48 | up | 0.03851 |
| rc_AA433930_at | AA433930 | 1032 | chondroitin 4-sulfotransferase | 7.68 | up | 0.02445 |
| rc_AA434418_at | AA434418 | 1036 | KIAA1115 protein | 5.12 | up | 0.00498 |
| rc_AA435526_s_at | AA435526 | 1037 | transferrin receptor (p90, CD71) | 3.69 | up | 0.00139 |
| rc_AA435665_at | AA435665 | 1040 | EST | 8.66 | up | 0.00001 |
| rc_AA436027_at | AA436027 | 1050 | EST | 3.71 | up | 0.03676 |
| rc_AA436473_s_at | AA436473 | 1052 | EST | 3.03 | up | 0.00133 |
| rc_AA436616_at | AA436616 | 1056 | EST | 3.18 | up | 0.04402 |
| rc_AA437368_at | AA437368 | 1063 | EST | 3.75 | up | 0.01317 |
| rc_AA437387_s_at | AA437387 | 1064 | EST | 3.81 | up | 0.01478 |
| rc_AA441911_at | AA441911 | 1066 | EST | 6.14 | up | 0.00003 |
| AA442054_s_at | AA442054 | 1067 | phospholipase C, gamma 1 (formerly subtype 148) | 16.89 | up | 0.00205 |
| rc_AA442763_at | AA442763 | 1072 | cyclin B2 | 5.09 | up | 0.02168 |
| rc_AA443271_at | AA443271 | 1073 | KIAA0546 protein | 3.6 | up | 0.01228 |
| rc_AA443316_s_at | AA443316 | 1075 | v-Ha-ras Harvey rat sarcoma viral oncogene homolog | 4.13 | up | 0.01729 |
| rc_AA443941_at | AA443941 | 1085 | tumor suppressing subtransferable candidate 1 | 3.57 | up | 0.01685 |
| rc_AA446949_at | AA446949 | 1096 | EST | 3.41 | up | 0.03411 |
| rc_AA446968_at | AA446968 | 1097 | EST | 3.45 | up | 0.02232 |
| rc_AA447118_s_at | AA447118 | 1099 | EST | 3.03 | up | 0.01702 |
| rc_AA447687_at | AA447687 | 1104 | EST | 11.42 | up | 0.00362 |
| rc_AA447732_at | AA447732 | 1105 | EST | 3.2 | up | 0.00591 |
| rc_AA447991_at | AA447991 | 1112 | EST | 4.99 | up | 0.00173 |
| rc_aa449073_s_at | AA449073 | 1117 | EST | 6.89 | up | 0.01445 |
| rc_AA449122_at | AA449122 | 1119 | EST | 3.65 | up | 0.00369 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|----------|--|-------------|-----------|---------|
| rc_AA449456_at | AA449456 | 1126 EST | | 6.29 | up | 0.00087 |
| rc_AA449458_at | AA449458 | 1127 EST | | 3.22 | up | 0.03098 |
| rc_AA449475_at | AA449475 | 1128 EST | | 3.06 | up | 0.00291 |
| rc_AA449479_at | AA449479 | 1129 EST | | 3.09 | up | 0.03495 |
| rc_AA450247_at | AA450247 | 1133 EST | | 5.27 | up | 0.02833 |
| rc_AA451676_at | AA451676 | 1135 EST | | 14.72 | up | 0.00056 |
| | | | hepatocellular carcinoma associated protein; breast cancer | | | |
| rc_AA451680_at | AA451680 | 1136 | associated gene 1 | 3.55 | up | 0.00708 |
| rc_AA451877_at | AA451877 | 1138 EST | | 8.63 | up | 0.00489 |
| rc_AA452259_at | AA452259 | 1143 EST | | 3.49 | up | 0.00114 |
| rc_AA452536_at | AA452536 | 1145 | v-ral simian leukemia viral oncogene homolog A (ras related) | 5.6 | up | 0.00481 |
| AA452724_at | AA452724 | 1149 | programmed cell death 5 | 7.2 | up | 0.00908 |
| rc_AA453477_at | AA453477 | 1153 | X-prolyl aminopeptidase (aminopeptidase P)-like | 4.23 | up | 0.0001 |
| rc_AA453783_s_at | AA453783 | 1158 EST | | 6.16 | up | 0.00167 |
| rc_AA454597_s_at | AA454597 | 1166 EST | | 3.63 | up | 0.0067 |
| rc_AA454710_at | AA454710 | 1168 EST | | 3.42 | up | 0.00653 |
| AA454908_s_at | AA454908 | 1171 | KIAA0144 gene product | 9.3 | up | 0.00539 |
| rc_AA455521_s_at | AA455521 | 1178 | E2F transcription factor 5, p130-binding | 4.6 | up | 0.00773 |
| rc_AA455522_s_at | AA455522 | 1179 EST | | 3.83 | up | 0.00017 |
| rc_aa458852_f_at | AA458852 | 1203 | KIAA0440 protein | 3.2 | up | 0.00038 |
| rc_AA458890_at | AA458890 | 1206 EST | | 3.36 | up | 0.00303 |
| rc_AA459254_at | AA459254 | 1211 EST | | 5.36 | up | 0.0259 |
| rc_AA459310_r_at | AA459310 | 1214 EST | | 3.45 | up | 0.00179 |
| rc_AA459388_s_at | AA459388 | 1215 | copine I | 5.23 | up | 0.00691 |
| rc_AA459703_at | AA459703 | 1222 | v-myc avian myelocytomatosis viral oncogene homolog | 4.75 | up | 0.02413 |
| rc_AA459961_at | AA459961 | 1223 EST | | 3.24 | up | 0.00316 |
| rc_AA460017_i_at | AA460017 | 1225 EST | | 10.76 | up | 0.00106 |
| rc_AA460017_f_at | AA460017 | 1225 EST | | 3.61 | up | 0.00109 |
| rc_AA461187_at | AA461187 | 1236 EST | | 8.15 | up | 0.00068 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA461473_at | AA461473 | 1242 | nebulette | 3.35 | up | 0.03855 |
| rc_AA461476_at | AA461476 | 1243 | EST | 4.12 | up | 0.00871 |
| rc_AA463234_at | AA463234 | 1246 | KIAA0792 gene product | 5.94 | up | 0.01182 |
| rc_AA463725_at | AA463725 | 1249 | mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase | 7.4 | up | 0.04715 |
| rc_AA463861_at | AA463861 | 1251 | EST | 24.79 | up | 0.00096 |
| rc_AA464414_i_at | AA464414 | 1258 | EST | 4.99 | up | 0.00529 |
| rc_AA464698_at | AA464698 | 1262 | EST | 3.24 | up | 0.04854 |
| rc_AA464963_at | AA464963 | 1265 | EST | 5.01 | up | 0.00107 |
| AA471278_at | AA471278 | 1277 | BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog | 5.14 | up | 0.00873 |
| rc_AA476216_at | AA476216 | 1279 | EST | 4.97 | up | 0.00359 |
| rc_AA478017_at | AA478017 | 1295 | zyxin | 5.77 | up | 0.00484 |
| rc_AA478300_at | AA478300 | 1298 | CD39-like 2 | 6.15 | up | 0.01625 |
| rc_AA478415_at | AA478415 | 1299 | EST | 4.56 | up | 0.00095 |
| rc_AA478599_at | AA478599 | 1304 | G protein-coupled receptor 56 | 3.31 | up | 0.00182 |
| rc_AA479044_s_at | AA479044 | 1307 | EST | 6.9 | up | 0.04668 |
| rc_AA479727_s_at | AA479727 | 1315 | EST | 6.06 | up | 0.00389 |
| rc_AA479797_at | AA479797 | 1316 | EST | 7.93 | up | 0.00006 |
| rc_AA479945_s_at | AA479945 | 1319 | plakophilin 3 | 3.17 | up | 0.01767 |
| rc_AA482007_at | AA482007 | 1331 | EST | 3.49 | up | 0.00167 |
| rc_AA482127_at | AA482127 | 1333 | protein kinase related to <i>S. cerevisiae</i> STE20, effector for Cdc42Hs | 4.88 | up | 0.00017 |
| rc_AA482224_f_at | AA482224 | 1334 | putative type II membrane protein | 4.62 | up | 0.0105 |
| AA482319_f_at | AA482319 | 1335 | putative type II membrane protein | 5.11 | up | 0.00177 |
| rc_AA482546_s_at | AA482546 | 1336 | KIAA0124 protein | 4.41 | up | 0.00604 |
| rc_AA482613_at | AA482613 | 1338 | DKFZP434B203 protein | 4.14 | up | 0.00186 |
| rc_AA485405_at | AA485405 | 1343 | EST | 5.35 | up | 0.03475 |
| rc_AA485697_at | AA485697 | 1346 | EST | 14.74 | up | 0.00102 |
| rc_AA488987_s_at | AA488987 | 1365 | synaptogyrin 2 | 3.24 | up | 0.01444 |
| rc_AA489707_at | AA489707 | 1371 | EST | 3.47 | up | 0.03433 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA489712_at | AA489712 | 1372 | EST | 4.93 | up | 0.00726 |
| rc_AA490212_at | AA490212 | 1375 | H2A histone family, member Y | 3.71 | up | 0.01226 |
| rc_AA490494_at | AA490494 | 1377 | EST | 5.16 | up | 0.01696 |
| rc_AA491223_at | AA491223 | 1389 | EST | 3.03 | up | 0.00557 |
| rc_AA496204_at | AA496204 | 1397 | EST | 3.69 | up | 0.01097 |
| rc_AA496245_at | AA496245 | 1398 | EST | 3.96 | up | 0.0039 |
| rc_AA496981_at | AA496981 | 1404 | v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 | 4.93 | up | 0.01096 |
| rc_AA497031_at | AA497031 | 1407 | EST | 11.05 | up | 0.04381 |
| rc_AA504111_at | AA504111 | 1409 | EST | 3.2 | up | 0.00544 |
| rc_AA504264_at | AA504264 | 1410 | EST | 3.81 | up | 0.00684 |
| rc_AA504270_at | AA504270 | 1411 | EST | 4.96 | up | 0.01919 |
| AA504413_at | AA504413 | 1413 | EST | 3.35 | up | 0.00079 |
| rc_AA504806_at | AA504806 | 1416 | EST | 3.54 | up | 0.00221 |
| rc_AA598405_at | AA598405 | 1424 | membrane interacting protein of RGS16 | 4.69 | up | 0.0122 |
| rc_AA598506_s_at | AA598506 | 1430 | KIAA0179 protein | 3.17 | up | 0.01694 |
| rc_AA598712_at | AA598712 | 1436 | EST | 3.03 | up | 0.03656 |
| rc_AA598988_at | AA598988 | 1442 | EST | 4.32 | up | 0.00044 |
| rc_AA599244_at | AA599244 | 1448 | KIAA0530 protein | 3.39 | up | 0.01246 |
| rc_AA599522_f_at | AA599522 | 1452 | squamous cell carcinoma antigen recognised by T cells | 6.75 | up | 0.04229 |
| rc_AA608579_s_at | AA608579 | 1464 | paired-like homeodomain transcription factor 2 | 4.29 | up | 0.04435 |
| rc_AA608897_at | AA608897 | 1473 | EST | 9.92 | up | 0.00087 |
| rc_AA608965_at | AA608965 | 1474 | Hermansky-Pudlak syndrome | 3.19 | up | 0.00204 |
| rc_AA609008_at | AA609008 | 1475 | EST | 3.46 | up | 0.02935 |
| rc_AA609013_s_at | AA609013 | 1477 | dipeptidase 1 (renal) | 10.17 | up | 0.00109 |
| rc_AA609614_at | AA609614 | 1487 | EST | 6.5 | up | 0.00406 |
| rc_AA609786_s_at | AA609786 | 1491 | nucleolar protein 1 (120kD) | 4.75 | up | 0.00261 |
| rc_AA610053_at | AA610053 | 1496 | EST | 7.01 | up | 0.00003 |
| rc_AA610116_i_at | AA610116 | 1499 | tetraspan NET-6 protein | 33.68 | up | 0.00171 |
| rc_AA620466_at | AA620466 | 1502 | EST | 5.14 | up | 0.00004 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-----------------|----------|--------|---|-------------|-----------|---------|
| rc_AA620881_at | AA620881 | 1510 | trinucleotide repeat containing 3 | 8.66 | up | 0.00735 |
| rc_AA620995_at | AA620995 | 1512 | EST | 3.74 | up | 0.03414 |
| rc_AA621277_at | AA621277 | 1520 | EST | 3.81 | up | 0.00194 |
| rc_AA621780_at | AA621780 | 1530 | CGI-96 protein | 3.65 | up | 0.01582 |
| AB000584_at | AB000584 | 1533 | prostate differentiation factor | 4.7 | up | 0.00071 |
| AB002533_at | AB002533 | 1539 | karyopherin alpha 4 (importin alpha 3) | 6.38 | up | 0.00003 |
| AB006781_s_at | AB006781 | 1540 | lectin, galactoside-binding, soluble, 4 (galectin 4) | 7.05 | up | 0.00913 |
| AF001294_at | AF001294 | 1544 | tumor suppressing subtransferable candidate 3 | 7.45 | up | 0.00009 |
| AF003521_at | AF003521 | 1545 | jagged 2 | 11.26 | up | 0.00008 |
| AF004709_at | AF004709 | 1547 | mitogen-activated protein kinase 13 | 3.92 | up | 0.0009 |
| | | | stress-associated endoplasmic reticulum protein 1; ribosome | | | |
| C00021_s_at | C00021 | 1551 | associated membrane protein 4 | 3.33 | up | 0.00215 |
| C01766_s_at | C01766 | 1559 | EST | 13.67 | up | 0.00003 |
| rc_C13992_f_at | C13992 | 1564 | EST | 6.39 | up | 0.00059 |
| rc_C14051_f_at | C14051 | 1565 | phosphoprotein enriched in astrocytes 15 | 3.68 | up | 0.01453 |
| rc_C14098_f_at | C14098 | 1566 | EST | 3.53 | up | 0.04401 |
| rc_C14348_at | C14348 | 1568 | EST | 4.06 | up | 0.00111 |
| C14412_s_at | C14412 | 1569 | HSPC038 protein | 3.9 | up | 0.00036 |
| rc_C14756_f_at | C14756 | 1570 | MLN51 protein | 5.36 | up | 0.00001 |
| rc_C15324_f_at | C15324 | 1574 | EST | 5.22 | up | 0.00344 |
| rc_C21248_at | C21248 | 1585 | pituitary tumor-transforming 1 | 3.85 | up | 0.00456 |
| D00017_at | D00017 | 1587 | annexin A2 | 11.38 | up | 0 |
| | | | interleukin 2 receptor, gamma (severe combined | | | |
| D11086_at | D11086 | 1595 | immunodeficiency) | 5.61 | up | 0.00873 |
| | | | heterogeneous nuclear ribonucleoprotein U (scaffold | | | |
| D13413_ma1_s_at | D13413 | 1604 | attachment factor A) | 4.79 | up | 0.00092 |
| D13639_at | D13639 | 1607 | cyclin D2 | 7.49 | up | 0.01641 |
| D14520_at | D14520 | 1613 | basic transcription element binding protein 2 | 4.93 | up | 0.00004 |
| D14530_at | D14530 | 1614 | ribosomal protein S23 | 3.1 | up | 0.00331 |
| D14657_at | D14657 | 1615 | KIAA0101 gene product | 3.7 | up | 0.04079 |
| rc_D19737_at | D19737 | 1623 | golgi autoantigen, golgin subfamily a, 3 | 3.44 | up | 0.02212 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_D20464_at | D20464 | 1625 | bromodomain adjacent to zinc finger domain, 2B | 3.27 | up | 0.04897 |
| rc_D20906_at | D20906 | 1627 | EST | 5.18 | up | 0.02189 |
| D21063_at | D21063 | 1628 | minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) | 3.83 | up | 0.00983 |
| D21261_at | D21261 | 1629 | transgelin 2 | 3.46 | up | 0.00685 |
| D23660_at | D23660 | 1630 | ribosomal protein L4 | 3.22 | up | 0.00316 |
| D25216_at | D25216 | 1631 | KIAA0014 gene product | 3.17 | up | 0.02125 |
| D25274_at | D25274 | 1632 | EST | 3.39 | up | 0.00238 |
| D25328_at | D25328 | 1633 | phosphofructokinase, platelet | 3.17 | up | 0.04925 |
| rc_D25560_i_at | D25560 | 1634 | EST | 4.72 | up | 0.00661 |
| D26129_at | D26129 | 1635 | ribonuclease, RNase A family, 1 (pancreatic) neuroblastoma candidate region, suppression of tumorigenicity 1 | 5.68 | up | 0.03827 |
| D28124_at | D28124 | 1636 | G8 protein | 6.38 | up | 0.00015 |
| D31094_at | D31094 | 1639 | secreted protein of unknown function | 4.41 | up | 0.04845 |
| D31417_at | D31417 | 1645 | | 4.56 | up | 0.00014 |
| D38073_at | D38073 | 1651 | minichromosome maintenance deficient (S. cerevisiae) 3 | 3.65 | up | 0.01869 |
| D38548_at | D38548 | 1655 | KIAA0076 gene product | 4.5 | up | 0.00036 |
| D38583_at | D38583 | 1656 | S100 calcium-binding protein A11 (calgizzarin) | 18.7 | up | 0.00003 |
| D42085_at | D42085 | 1658 | KIAA0095 gene product | 3.83 | up | 0.00036 |
| D43949_at | D43949 | 1659 | KIAA0082 protein | 3.32 | up | 0.0014 |
| D43950_at | D43950 | 1660 | chaperonin containing TCP1, subunit 5 (epsilon) | 3.61 | up | 0.00672 |
| D49400_at | D49400 | 1667 | ATPase, vacuolar, 14 kD | 4.01 | up | 0.00287 |
| D50663_at | D50663 | 1671 | t-complex-associated-testis-expressed 1-like 1 | 4.09 | up | 0.00208 |
| D50913_at | D50913 | 1672 | KIAA0123 protein | 3.32 | up | 0.01202 |
| D50914_at | D50914 | 1673 | KIAA0124 protein | 4.74 | up | 0.00752 |
| rc_D51112_s_at | D51112 | 1675 | collapsin response mediator protein 1 | 10.48 | up | 0.00076 |
| rc_D51133_f_at | D51133 | 1676 | tubulin, beta, 4 | 4.84 | up | 0.02875 |
| rc_D51276_f_at | D51276 | 1678 | leukemia-associated phosphoprotein p18 (statmin) | 4.81 | up | 0.00514 |
| rc_D51287_f_at | D51287 | 1680 | ribosomal protein S12 | 3.3 | up | 0.02829 |
| rc_D51393_f_at | D51393 | 1681 | ribosomal protein L4 | 5.64 | up | 0.00074 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_D52632_f_at | D52632 | 1683 | ribosomal protein S6 | 3.12 | up | 0.00498 |
| rc_D53139_f_at | D53139 | 1684 | ribosomal protein S28 | 4.38 | up | 0.0009 |
| rc_D54296_f_at | D54296 | 1685 | KIAA0255 gene product | 3.8 | up | 0.01059 |
| D55716_at | D55716 | 1686 | minichromosome maintenance deficient (S. cerevisiae) 7 | 6.6 | up | 0.00151 |
| rc_D57489_at | D57489 | 1689 | chaperonin containing TCP1, subunit 7 (eta) | 4.08 | up | 0.00001 |
| rc_D59322_f_at | D59322 | 1694 | EST | 4.18 | up | 0.00006 |
| rc_D59847_at | D59847 | 1701 | EST | 3.09 | up | 0.02206 |
| rc_D60811_s_at | D60811 | 1704 | EST | 3.22 | up | 0.0098 |
| | | | platelet-activating factor acetylhydrolase, isoform lb, gamma subunit (29kD) | | | |
| D63391_at | D63391 | 1710 | | 3.91 | up | 0.00062 |
| D63486_at | D63486 | 1712 | KIAA0152 gene product | 6.33 | up | 0.00078 |
| D63487_at | D63487 | 1713 | KIAA0153 protein | 5.4 | up | 0.00027 |
| D63874_at | D63874 | 1714 | high-mobility group (nonhistone chromosomal) protein 1 | 3.64 | up | 0.00228 |
| D63880_at | D63880 | 1715 | KIAA0159 gene product | 4.26 | up | 0.00253 |
| D78361_at | D78361 | 1718 | EST | 3.14 | up | 0.00023 |
| D78676_at | D78676 | 1719 | EST | 3.2 | up | 0.00635 |
| D79205_at | D79205 | 1721 | ribosomal protein L39 | 3.07 | up | 0.00021 |
| rc_D80237_s_at | D80237 | 1729 | actin related protein 2/3 complex, subunit 4 (20 kD) | 3.27 | up | 0.00137 |
| rc_D80662_s_at | D80662 | 1733 | adaptor-related protein complex 1, gamma 2 subunit | 3.43 | up | 0.00108 |
| rc_D80710_f_at | D80710 | 1734 | integral type I protein | 7.08 | up | 0.00213 |
| rc_D80917_f_at | D80917 | 1736 | KIAA0670 protein/acinus | 3.58 | up | 0.00007 |
| rc_D80946_f_at | D80946 | 1737 | SFRS protein kinase 1 | 8.53 | up | 0.00455 |
| | | | 5-aminimidazole-4-carboxamide ribonucleotide | | | |
| D82348_at | D82348 | 1744 | formyltransferase/IMP cyclohydrolase | 3.93 | up | 0.00037 |
| D82558_at | D82558 | 1746 | novel centrosomal protein RanBPM | 5.94 | up | 0.00752 |
| D83735_at | D83735 | 1747 | calponin 2 | 10.42 | up | 0.00001 |
| | | | trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit) | | | |
| D83783_at | D83783 | 1748 | | 6.55 | up | 0.00176 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| D83783_at | D83783 | 1748 | trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit) | 3.33 | up | 0.00748 |
| D86956_at | D86956 | 1753 | heat shock 105kD | 4 | up | 0.03013 |
| D86974_at | D86974 | 1756 | KIAA0220 protein | 3.85 | up | 0.0161 |
| D87735_at | D87735 | 1764 | ribosomal protein L14 | 3.92 | up | 0.00015 |
| D87953_at | D87953 | 1765 | N-myc downstream regulated | 6.12 | up | 0.00033 |
| D88154_at | D88154 | 1766 | villin-like | 4.18 | up | 0.00051 |
| rc_F01444_f_at | F01444 | 1770 | KIAA0440 protein | 6.78 | up | 0.00028 |
| rc_F01568_at | F01568 | 1772 | EST | 3.24 | up | 0.0018 |
| rc_F02800_at | F02800 | 1780 | EST | 3.45 | up | 0.03238 |
| rc_F02863_at | F02863 | 1782 | EST | 3.21 | up | 0.01039 |
| rc_F04320_s_at | F04320 | 1786 | replication factor C (activator 1) 4 (37kD) | 3.63 | up | 0.01119 |
| rc_F04444_at | F04444 | 1788 | EST | 4.57 | up | 0.01132 |
| rc_F04531_s_at | F04531 | 1791 | Kell blood group precursor (McLeod phenotype) | 7.79 | up | 0.03205 |
| rc_F04674_at | F04674 | 1793 | KIAA0746 protein | 8.2 | up | 0.00028 |
| rc_F09297_s_at | F09297 | 1800 | EST | 3.94 | up | 0.0016 |
| rc_F09394_s_at | F09394 | 1803 | KIAA0715 protein | 22.89 | up | 0.01753 |
| rc_F09684_at | F09684 | 1805 | EST | 3.78 | up | 0.00277 |
| rc_F09788_at | F09788 | 1808 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II | 4.14 | up | 0.00003 |
| rc_F13809_f_at | F13809 | 1828 | tropomyosin 1 (alpha) | 7.62 | up | 0.00012 |
| rc_H04753_f_at | H04753 | 1839 | EST | 3.38 | up | 0.02447 |
| rc_H04799_at | H04799 | 1841 | EST | 3.71 | up | 0.04109 |
| rc_H05394_f_at | H05394 | 1845 | KIAA0266 gene product | 4.06 | up | 0.0015 |
| rc_H05525_s_at | H05525 | 1846 | hypothetical protein | 4.6 | up | 0.0033 |
| rc_H05625_f_at | H05625 | 1847 | EST | 5.17 | up | 0.04551 |
| rc_H08863_at | H08863 | 1859 | hypothetical protein | 3.48 | up | 0.00205 |
| rc_H09241_s_at | H09241 | 1861 | EST | 4.17 | up | 0.00727 |
| rc_H09271_f_at | H09271 | 1862 | EST | 5.06 | up | 0.0016 |
| rc_H09281_at | H09281 | 1863 | EST | 6 | up | 0.00966 |
| rc_H13532_f_at | H13532 | 1881 | ribosomal protein L18a | 3.97 | up | 0.00061 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_H17476_at | H17476 | 1889 | EST | 3.44 | up | 0.00479 |
| rc_H18412_s_at | H18412 | 1890 | isocitrate dehydrogenase 3 (NAD+) gamma | 4.37 | up | 0.00262 |
| rc_H18442_f_at | H18442 | 1891 | creatine kinase, brain | 17.42 | up | 0.02391 |
| rc_H20989_s_at | H20989 | 1899 | pyruvate kinase, muscle | 11.37 | up | 0.0375 |
| rc_H24077_at | H24077 | 1900 | EST | 3.05 | up | 0.0324 |
| rc_H27188_f_at | H27188 | 1908 | collagen-binding protein 2 (colligen 2) | 4.16 | up | 0.02073 |
| rc_H28333_f_at | H28333 | 1912 | melanoma adhesion molecule | 3.11 | up | 0.00172 |
| rc_H29565_at | H29565 | 1913 | EST | 3.89 | up | 0.01856 |
| rc_H38240_s_at | H38240 | 1916 | thrombospondin 2 | 4.28 | up | 0.0066 |
| rc_H38568_s_at | H38568 | 1918 | EST | 4.86 | up | 0.0003 |
| rc_H42321_f_at | H42321 | 1928 | ribosomal protein L18a | 3.23 | up | 0.01102 |
| H43286_s_at | H43286 | 1929 | gamma-aminobutyric acid (GABA) B receptor, 1 | 5.02 | up | 0.01972 |
| rc_H43646_at | H43646 | 1930 | H2A histone family, member Y | 4.6 | up | 0.00147 |
| H46486_s_at | H46486 | 1932 | nesca protein | 4.77 | up | 0.00421 |
| rc_H49637_s_at | H49637 | 1940 | EST | 3.79 | up | 0.01092 |
| rc_H52673_s_at | H52673 | 1943 | BCL2-antagonist/killer 1 | 3.03 | up | 0.0393 |
| H53657_s_at | H53657 | 1945 | adenylate cyclase 3 | 3.98 | up | 0.0045 |
| H55437_at | H55437 | 1948 | kraken-like | 3.53 | up | 0.02344 |
| rc_H56345_r_at | H56345 | 1950 | EST | 4.15 | up | 0.00488 |
| | | | solute carrier family 2 (facilitated glucose transporter), member 1 | | | |
| rc_H58873_s_at | H58873 | 1961 | 1 | 57.98 | up | 0.00063 |
| rc_H59617_at | H59617 | 1964 | EST | 3.3 | up | 0.04588 |
| rc_H75933_f_at | H75933 | 1998 | laminin receptor 1 (67kD, ribosomal protein SA) | 5.81 | up | 0.00024 |
| rc_H78211_at | H78211 | 2001 | EST | 6.73 | up | 0.02488 |
| rc_H78323_at | H78323 | 2002 | transcription factor Dp-1 | 3.69 | up | 0.00326 |
| | | | high-mobility group (nonhistone chromosomal) protein isoforms I and Y | | | |
| rc_H81413_f_at | H81413 | 2007 | I and Y | 5.82 | up | 0.00769 |
| rc_H88674_s_at | H88674 | 2021 | collagen, type I, alpha 2 | 5.06 | up | 0.00866 |
| H89551_s_at | H89551 | 2024 | EST | 9.94 | up | 0.00137 |
| rc_H93021_at | H93021 | 2033 | peptidylprolyl isomerase A (cyclophilin A) | 3.31 | up | 0.0183 |
| rc_H93492_at | H93492 | 2037 | EST | 3.94 | up | 0.01136 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_H93652_f_at | H93652 | 2039 | ribosomal protein S5 | 3.31 | up | 0.00788 |
| rc_H94471_at | H94471 | 2042 | occludin | 43.09 | up | 0 |
| rc_H95233_s_at | H95233 | 2048 | serine protease inhibitor, Kunitz type, 2 | 47.06 | up | 0 |
| rc_H96975_at | H96975 | 2057 | EST | 3.22 | up | 0.0141 |
| rc_H97013_at | H97013 | 2059 | ephrin-A4 | 9.14 | up | 0.00346 |
| rc_H97809_at | H97809 | 2063 | EST | 4.05 | up | 0.00111 |
| rc_H98924_at | H98924 | 2072 | chromatin assembly factor 1, subunit A (p150) | 3.53 | up | 0.02106 |
| rc_H99473_s_at | H99473 | 2077 | regulator of nonsense transcripts 1 | 5.37 | up | 0.00177 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-----------------|---------|--------|---|-------------|-----------|---------|
| J03459_at | J03459 | 2093 | leukotriene A4 hydrolase | 3.03 | up | 0.04041 |
| J03464_s_at | J03464 | 2094 | collagen, type I, alpha 2 | 9.81 | up | 0.00028 |
| J03592_at | J03592 | 2096 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | 10.05 | up | 0 |
| J03827_at | J03827 | 2100 | nuclease sensitive element binding protein 1 | 4.45 | up | 0.00015 |
| J04152_ma1_s_at | J04152 | 2107 | membrane component, chromosome 1, surface marker 1 | 5.26 | up | 0.02466 |
| J04164_at | J04164 | 2108 | (40kD glycoprotein, identified by monoclonal antibody GA733) | 12.37 | up | 0.00001 |
| AFFX-BioDn-3_at | J04423 | 2109 | interferon induced transmembrane protein 1 (9-27) | 54.11 | up | 0.02774 |
| AFFX-BioDn-3_at | J04423 | 2109 | EST | 48.05 | up | 0.02203 |
| AFFX-BioDn-3_at | J04423 | 2109 | EST | 21.46 | up | 0.04283 |
| AFFX-BioB-3_at | J04423 | 2109 | EST | 5.13 | up | 0.02791 |
| AFFX-BioB-5_at | J04423 | 2109 | EST | 4.47 | up | 0.02754 |
| AFFX-BioDn-3_st | J04423 | 2109 | EST | 4.35 | up | 0.01245 |
| J04469_at | J04469 | 2111 | creatine kinase, mitochondrial 1 (ubiquitous) | 7.9 | up | 0.00705 |
| J04823_ma1_at | J04823 | 2115 | cytochrome c oxidase subunit VIII | 3.35 | up | 0.00075 |
| J05257_at | J05257 | 2118 | dipeptidase 1 (renal) | 12.02 | up | 0.02099 |
| J05582_s_at | J05582 | 2121 | mucin 1, transmembrane | 5.39 | up | 0.00056 |
| K03195_at | K03195 | 2128 | solute carrier family 2 (facilitated glucose transporter), member 1 | 10.73 | up | 0.00139 |
| K03460_at | K03460 | 2129 | tubulin, alpha 1 (testis specific) | 7.5 | up | 0.00002 |
| L03411_s_at | L03411 | 2134 | RD RNA-binding protein | 3.97 | up | 0.00422 |
| L04483_s_at | L04483 | 2136 | ribosomal protein S21 | 4.2 | up | 0.00057 |
| L04490_at | L04490 | 2137 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD) | 5.22 | up | 0.02192 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|---------------|---------|--------|---|-------------|-----------|---------|
| L06499_at | L06499 | 2141 | ribosomal protein L37a | 4.34 | up | 0.01103 |
| L06505_at | L06505 | 2142 | ribosomal protein L12 | 5 | up | 0.00163 |
| L08044_s_at | L08044 | 2149 | trefoil factor 3 (intestinal) | 21.42 | up | 0.01674 |
| L08044_s_at | L08044 | 2149 | trefoil factor 3 (intestinal) | 14.18 | up | 0.02124 |
| L09604_at | L09604 | 2151 | proteolipid protein 2 (colonic epithelium-enriched) | 8.68 | up | 0 |
| L11566_at | L11566 | 2156 | ribosomal protein L18 | 4.29 | up | 0.00014 |
| L11669_at | L11669 | 2157 | tetracycline transporter-like protein | 6.75 | up | 0.00101 |
| L12350_at | L12350 | 2160 | thrombospondin 2 | 3.78 | up | 0.00061 |
| L12711_s_at | L12711 | 2161 | transketolase (Wernicke-Korsakoff syndrome) | 3.08 | up | 0.03362 |
| | | | high-mobility group (nonhistone chromosomal) protein isoforms I and Y | | | |
| L17131_ma1_at | L17131 | 2168 | | 20.57 | up | 0.00058 |
| L19527_at | L19527 | 2169 | ribosomal protein L27 | 3.54 | up | 0.00025 |
| L19605_at | L19605 | 2170 | annexin A11 | 6.38 | up | 0.00017 |
| | | | macrophage migration inhibitory factor (glycosylation-inhibiting factor) | | | |
| L19686_ma1_at | L19686 | 2171 | | 5.26 | up | 0.00562 |
| L20591_at | L20591 | 2173 | annexin A3 | 4.64 | up | 0.00065 |
| L20941_at | L20941 | 2174 | ferritin, heavy polypeptide 1 | 3.3 | up | 0.01172 |
| L21954_at | L21954 | 2177 | benzodiazepine receptor (peripheral) | 8.53 | up | 0.00001 |
| L23808_at | L23808 | 2179 | matrix metalloproteinase 12 (macrophage elastase) | 6.18 | up | 0.02195 |
| L25081_at | L25081 | 2180 | ras homolog gene family, member C | 3.67 | up | 0.00005 |
| L33075_at | L33075 | 2195 | IQ motif containing GTPase activating protein 1 | 3.83 | up | 0.00015 |
| L33842_ma1_at | L33842 | 2197 | IMP (inosine monophosphate) dehydrogenase 2 | 11.03 | up | 0.00001 |
| | | | CD24 antigen (small cell lung carcinoma cluster 4 antigen) | | | |
| L33930_s_at | L33930 | 2198 | | 9.16 | up | 0.01252 |
| | | | transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) | | | |
| L34587_at | L34587 | 2200 | | 4.32 | up | 0.00287 |
| L36720_at | L36720 | 2205 | bystin-like | 3.46 | up | 0.00094 |
| L38696_at | L38696 | 2208 | RNA-binding protein (autoantigenic) | 3.7 | up | 0.00093 |
| | | | thyroid receptor interacting protein 10 (CDC42-interacting protein) | | | |
| L40379_at | L40379 | 2210 | | 3.87 | up | 0.00207 |
| L40904_at | L40904 | 2212 | peroxisome proliferative activated receptor, gamma | 3.43 | up | 0.03511 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|--------------------|---------|--------|---|-------------|-----------|---------|
| L41351_at | L41351 | 2214 | protease, serine, 8 (prostasin) | 6.34 | up | 0.01132 |
| L44538_at | L44538 | 2217 | EST | 4.34 | up | 0.04319 |
| L76191_at | L76191 | 2222 | interleukin-1 receptor-associated kinase 1 | 5.66 | up | 0.00089 |
| L76200_at | L76200 | 2223 | guanylate kinase 1 | 3.24 | up | 0.0097 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 11.55 | up | 0.00099 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 10.2 | up | 0.00027 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 5.62 | up | 0.00251 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 5.61 | up | 0.01238 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 5.35 | up | 0.00186 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 4.79 | up | 0.00328 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 4.66 | up | 0.00405 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 3.73 | up | 0.01794 |
| AFFX-HUMRGE/M10098 | M10098 | 2231 | EST | 10.83 | up | 0.00191 |
| M12125_at | M12125 | 2241 | tropomyosin 2 (beta) | 3.99 | up | 0 |
| M13934_cds2_at | M13934 | 2255 | ribosomal protein S14 | 7.01 | up | 0 |
| M14199_s_at | M14199 | 2258 | laminin receptor 1 (67kD, ribosomal protein SA) | 4.46 | up | 0.00686 |
| M14483_ma1_s_at | M14483 | 2261 | prothymosin, alpha (gene sequence 28) | 3.11 | up | 0.00013 |
| M14949_at | M14949 | 2264 | related RAS viral (v-ras) oncogene homolog | 3.75 | up | 0.00159 |
| M15205_at | M15205 | 2265 | thymidine kinase 1, soluble | 12.69 | up | 0.03633 |
| M16364_s_at | M16364 | 2269 | creatine kinase, brain | 4.15 | up | 0.00009 |
| M17733_at | M17733 | 2280 | thymosin, beta 4, X chromosome | 3.92 | up | 0.00003 |
| M17885_at | M17885 | 2281 | ribosomal protein, large, P0 | 4.34 | up | 0.00004 |
| M17886_at | M17886 | 2282 | ribosomal protein, large, P1 | 3.79 | up | 0.00004 |
| M18000_at | M18000 | 2283 | ribosomal protein S17 | | | |
| | | | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | 44.82 | up | 0.00291 |
| M18728_at | M18728 | 2285 | | 5.32 | up | 0.00344 |
| M20471_at | M20471 | 2289 | clathrin, light polypeptide (Lca) | | | |
| M22960_at | M22960 | 2296 | protective protein for beta-galactosidase (galactosialidosis) | 4.49 | up | 0.00898 |
| M23613_at | M23613 | 2301 | nucleophosmin (nucleolar phosphoprotein B23, numatrin) | 3.67 | up | 0.00977 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------------|---------|--------|--|-------------|-----------|---------|
| M24194_at | M24194 | 2302 | guanine nucleotide binding protein (G protein), beta polypeptide | 4.55 | up | 0.00017 |
| M24485_s_at | M24485 | 2304 | 2-like 1 | 10.2 | up | 0.00003 |
| M26708_s_at | M26708 | 2311 | glutathione S-transferase pi | 3.35 | up | 0.00064 |
| M27826_at | M27826 | 2313 | prothymosin, alpha (gene sequence 28) | 26.36 | up | 0.00342 |
| AFEX-M27830_5_at | M27830 | 2314 | endogenous retroviral protease | 15.53 | up | 0.00022 |
| AFEX-M27830_5_at | M27830 | 2314 | EST | 14.86 | up | 0.00043 |
| AFEX-M27830_5_at | M27830 | 2314 | EST | 10.64 | up | 0.00213 |
| AFEX-M27830_M_at | M27830 | 2314 | EST | 9.8 | up | 0.00041 |
| AFEX-M27830_M_at | M27830 | 2314 | EST | 8.78 | up | 0.00003 |
| AFEX-M27830_5_at | M27830 | 2314 | EST | 8.2 | up | 0.00294 |
| AFEX-M27830_M_at | M27830 | 2314 | EST | 6.25 | up | 0.00046 |
| AFEX-M27830_M_at | M27830 | 2314 | EST | 5.78 | up | 0.0017 |
| M29277_at | M29277 | 2316 | melanoma adhesion molecule | 3.91 | up | 0.00112 |
| M29540_at | M29540 | 2317 | carcinoembryonic antigen-related cell adhesion molecule 5 | 36.57 | up | 0.0116 |
| M30496_at | M30496 | 2324 | ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) | 3.8 | up | 0.00478 |
| M31303_rna1_at | M31303 | 2327 | leukemia-associated phosphoprotein p18 (stathmin) | 7.48 | up | 0.00021 |
| M31520_rna1_s_at | M31520 | 2328 | ribosomal protein S24 | 3.37 | up | 0.00077 |
| M31520_at | M31520 | 2328 | ribosomal protein S24 | 3.13 | up | 0.00014 |
| M32405_at | M32405 | 2334 | ribosomal protein S15 | 4.01 | up | 0.00055 |
| M32886_at | M32886 | 2335 | sorcin | 8.35 | up | 0.00215 |
| AFEX-HUMGAPDH/M33 | M33197 | 2337 | glyceraldehyde-3-phosphate dehydrogenase | 3.31 | up | 0.00009 |
| M34182_at | M34182 | 2340 | protein kinase, cAMP-dependent, catalytic, gamma | 4.51 | up | 0.00043 |
| M35252_at | M35252 | 2343 | transmembrane 4 superfamily member 3 | 39.12 | up | 0 |
| M36072_at | M36072 | 2347 | ribosomal protein L7a | 3.1 | up | 0.00006 |
| M38591_at | M38591 | 2350 | S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) | 14.87 | up | 0 |
| M38690_at | M38690 | 2351 | CD9 antigen (p24) | 9.08 | up | 0.00059 |
| M55998_s_at | M55998 | 2356 | collagen, type I, alpha 1 | 6.99 | up | 0.00103 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| M57710_at | M57710 | 2357 | lectin, galactoside-binding, soluble, 3 (galectin 3) | 27.12 | up | 0.00001 |
| M60784_s_at | M60784 | 2366 | small nuclear ribonucleoprotein polypeptide A | 5.74 | up | 0.00126 |
| M60854_at | M60854 | 2367 | ribosomal protein S16 | 3.4 | up | 0.00001 |
| M62895_s_at | M62895 | 2375 | annexin A2, annexin A2 pseudogene 2 | 6.11 | up | 0.00013 |
| M64716_at | M64716 | 2382 | ribosomal protein S25 | 3.16 | up | 0.00039 |
| M68864_at | M68864 | 2389 | ORF | 3.1 | up | 0.00603 |
| M77232_ma1_at | M77232 | 2399 | ribosomal protein S6 | 3.82 | up | 0.00045 |
| M77349_at | M77349 | 2400 | transforming growth factor, beta-induced, 68kD | 4.81 | up | 0.00546 |
| M77836_at | M77836 | 2401 | pyrroline-5-carboxylate reductase 1 | 3.43 | up | 0.00759 |
| M79463_s_at | M79463 | 2402 | promyelocytic leukemia | 4.88 | up | 0.01821 |
| M81757_at | M81757 | 2406 | ribosomal protein S19 | 5.46 | up | 0 |
| M86400_at | M86400 | 2410 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase | 5.62 | up | 0.00016 |
| M86667_at | M86667 | 2411 | activation protein, zeta polypeptide | 3.03 | up | 0.04853 |
| M86752_at | M86752 | 2412 | nucleosome assembly protein 1-like 1 | 7.32 | up | 0.00001 |
| M87339_at | M87339 | 2415 | stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) | 4.07 | up | 0.00316 |
| M91083_at | M91083 | 2419 | replication factor C (activator 1) 4 (37kD) | 3.3 | up | 0.00163 |
| M93036_at | M93036 | 2422 | chromosome 11 open reading frame 13 | 16.45 | up | 0.00308 |
| M94250_at | M94250 | 2426 | membrane component, chromosomal 4, surface marker (35kD glycoprotein) | 10.39 | up | 0.01818 |
| M94345_at | M94345 | 2427 | midkine (neurite growth-promoting factor 2) | 22.38 | up | 0.00003 |
| M96739_at | M96739 | 2434 | capping protein (actin filament), gelsolin-like | 3.72 | up | 0.00015 |
| rc_N20198_s_at | N20198 | 2440 | nescient helix loop helix 1 | 5.17 | up | 0.00508 |
| rc_N21359_at | N21359 | 2442 | ubiquitin-conjugating enzyme E2 variant 1 | 4.43 | up | 0.00078 |
| rc_N22015_at | N22015 | 2448 | EST | 46.61 | up | 0.00025 |
| rc_N22107_at | N22107 | 2449 | EST | 6.88 | up | 0.04259 |
| rc_N24899_at | N24899 | 2461 | EST | 3.06 | up | 0.00353 |
| rc_N26186_at | N26186 | 2468 | EST | 6.15 | up | 0.00135 |
| rc_N27186_at | N27186 | 2470 | EST | 3.79 | up | 0.00112 |
| rc_N27334_at | N27334 | 2471 | EST | 3.65 | up | 0.03437 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_N29888_at | N29888 | 2483 | EST | 3.7 | up | 0.00226 |
| rc_N30436_f_at | N30436 | 2484 | EST | 3.45 | up | 0.02356 |
| rc_N31570_at | N31570 | 2486 | TNF receptor-associated factor 5 | 10.39 | up | 0.00018 |
| rc_N31597_s_at | N31597 | 2487 | DKFZP564G2022 protein | 4.44 | up | 0.00085 |
| N36432_at | N36432 | 2507 | erythrocyte membrane protein band 4.1-like 2 | 3.03 | up | 0.03086 |
| rc_N39099_at | N39099 | 2508 | EST | 4.42 | up | 0.00643 |
| rc_N39237_at | N39237 | 2511 | EST | 9.29 | up | 0.00001 |
| rc_N39254_s_at | N39254 | 2512 | EST | 4.42 | up | 0.00478 |
| rc_N46423_at | N46423 | 2521 | EST | 9.64 | up | 0.00027 |
| rc_N47956_at | N47956 | 2524 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) | 6.34 | up | 0.00251 |
| rc_N49284_s_at | N49284 | 2537 | v-myb avian myeloblastosis viral oncogene homolog | 11.82 | up | 0.01981 |
| rc_N49738_at | N49738 | 2539 | EST | 3.81 | up | 0.02479 |
| rc_N50048_at | N50048 | 2542 | EST | 4.08 | up | 0.00085 |
| rc_N51053_s_at | N51053 | 2543 | eukaryotic translation initiation factor 5 | 3.42 | up | 0.01326 |
| rc_N51342_at | N51342 | 2545 | EST | 3.56 | up | 0.0001 |
| rc_N52168_at | N52168 | 2551 | EST | 5.65 | up | 0.00003 |
| rc_N54841_at | N54841 | 2572 | EST | 42.96 | up | 0.00002 |
| rc_N56935_s_at | N56935 | 2575 | EST | 3.57 | up | 0.00282 |
| rc_N58463_at | N58463 | 2580 | PCTAIRE protein kinase 1 | 3.18 | up | 0.00649 |
| rc_N62126_at | N62126 | 2589 | EST | 8.51 | up | 0.00016 |
| rc_N62675_s_at | N62675 | 2594 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 | 3.61 | up | 0.04034 |
| rc_N62819_at | N62819 | 2595 | EST | 3.25 | up | 0.01137 |
| rc_N64616_at | N64616 | 2611 | EST | 3.11 | up | 0.0074 |
| rc_N66139_s_at | N66139 | 2615 | neurochondrin | 4.03 | up | 0.00118 |
| rc_N66624_at | N66624 | 2618 | homolog of mouse quaking QKI (KH domain RNA binding protein) | 6.25 | up | 0 |
| rc_N66951_at | N66951 | 2621 | EST | 5.54 | up | 0.02442 |
| rc_N67205_at | N67205 | 2625 | EST | 3.1 | up | 0.00626 |
| rc_N68038_f_at | N68038 | 2632 | phorbolin (similar to apolipoprotein B mRNA editing protein) | 3.75 | up | 0.01041 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_N68385_f_at | N68385 | 2635 | ribosomal protein L13a | 3.57 | up | 0.00417 |
| rc_N68921_at | N68921 | 2639 | EST | 4.4 | up | 0.00989 |
| rc_N69252_f_at | N69252 | 2647 | ferritin, light polypeptide | 5.33 | up | 0.01554 |
| rc_N69263_at | N69263 | 2648 | EST | 7.47 | up | 0.00004 |
| rc_N70577_at | N70577 | 2659 | EST | 3.07 | up | 0.01975 |
| rc_N70678_s_at | N70678 | 2660 | TAR (HIV) RNA-binding protein 1 | 4.2 | up | 0.00119 |
| rc_N70903_at | N70903 | 2662 | EST | 4.41 | up | 0.0078 |
| rc_N71072_at | N71072 | 2664 | EST | 5.57 | up | 0.03881 |
| rc_N71781_at | N71781 | 2666 | EST | 7.01 | up | 0.02952 |
| rc_N72116_s_at | N72116 | 2668 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | 9.01 | up | 0.00051 |
| rc_N73762_f_at | N73762 | 2678 | EST | 6.65 | up | 0.0023 |
| rc_N73808_f_at | N73808 | 2679 | EST | 8.46 | up | 0.01886 |
| rc_N73846_at | N73846 | 2680 | EST | 3.27 | up | 0.00012 |
| rc_N77947_s_at | N77947 | 2698 | EST | 5 | up | 0.00117 |
| rc_N80703_at | N80703 | 2704 | EST | 6.06 | up | 0.00003 |
| rc_N89670_at | N89670 | 2709 | EST | 4.26 | up | 0.00002 |
| rc_N89937_at | N89937 | 2711 | LIM domain only 7 | 3.6 | up | 0.00375 |
| rc_N90238_i_at | N90238 | 2712 | EST | 3.06 | up | 0.00354 |
| rc_N91023_at | N91023 | 2716 | EST | 3.87 | up | 0.00008 |
| rc_N92775_at | N92775 | 2723 | amyloid beta (A4) precursor protein-binding, family A, member 3 (X11-like 2) | 3.86 | up | 0.00577 |
| rc_N92915_at | N92915 | 2724 | brefeldin A-inhibited guanine nucleotide-exchange protein 1 | 3.1 | up | 0.00807 |
| rc_N92934_s_at | N92934 | 2725 | cysteine-rich protein 1 (intestinal) | 35.52 | up | 0.002 |
| rc_N93105_f_at | N93105 | 2728 | EST | 3.77 | up | 0.02195 |
| rc_N93798_at | N93798 | 2738 | protein tyrosine phosphatase type IVA, member 3 | 4.65 | up | 0.00118 |
| rc_N98464_s_at | N98464 | 2744 | EST | 15.95 | up | 0.00004 |
| rc_N98758_f_at | N98758 | 2745 | EST | 3.87 | up | 0.0074 |
| N99505_at | N99505 | 2746 | EST | 3.6 | up | 0.04499 |
| rc_R02036_at | R02036 | 2754 | EST | 8.01 | up | 0.01012 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_R06251_f_at | R06251 | 2764 | tumor protein D52-like 2 | 5.57 | up | 0.00037 |
| rc_R06254_f_at | R06254 | 2765 | tumor protein D52-like 2 | 4.64 | up | 0.00039 |
| rc_R06866_s_at | R06866 | 2774 | EST | 5.18 | up | 0.00187 |
| rc_R06986_f_at | R06986 | 2776 | peptidylprolyl isomerase B (cyclophilin B) | 3.01 | up | 0.04418 |
| rc_R22565_at | R22565 | 2800 | EST | 4.8 | up | 0.0424 |
| rc_R26706_s_at | R26706 | 2803 | EST | 3.21 | up | 0.03858 |
| rc_R26744_at | R26744 | 2804 | midline 1 (Opitz/BBB syndrome) | 4.32 | up | 0.00532 |
| rc_R27432_at | R27432 | 2808 | EST | 3.62 | up | 0.00014 |
| rc_R28636_at | R28636 | 2809 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3 | 3.78 | up | 0.00765 |
| rc_R31107_at | R31107 | 2812 | EST | 4.12 | up | 0.00003 |
| rc_R33498_s_at | R33498 | 2820 | EST | 41.34 | up | 0.00001 |
| rc_R36947_s_at | R36947 | 2825 | calcium channel, voltage-dependent, beta 3 subunit | 4.11 | up | 0.00006 |
| rc_R38076_s_at | R38076 | 2828 | EST | 4.08 | up | 0.00374 |
| rc_R38239_at | R38239 | 2830 | EST | 7.14 | up | 0.00249 |
| rc_R38280_at | R38280 | 2831 | BCS1 (yeast homolog)-like | 3.68 | up | 0.0009 |
| rc_R38511_s_at | R38511 | 2832 | protein similar to E.coli yhdg and R. capsulatus nifR3 | 5.19 | up | 0.00015 |
| rc_R39191_s_at | R39191 | 2834 | KIAA1020 protein | 4.69 | up | 0.00456 |
| rc_R40254_at | R40254 | 2840 | EST | 5.82 | up | 0.00304 |
| rc_R43952_at | R43952 | 2853 | homeo box B5 | 4.11 | up | 0.04316 |
| rc_R44479_at | R44479 | 2855 | KIAA0552 gene product | 4.14 | up | 0.0181 |
| rc_R44538_at | R44538 | 2856 | EST | 5.73 | up | 0.01015 |
| rc_R45698_at | R45698 | 2866 | EST | 3.01 | up | 0.04766 |
| rc_R45994_f_at | R45994 | 2867 | EST | 7.81 | up | 0.0018 |
| rc_R48447_at | R48447 | 2871 | EST | 7.75 | up | 0.00049 |
| rc_R48589_at | R48589 | 2874 | EST | 4.95 | up | 0.01346 |
| rc_R49084_s_at | R49084 | 2879 | KIAA0770 protein | 3.57 | up | 0.00447 |
| rc_R49216_at | R49216 | 2880 | EST | 3.64 | up | 0.0004 |
| rc_R49395_s_at | R49395 | 2881 | EST | 4.38 | up | 0.00112 |
| rc_R49476_at | R49476 | 2883 | EST | 10.95 | up | 0.00014 |
| rc_R52161_at | R52161 | 2893 | EST | 5.84 | up | 0.03253 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_R53109_f_at | R53109 | 2899 | dimethylarginine dimethylaminohydrolase 2 | 3.31 | up | 0.02389 |
| rc_R53109_r_at | R53109 | 2899 | dimethylarginine dimethylaminohydrolase 2 | 3.22 | up | 0.00724 |
| rc_R54614_s_at | R54614 | 2902 | EST | 3.24 | up | 0.00526 |
| rc_R55470_at | R55470 | 2904 | EST | 3.59 | up | 0.00515 |
| rc_R56095_s_at | R56095 | 2906 | EST | 8.16 | up | 0.00023 |
| R56678_at | R56678 | 2908 | EST | 3.81 | up | 0.02242 |
| rc_R56880_at | R56880 | 2909 | EST | 6.82 | up | 0.02559 |
| rc_R58974_at | R58974 | 2910 | EST | 4.95 | up | 0.00498 |
| rc_R59352_s_at | R59352 | 2915 | KIAA0296 gene product | 4.19 | up | 0.00393 |
| rc_R61297_s_at | R61297 | 2920 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | 6.42 | up | 0.00126 |
| R69700_at | R69700 | 2943 | EST | 6.71 | up | 0.0021 |
| rc_R70005_at | R70005 | 2944 | EST | 4.61 | up | 0.00037 |
| rc_R70801_s_at | R70801 | 2950 | EST | 6.36 | up | 0.00563 |
| rc_R71082_s_at | R71082 | 2951 | programmed cell death 5 | 3.6 | up | 0.01338 |
| rc_R71395_at | R71395 | 2952 | EST | 10.42 | up | 0.00422 |
| rc_R73565_at | R73565 | 2959 | EST | 3.29 | up | 0.03489 |
| rc_R76782_s_at | R76782 | 2963 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) | 5.83 | up | 0.01126 |
| rc_R77631_at | R77631 | 2967 | EST | 3.43 | up | 0.00006 |
| rc_R79580_at | R79580 | 2970 | EST | 6.25 | up | 0.00593 |
| rc_R87989_at | R87989 | 2979 | centrosome associated protein | 3.64 | up | 0.00008 |
| rc_R91819_at | R91819 | 2984 | EST | 8.95 | up | 0.00009 |
| rc_R92994_s_at | R92994 | 2990 | matrix metalloproteinase 12 (macrophage elastase) | 11.05 | up | 0.00248 |
| rc_R95966_i_at | R95966 | 2997 | EST | 11.22 | up | 0.00682 |
| rc_R96924_s_at | R96924 | 3001 | EST | 6.18 | up | 0.03417 |
| rc_R97759_at | R97759 | 3006 | serum/glucocorticoid regulated kinase | 5.99 | up | 0.00221 |
| S54005_s_at | S54005 | 3020 | thymosin, beta 10 | 7.03 | up | 0.00334 |
| S56151_s_at | S56151 | 3021 | milk fat globule-EGF factor 8 protein | 4.59 | up | 0.0091 |
| S69272_s_at | S69272 | 3028 | protease inhibitor 6 (placental thrombin inhibitor) | 5.15 | up | 0.00003 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| S73885_s_at | S73885 | 3032 | transcription factor AP-4 (activating enhancer-binding protein 4) | 4.18 | up | 0.00005 |
| S78187_at | S78187 | 3036 | cell division cycle 25B | 8.07 | up | 0.00009 |
| S81914_at | S81914 | 3038 | immediate early response 3 | 5.46 | up | 0.01798 |
| rc_T03313_at | T03313 | 3042 | dyskeratosis congenita 1, dyskerin | 9.63 | up | 0.00001 |
| rc_T03438_s_at | T03438 | 3043 | EST | 8.18 | up | 0.00032 |
| rc_T03580_f_at | T03580 | 3046 | pyruvate kinase, muscle | 24.91 | up | 0.0001 |
| rc_T12599_f_at | T12599 | 3056 | ribosomal protein L21 | 3.54 | up | 0.01437 |
| rc_T15442_f_at | T15442 | 3057 | calpain, large polypeptide L1 | 5.01 | up | 0.00255 |
| rc_T15473_at | T15473 | 3058 | muscle specific gene | 5.81 | up | 0.02404 |
| rc_T15477_at | T15477 | 3059 | EST | 3.61 | up | 0.00005 |
| rc_T15903_s_at | T15903 | 3063 | EST | 3.23 | up | 0.01377 |
| rc_T16308_f_at | T16308 | 3069 | EST | 5.29 | up | 0.00119 |
| rc_T16983_s_at | T16983 | 3074 | cleavage and polyadenylation specific factor 4, 30kD subunit | 5.23 | up | 0.00075 |
| rc_T23465_at | T23465 | 3081 | EST | 4.4 | up | 0.017 |
| rc_T23490_i_at | T23490 | 3082 | EST | 11.86 | up | 0.03242 |
| rc_T23516_f_at | T23516 | 3083 | 3-phosphoglycerate dehydrogenase | 5.38 | up | 0.00001 |
| rc_T24068_s_at | T24068 | 3088 | EST | 15.26 | up | 0.00046 |
| rc_T25725_at | T25725 | 3091 | EST | 3.26 | up | 0.00099 |
| rc_T26366_f_at | T26366 | 3093 | EST | 30.43 | up | 0.00153 |
| rc_T26471_at | T26471 | 3094 | EST | 4.62 | up | 0.01091 |
| rc_T26513_i_at | T26513 | 3095 | protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform | 5.07 | up | 0.0016 |
| rc_T26574_s_at | T26574 | 3096 | catenin (cadherin-associated protein), delta 1 | 3.17 | up | 0.00828 |
| rc_T30193_s_at | T30193 | 3098 | protease, serine, 8 (prostasin) | 8.39 | up | 0.00043 |
| rc_T32072_s_at | T32072 | 3102 | EST | 5.95 | up | 0.00029 |
| rc_T32108_at | T32108 | 3103 | EST | 6.96 | up | 0.00723 |
| rc_T33489_s_at | T33489 | 3105 | EST | 8.04 | up | 0.00469 |
| rc_T33508_s_at | T33508 | 3106 | phosphatidylinositol-4-phosphate 5-kinase, type II, beta | 3.31 | up | 0.00416 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| T35341_s_at | T35341 | 3112 | EST | 4.73 | up | 0.00057 |
| T35725_s_at | T35725 | 3113 | EST | 3.4 | up | 0.00149 |
| rc_T40849_s_at | T40849 | 3116 | maternal G10 transcript | 4.11 | up | 0.00449 |
| rc_T47032_s_at | T47032 | 3124 | partner of RAC1 (arfaplin 2) | 3.27 | up | 0.00503 |
| rc_T47325_s_at | T47325 | 3125 | EST | 5.63 | up | 0.01015 |
| rc_T47601_at | T47601 | 3126 | EST | 4.05 | up | 0.00878 |
| rc_T47969_s_at | T47969 | 3128 | ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeier-Vogt disease) | 3.03 | up | 0.03452 |
| T48195_s_at | T48195 | 3131 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) | 3.75 | up | 0.00012 |
| rc_T48293_f_at | T48293 | 3133 | EST | 3.55 | up | 0.01355 |
| rc_T53404_at | T53404 | 3143 | EST | 10.68 | up | 0.00582 |
| rc_T55004_s_at | T55004 | 3146 | EST | 4.83 | up | 0.00156 |
| rc_T55196_at | T55196 | 3147 | EST | 4.04 | up | 0.00012 |
| rc_T58153_s_at | T58153 | 3154 | heat shock 105kD | 3.08 | up | 0.01317 |
| rc_T58607_at | T58607 | 3155 | EST | 3.52 | up | 0.04102 |
| rc_T59161_s_at | T59161 | 3159 | thymosin, beta 10 | 3.41 | up | 0.01885 |
| rc_T59668_s_at | T59668 | 3160 | lysyl oxidase | 3.28 | up | 0.00588 |
| rc_T66935_at | T66935 | 3179 | EST | 3.97 | up | 0.00188 |
| rc_T77733_s_at | T77733 | 3219 | tubulin, gamma 1 | 4.42 | up | 0.00049 |
| rc_T78922_s_at | T78922 | 3222 | stem cell growth factor; lymphocyte secreted C-type lectin | 3.42 | up | 0.02419 |
| rc_T91116_at | T91116 | 3252 | EST | 4.01 | up | 0.02721 |
| rc_T92935_at | T92935 | 3255 | EST | 3.48 | up | 0.03578 |
| rc_T95057_f_at | T95057 | 3259 | EST | 10.39 | up | 0.00003 |
| rc_T98284_at | T98284 | 3268 | EST | 4.47 | up | 0.00054 |
| U01062_at | U01062 | 3273 | inositol 1,4,5-triphosphate receptor, type 3 | 7.41 | up | 0 |
| U01147_at | U01147 | 3275 | active BCR-related gene | 3.22 | up | 0.00103 |
| U02493_at | U02493 | 3279 | non-Pou domain-containing octamer (ATGCAAAAT) binding protein | 3.04 | up | 0.0019 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|---|-------------|-----------|---------|
| U03891_at | U03891 | 3283 | phorbolin (similar to apolipoprotein B mRNA editing protein) | 3 | up | 0.00065 |
| U04313_at | U04313 | 3284 | protease inhibitor 5 (maspin) | 4.54 | up | 0.02986 |
| U05875_at | U05875 | 3286 | interferon gamma receptor 2 (interferon gamma transducer 1) | 3.09 | up | 0.00549 |
| U07969_s_at | U07969 | 3289 | cadherin 17, LI cadherin (liver-intestine) | 10.78 | up | 0.02002 |
| U09117_at | U09117 | 3294 | phospholipase C, delta 1 | 7.96 | up | 0.00001 |
| U09564_at | U09564 | 3295 | SFRS protein kinase 1 | 3.79 | up | 0.00765 |
| U09770_at | U09770 | 3296 | cysteine-rich protein 1 (intestinal) | 13.03 | up | 0.0072 |
| U11861_at | U11861 | 3298 | maternal G10 transcript | 3.8 | up | 0.00001 |
| U12404_at | U12404 | 3299 | ribosomal protein L10a | 4.18 | up | 0.00004 |
| U12465_at | U12465 | 3300 | ribosomal protein L35 | 4.69 | up | 0.00001 |
| U14968_at | U14968 | 3303 | ribosomal protein L27a | 4.01 | up | 0.00003 |
| U14969_at | U14969 | 3304 | ribosomal protein L28 | 4.63 | up | 0.00004 |
| U14970_at | U14970 | 3305 | ribosomal protein S5 | 3.45 | up | 0.00915 |
| U14971_at | U14971 | 3306 | ribosomal protein S9 | 3.93 | up | 0.00026 |
| U14972_at | U14972 | 3307 | ribosomal protein S10 | 5.24 | up | 0.00077 |
| U14973_at | U14973 | 3308 | ribosomal protein S29 | 3.1 | up | 0.00028 |
| U15008_at | U15008 | 3309 | small nuclear ribonucleoprotein D2 polypeptide (16.5kD) | 4.9 | up | 0.00396 |
| U17077_at | U17077 | 3314 | BENE protein | 4.98 | up | 0.00366 |
| U17760_ma1_at | U17760 | 3315 | laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD)) | 3.54 | up | 0.01853 |
| U20499_at | U20499 | 3321 | sulfotransferase family 1A, phenol-preferring, member 3 | 5.5 | up | 0.00299 |
| U20758_ma1_at | U20758 | 3323 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | 6.12 | up | 0.03448 |
| U21049_at | U21049 | 3325 | epithelial protein up-regulated in carcinoma, membrane associated protein 17 | 7.53 | up | 0.01667 |
| U22376_cds2_s_at | U22376 | 3328 | v-myb avian myeloblastosis viral oncogene homolog | 3.34 | up | 0.03416 |
| U25789_at | U25789 | 3334 | ribosomal protein L21 | 4.37 | up | 0.00045 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|--|-------------|-----------|---------|
| U26726_at | U26726 | 3336 | hydroxysteroid (11-beta) dehydrogenase 2 | 3.45 | up | 0.02342 |
| U27328_s_at | U27328 | 3338 | fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included) | 3.05 | up | 0.03224 |
| U31556_at | U31556 | 3346 | E2F transcription factor 5, p130-binding | 4.14 | up | 0.01157 |
| U33286_at | U33286 | 3349 | chromosome segregation 1 (yeast homolog)-like | 3.39 | up | 0.00939 |
| U36341_rna1_at | U36341 | 3351 | solute carrier family 6 (neurotransmitter transporter, creatine), member 8 | 3.05 | up | 0.02622 |
| U37689_at | U37689 | 3356 | polymerase (RNA) II (DNA directed) polypeptide H | 3.65 | up | 0.00044 |
| U40990_at | U40990 | 3359 | potassium voltage-gated channel, KQT-like subfamily, member 1 | 3.18 | up | 0.00093 |
| U42408_at | U42408 | 3361 | ladinin 1 | 6.8 | up | 0.00305 |
| U43901_rna1_s_at | U43901 | 3362 | laminin receptor 1 (67kD, ribosomal protein SA) | 3.11 | up | 0.03145 |
| U46692_rna1_at | U46692 | 3367 | cystatin B (stefin B) | 5.54 | up | 0.00016 |
| U47025_s_at | U47025 | 3368 | phosphorylase, glycogen; brain | 8.52 | up | 0.00134 |
| U48705_rna1_s_at | U48705 | 3370 | discoidin domain receptor family, member 1 | 5.94 | up | 0.01323 |
| U51095_at | U51095 | 3382 | caudal type homeo box transcription factor 1 | 4.76 | up | 0.02664 |
| U51478_at | U51478 | 3385 | ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide | 5.75 | up | 0.00007 |
| U53347_at | U53347 | 3389 | solute carrier family 1 (neutral amino acid transporter), member 5 | 3.81 | up | 0.00273 |
| U53830_at | U53830 | 3391 | interferon regulatory factor 7 | 3.94 | up | 0.03147 |
| U58682_at | U58682 | 3396 | ribosomal protein S28 | 6.09 | up | 0.00001 |
| U62392_at | U62392 | 3403 | zinc finger protein 193 | 3.18 | up | 0.00269 |
| U62962_at | U62962 | 3404 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | 4.05 | up | 0.0047 |
| U67171_at | U67171 | 3409 | selenoprotein W, 1 | 3.08 | up | 0.0047 |
| U73379_at | U73379 | 3418 | ubiquitin carrier protein E2-C | 8.32 | up | 0.00101 |
| U73843_at | U73843 | 3421 | E74-like factor 3 (ets domain transcription factor) | 5.75 | up | 0.00017 |
| U75285_rna1_at | U75285 | 3422 | apoptosis inhibitor 4 (survivin) | 4.46 | up | 0.02212 |
| U76366_s_at | U76366 | 3424 | Treacher Collins-Franceschetti syndrome 1 | 3.44 | up | 0.00021 |
| U78027_rna3_at | U78027 | 3429 | EST | 4.15 | up | 0.00295 |
| U78095_at | U78095 | 3430 | serine protease inhibitor, Kunitz type, 2 | 18.85 | up | 0 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| U78525_at | U78525 | 3432 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) | 4.68 | up | 0.00132 |
| U78556_at | U78556 | 3433 | cisplatin resistance associated | 5.77 | up | 0.00241 |
| U79266_at | U79266 | 3434 | protein predicted by clone 23627 | 3.49 | up | 0.00004 |
| U79725_at | U79725 | 3438 | glycoprotein A33 (transmembrane) | 8.57 | up | 0.00299 |
| U83246_at | U83246 | 3443 | copine I | 3.57 | up | 0.01672 |
| U84720_at | U84720 | 3446 | RAE1 (RNA export 1, S.pombe) homolog | 3.37 | up | 0.03586 |
| U85773_at | U85773 | 3449 | phosphomannomutase 2 | 3.94 | up | 0.00288 |
| U86409_at | U86409 | 3450 | EST | 3.38 | up | 0.00003 |
| U89606_at | U89606 | 3452 | pyridoxal (pyridoxine, vitamin B6) kinase | 3.58 | up | 0.00322 |
| U90549_at | U90549 | 3456 | high-mobility group (nonhistone chromosomal) protein 17-like 3 | 3.2 | up | 0.0401 |
| U90913_at | U90913 | 3459 | Tax interaction protein 1 | 4.35 | up | 0.00159 |
| U93205_at | U93205 | 3461 | chloride intracellular channel 1 | 6.14 | up | 0.00058 |
| U93868_at | U93868 | 3463 | polymerase (RNA) III (DNA directed) (32kD) | 3.5 | up | 0.01235 |
| rc_W02041_at | W02041 | 3466 | EST | 4.83 | up | 0.00158 |
| rc_W20391_s_at | W20391 | 3479 | kinesin-like 2 | 3.98 | up | 0.01788 |
| W28362_at | W28362 | 3488 | KIAA0974 protein | 3.98 | up | 0.00626 |
| rc_W31382_at | W31382 | 3495 | EST | 4 | up | 0.00058 |
| rc_W37680_at | W37680 | 3503 | EST | 3.55 | up | 0.01036 |
| rc_W37937_at | W37937 | | EST | 3.07 | up | 0.00776 |
| rc_W38044_s_at | W38044 | | myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7 | 7.28 | up | 0.03105 |
| W39183_s_at | W39183 | 3508 | KIAA0601 protein | 3.66 | up | 0.00018 |
| rc_W42627_f_at | W42627 | 3511 | EST | 3.56 | up | 0.00198 |
| rc_W42957_at | W42957 | 3516 | calmodulin 2 (phosphorylase kinase, delta) | 15.22 | up | 0.00007 |
| rc_W44557_at | W44557 | 3518 | chromosome 1 open reading frame 2 | 4.32 | up | 0.00128 |
| rc_W44733_at | W44733 | 3519 | EST | 3.02 | up | 0.00097 |
| rc_W45487_s_at | W45487 | 3524 | dynamitin 2 | 4.2 | up | 0.00325 |
| rc_W49574_at | W49574 | 3538 | EST | 5.97 | up | 0.00045 |
| rc_W49661_s_at | W49661 | 3539 | FK506-binding protein 9 (63 kD) | 3.01 | up | 0.02259 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| W52858_at | W52858 | 3545 | DKFZP564F0522 protein | 4.38 | up | 0.00088 |
| rc_W60486_at | W60486 | 3558 | EST | 4.29 | up | 0.00964 |
| rc_W67251_s_at | W67251 | 3570 | EST | 6.13 | up | 0.01463 |
| rc_W70336_at | W70336 | 3579 | EST | 3.65 | up | 0.01776 |
| rc_W72276_at | W72276 | 3583 | EST | 27.39 | up | 0.00183 |
| rc_W72861_at | W72861 | 3586 | protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (lprn), alpha 3 | 3.01 | up | 0.00055 |
| rc_W73189_at | W73189 | 3589 | EphB2 | 3.69 | up | 0.02909 |
| rc_W73914_at | W73914 | 3595 | EST | 3.5 | up | 0.04782 |
| rc_W74233_s_at | W74233 | 3597 | related RAS viral (r-ras) oncogene homolog | 6.02 | up | 0.01815 |
| W76097_at | W76097 | 3599 | EST | 3.83 | up | 0.00001 |
| rc_W78057_at | W78057 | 3600 | EST | 9.06 | up | 0.0034 |
| rc_W80730_at | W80730 | 3607 | EST | 6.59 | up | 0.00425 |
| rc_W80763_at | W80763 | 3608 | EST | 3.83 | up | 0.01319 |
| rc_W81375_at | W81375 | 3613 | EST | 3.58 | up | 0.00322 |
| rc_W81540_at | W81540 | 3614 | serine/threonine kinase 24 (Ste20, yeast homolog) | 6.72 | up | 0.00164 |
| rc_W90146_f_at | W90146 | 3644 | EST | 6.23 | up | 0.01558 |
| rc_W92207_at | W92207 | 3651 | EST | 6.77 | up | 0.00002 |
| rc_W92449_at | W92449 | 3652 | EST | 31.67 | up | 0.00011 |
| rc_W92608_s_at | W92608 | 3653 | BAI1-associated protein 3 | 5.12 | up | 0.00075 |
| rc_W93726_s_at | W93726 | 3656 | protease inhibitor 5 (maspin) | 16.48 | up | 0.00014 |
| rc_W93943_at | W93943 | 3657 | EST | 4.3 | up | 0.00296 |
| W95348_at | W95348 | 3663 | HSPC113 protein | 10.89 | up | 0.01065 |
| rc_W95477_at | W95477 | 3664 | EST | 26.51 | up | 0.00161 |
| X03342_at | X03342 | 3675 | ribosomal protein L32 | 4.09 | up | 0.00008 |
| AFFX-CreX-5_at | X03453 | 3677 | EST | 3.03 | up | 0.0025 |
| X04347_s_at | X04347 | 3680 | heterogeneous nuclear ribonucleoprotein A1 | 7.26 | up | 0.00018 |
| X05610_at | X05610 | 3685 | collagen, type IV, alpha 2 | 3.58 | up | 0.01351 |
| X06617_at | X06617 | 3687 | ribosomal protein S11 | 4.32 | up | 0.0002 |
| X07820_at | X07820 | 3695 | matrix metalloproteinase 10 (stromelysin 2) | 3.49 | up | 0.00689 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| X12447_at | X12447 | 3696 | aldolase A, fructose-bisphosphate | 10.52 | up | 0.00038 |
| X13956_at | X13956 | 3701 | EST | 3.2 | up | 0.00321 |
| X14850_at | X14850 | 3706 | H2A histone family, member X | 4.11 | up | 0.0001 |
| X15940_at | X15940 | 3709 | ribosomal protein L31 | 4.45 | up | 0.00004 |
| X17093_at | X17093 | 3716 | EST | 4.82 | up | 0.00176 |
| X17206_at | X17206 | 3718 | ribosomal protein S2 | 5.14 | up | 0 |
| X17567_s_at | X17567 | 3719 | small nuclear ribonucleoprotein polypeptides B and B1 | 3.6 | up | 0.00586 |
| X51466_at | X51466 | 3720 | eukaryotic translation elongation factor 2 | 3.25 | up | 0.00019 |
| X51521_at | X51521 | 3721 | villin 2 (ezrin) | 3.89 | up | 0.00001 |
| X52851_rna1_at | X52851 | 3725 | EST | 3.38 | up | 0.0001 |
| X52966_at | X52966 | 3726 | ribosomal protein L35a | 3.93 | up | 0.00217 |
| X53331_at | X53331 | 3727 | matrix Gla protein | 3.66 | up | 0.04038 |
| X54667_s_at | X54667 | 3731 | cystatin S, cystatin SN | 8.53 | up | 0.00059 |
| X55715_at | X55715 | 3735 | ribosomal protein S3 | 3.72 | up | 0.00755 |
| X55954_at | X55954 | 3736 | ribosomal protein L23 | 3.81 | up | 0.00025 |
| X56494_at | X56494 | 3738 | pyruvate kinase, muscle | 22.97 | up | 0.00001 |
| X56932_at | X56932 | 3740 | ribosomal protein L13a | 3.26 | up | 0 |
| X56997_rna1_at | X56997 | 3741 | ubiquitin A-52 residue ribosomal protein fusion product 1 | 3.18 | up | 0.00006 |
| X57348_s_at | X57348 | 3744 | stratifin | 12.53 | up | 0.0013 |
| X62535_at | X62535 | 3756 | diacylglycerol kinase, alpha (80kD) | 4.72 | up | 0.00315 |
| X62691_at | X62691 | 3757 | ribosomal protein S15a | 4.09 | up | 0.00005 |
| X63527_at | X63527 | 3761 | ribosomal protein L19 | 3.17 | up | 0.02488 |
| X63629_at | X63629 | 3762 | cadherin 3, P-cadherin (placental) | 3.02 | up | 0.01654 |
| X64364_at | X64364 | 3764 | basigin | 6.45 | up | 0.00041 |
| X64707_at | X64707 | 3765 | ribosomal protein L13 | 4.28 | up | 0.00257 |
| X65614_at | X65614 | 3767 | S100 calcium-binding protein P | 12.2 | up | 0.00065 |
| X66364_at | X66364 | 3770 | cyclin-dependent kinase 5 | 3.55 | up | 0.02824 |
| | | | proteasome (prosome, macropain) subunit, beta type, 9 (large | | | |
| X66401_cds1_at | X66401 | 3771 | multifunctional protease 2) | 3.68 | up | 0.01385 |
| X66899_at | X66899 | 3772 | Ewing sarcoma breakpoint region 1 | 4.72 | up | 0.00011 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-----------------|---------|--------|---|-------------|-----------|---------|
| X67247_ma1_at | X67247 | 3774 | mitogen-activated protein kinase kinase kinase kinase 3 | 3.48 | up | 0.00012 |
| X67325_at | X67325 | 3775 | interferon, alpha-inducible protein 27 | 9.67 | up | 0.03245 |
| X68314_at | X68314 | 3778 | glutathione peroxidase 2 (gastrointestinal) | 14.4 | up | 0.00222 |
| X68688_ma1_s_at | X68688 | 3780 | zinc finger protein 33a (KOX 31) | 4.7 | up | 0.00062 |
| X68688_ma1_s_at | X68688 | 3780 | zinc finger protein 33a (KOX 31) | 3.62 | up | 0.00319 |
| X69150_at | X69150 | 3782 | ribosomal protein S18 | 4.5 | up | 0.00003 |
| X69391_at | X69391 | 3783 | ribosomal protein L6 | 3.18 | up | 0.00003 |
| | | | CD47 antigen (Rh-related antigen, integrin-associated signal transducer) | | | |
| X69398_at | X69398 | 3784 | transducer | 3.68 | up | 0.02332 |
| X69654_at | X69654 | 3785 | ribosomal protein S26 | 3.11 | up | 0.02683 |
| | | | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 | | | |
| X69908_ma1_at | X69908 | 3786 | macrophage stimulating 1 receptor (c-met-related tyrosine kinase) | 3.73 | up | 0.00685 |
| X70040_at | X70040 | 3788 | kinase | 4 | up | 0.00402 |
| X74929_s_at | X74929 | 3792 | keratin 8 | 4.73 | up | 0.00018 |
| X76180_at | X76180 | 3795 | sodium channel, nonvoltage-gated 1 alpha | 11.68 | up | 0 |
| X77588_s_at | X77588 | 3799 | N-acetyltransferase, homolog of S. cerevisiae ARD1 | 3.91 | up | 0.0221 |
| X78687_at | X78687 | 3800 | sialidase 1 (lysosomal sialidase) | 3.18 | up | 0.031 |
| X79234_at | X79234 | 3803 | ribosomal protein L11 | 3.59 | up | 0.00051 |
| X79882_at | X79882 | 3805 | lung resistance-related protein | 6.71 | up | 0.0362 |
| X80198_at | X80198 | 3807 | steroidogenic acute regulatory protein related | 3.03 | up | 0.00044 |
| X80822_at | X80822 | 3808 | ribosomal protein L18a | 4.13 | up | 0.0006 |
| X80822_f_at | X80822 | 3808 | ribosomal protein L18a | 3.08 | up | 0.02481 |
| X80909_at | X80909 | 3809 | nascent-polypeptide-associated complex alpha polypeptide | 3.84 | up | 0.00399 |
| X83228_at | X83228 | 3810 | cadherin 17, L1 cadherin (liver-intestine) | 10.58 | up | 0.02147 |
| X89960_at | X89960 | 3818 | EST | 9.87 | up | 0 |
| | | | high-mobility group (nonhistone chromosomal) protein isoform I-C | | | |
| X92518_s_at | X92518 | 3825 | C | 3.12 | up | 0.00638 |
| X93036_at | X93036 | 3830 | FXYD domain-containing ion transport regulator 3 | 42.36 | up | 0.00167 |

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| X95404_at | X95404 | 3834 | cofilin 1 (non-muscle) | 3.18 | up | 0.00104 |
| X98482_r_at | X98482 | 3841 | EST | 5.03 | up | 0.00002 |
| X99133_at | X99133 | 3842 | lipocalin 2 (oncogene 24p3) | 6.27 | up | 0.0453 |
| Y00503_at | Y00503 | 3849 | keratin 19 | 14.19 | up | 0.00217 |
| Y00705_at | Y00705 | 3850 | serine protease inhibitor, Kazal type 1 | 9.83 | up | 0.03697 |
| Y10807_s_at | Y10807 | 3860 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2 | 4.28 | up | 0.00124 |
| Z23090_at | Z23090 | 3868 | heat shock 27kD protein 1 | 7.67 | up | 0.00008 |
| Z24727_at | Z24727 | 3871 | tropomyosin 1 (alpha) | 4.47 | up | 0.00121 |
| Z25749_rna1_at | Z25749 | 3872 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2 | 4.41 | up | 0.00031 |
| Z26876_at | Z26876 | 3874 | ribosomal protein L38 | 4.43 | up | 0.00022 |
| Z28407_at | Z28407 | 3876 | ribosomal protein L8 | 6.53 | up | 0.00004 |
| Z30643_at | Z30643 | 3879 | chloride channel Ka | 3.86 | up | 0.00204 |
| rc_Z38150_s_at | Z38150 | 3883 | EST | 3.06 | up | 0.00049 |
| rc_Z38266_at | Z38266 | 3886 | EST | 6.58 | up | 0.01909 |
| rc_Z38729_at | Z38729 | 3894 | EST | 3.13 | up | 0.04514 |
| rc_Z38909_at | Z38909 | 3897 | EST | 3.55 | up | 0.03195 |
| rc_Z39079_at | Z39079 | 3900 | KIAA1058 protein | 4.08 | up | 0.01781 |
| rc_Z39191_at | Z39191 | 3901 | EST | 8.84 | up | 0.00011 |
| rc_Z39200_at | Z39200 | 3902 | EST | 3.29 | up | 0.00586 |
| rc_Z39429_at | Z39429 | 3906 | EST | 7.84 | up | 0.00045 |
| rc_Z39930_f_at | Z39930 | 3914 | EST | 3.07 | up | 0.00002 |
| rc_Z40583_f_at | Z40583 | 3922 | EST | 4.24 | up | 0.02375 |
| rc_Z40898_at | Z40898 | 3925 | EST | 3.71 | up | 0.01168 |
| rc_Z40945_at | Z40945 | 3927 | trinucleotide repeat containing 15 | 7.82 | up | 0.00007 |
| rc_Z41103_at | Z41103 | 3929 | trinucleotide repeat containing 15 | 3.83 | up | 0.00444 |
| rc_Z41740_s_at | Z41740 | 3935 | EST | 6.76 | up | 0.00049 |
| rc_Z41798_s_at | Z41798 | 3937 | EST | 6 | up | 0.00073 |
| Z68228_s_at | Z68228 | 3947 | junction plakoglobin | 3.3 | up | 0.0237 |
| Z74615_at | Z74615 | 3949 | collagen, type I, alpha 1 | 10.47 | up | 0.00064 |
| Z74616_s_at | Z74616 | 3950 | collagen, type I, alpha 2 | 4.83 | up | 0.02364 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA001603_at | AA001603 | 3 | EST | 4.31 | down | 0.00883 |
| rc_AA001604_at | AA001604 | 4 | EST | 3.33 | down | 0.0215 |
| AA004231_at | AA004231 | 7 | EST | 3.16 | down | 0.03067 |
| rc_AA004521_at | AA004521 | 8 | prostate cancer overexpressed gene 1 | 8.03 | down | 0.00027 |
| rc_AA004905_at | AA004905 | 11 | KIAA0937 protein | 4.63 | down | 0.00082 |
| rc_AA005202_at | AA005202 | 12 | retinol-binding protein 4, interstitial | 3.18 | down | 0.00106 |
| rc_AA005358_at | AA005358 | 14 | EST | 5.2 | down | 0.00318 |
| rc_AA007629_at | AA007629 | 19 | EST | 8.01 | down | 0.00001 |
| rc_AA009719_at | AA009719 | 20 | peroxisomal membrane protein 2 (22kD) | 47.12 | down | 0.00008 |
| rc_AA010205_at | AA010205 | 23 | EST | 7.41 | down | 0 |
| rc_AA010360_at | AA010360 | 24 | EST | 6.55 | down | 0.00027 |
| rc_AA010530_at | AA010530 | 25 | EST | 3.74 | down | 0.0481 |
| rc_AA010619_at | AA010619 | 27 | EST | 8.55 | down | 0.00057 |
| AA010750_at | AA010750 | 28 | calmodulin 1 (phosphorylase kinase, delta) | 10.22 | down | 0.00959 |
| rc_AA015768_at | AA015768 | 34 | EST | 15.3 | down | 0.00008 |
| rc_AA017146_at | AA017146 | 36 | EST | 10.1 | down | 0.00052 |
| rc_AA017192_at | AA017192 | 37 | EST | 3.43 | down | 0.04865 |
| rc_AA018867_at | AA018867 | 39 | EST | 42.87 | down | 0.00002 |
| rc_AA021623_s_at | AA021623 | 43 | insulin induced gene 1 | 11.71 | down | 0.00094 |
| rc_AA025930_at | AA025930 | 52 | EST | 3.59 | down | 0.00372 |
| rc_AA031543_s_at | AA031543 | 68 | translocation protein 1 | 5.92 | down | 0.00405 |
| AA031548_at | AA031548 | 69 | cell division cycle 42 (GTP-binding protein, 25kD) | 3.65 | down | 0.03029 |
| rc_AA032005_at | AA032005 | 71 | EST | 5.3 | down | 0.01202 |
| AA032048_at | AA032048 | 72 | EST | 5.45 | down | 0.00383 |
| rc_AA032250_at | AA032250 | 73 | EST | 3.56 | down | 0.0009 |
| rc_AA034030_at | AA034030 | 75 | methylmalonyl Coenzyme A mutase | 14.32 | down | 0.00004 |
| rc_AA035245_s_at | AA035245 | 79 | aldehyde oxidase 1 | 69.82 | down | 0.00117 |
| rc_AA035457_at | AA035457 | 80 | EST | 10.06 | down | 0.00085 |
| rc_AA035638_at | AA035638 | 82 | EST | 9.91 | down | 0.00541 |
| rc_AA036662_s_at | AA036662 | 83 | EST | 4.16 | down | 0.00235 |
| rc_AA037357_f_at | AA037357 | 85 | EST | 3.53 | down | 0.02129 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA039335_s_at | AA039335 | 89 | coagulation factor XII (Hageman factor) | 32 | down | 0.0029 |
| rc_AA039616_at | AA039616 | 90 | EST | 9.36 | down | 0.00009 |
| AA039806_at | AA039806 | 91 | msh (Drosophila) homeo box homolog 1 | 3.53 | down | 0.00114 |
| rc_AA040087_at | AA040087 | 92 | EST | 4.13 | down | 0.00123 |
| rc_AA040270_at | AA040270 | 93 | EST | 3.03 | down | 0.01367 |
| rc_AA040291_at | AA040291 | 94 | KIAA0669 gene product | 3.55 | down | 0.00308 |
| rc_AA043501_at | AA043501 | 98 | v-maf musculoaponeurotic fibrosarcoma (avian) | 3.81 | down | 0.01304 |
| AA044622_at | AA044622 | 103 | EST | 3.62 | down | 0.03789 |
| AA044755_s_at | AA044755 | 104 | EST | 6.7 | down | 0.01228 |
| AA044842_at | AA044842 | 105 | Autosomal Highly Conserved Protein | 5.21 | down | 0.0009 |
| AA045870_at | AA045870 | 108 | EST | 5.93 | down | 0.00017 |
| rc_AA046457_at | AA046457 | 111 | EST | 3.2 | down | 0.00513 |
| AA046674_at | AA046674 | 112 | EST | 5.17 | down | 0.02561 |
| rc_AA046747_at | AA046747 | 114 | EST | 4.82 | down | 0.00022 |
| AA046840_at | AA046840 | 115 | CCAAT/enhancer binding protein (C/EBP), delta | 3.79 | down | 0.03319 |
| AA047151_at | AA047151 | 116 | EST | 7.13 | down | 0.00007 |
| rc_AA047187_at | AA047187 | 117 | EST | 3.04 | down | 0.04306 |
| rc_AA047290_at | AA047290 | 118 | EST | 3.39 | down | 0.00024 |
| rc_AA052980_at | AA052980 | 122 | EST | 4.52 | down | 0.023 |
| rc_AA055992_at | AA055992 | 136 | calumenin | 3.51 | down | 0.00604 |
| AA056170_at | AA056170 | 137 | EST | 3.82 | down | 0.0083 |
| rc_AA056247_at | AA056247 | 138 | EST | 3.48 | down | 0.03277 |
| rc_AA056482_at | AA056482 | 141 | EST | 4.82 | down | 0.00199 |
| rc_AA057678_at | AA057678 | 143 | EST | 6.88 | down | 0.00078 |
| AA059489_at | AA059489 | 145 | RGC32 protein | 3.74 | down | 0.00734 |
| rc_AA062744_at | AA062744 | 147 | EST | 3.31 | down | 0.01909 |
| rc_AA065173_at | AA065173 | 148 | EST | 4.08 | down | 0.00377 |
| rc_AA069456_at | AA069456 | 149 | KIAA0438 gene product | 3.47 | down | 0.02718 |
| rc_AA069768_s_at | AA069768 | 151 | hevin | 4.62 | down | 0.00202 |
| AA070090_at | AA070090 | 152 | EST | 3.24 | down | 0.00804 |
| rc_AA070091_at | AA070091 | 153 | EST | 5 | down | 0 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA074885_at | AA074885 | 161 | macrophage receptor with collagenous structure | 11.05 | down | 0.00786 |
| rc_AA074891_at | AA074891 | 162 | EST | 3.12 | down | 0.01897 |
| rc_AA076238_at | AA076238 | 168 | EST | 3.23 | down | 0.00395 |
| rc_AA076249_at | AA076249 | 169 | EST | 3.78 | down | 0.00029 |
| rc_AA076326_at | AA076326 | 170 | SEC14 (S. cerevisiae)-like 2 | 10.88 | down | 0.00616 |
| rc_AA079758_f_at | AA079758 | 174 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 7.83 | down | 0.00359 |
| rc_AA083812_at | AA083812 | 175 | DKFZP566F123 protein | 9.11 | down | 0.00167 |
| rc_AA084408_at | AA084408 | 179 | EST | 4.05 | down | 0.00864 |
| rc_aa084668_at | AA084668 | 180 | ubiquitin-like 3 | 3.19 | down | 0.0419 |
| rc_AA085987_s_at | AA085987 | 183 | UDP glycosyltransferase 1 | 40.87 | down | 0.00004 |
| rc_AA086201_at | AA086201 | 185 | EST | 5.8 | down | 0.00012 |
| rc_AA088698_at | AA088698 | 188 | EST | 3.23 | down | 0.02543 |
| AA090257_at | AA090257 | 190 | superoxide dismutase 2, mitochondrial | 11.72 | down | 0.02072 |
| AA090434_at | AA090434 | 191 | diaphanous (Drosophila, homolog) 1 | 4.61 | down | 0.01704 |
| AA090439_at | AA090439 | 192 | ribosomal protein S6 | 5.58 | down | 0.00501 |
| AA092596_at | AA092596 | 197 | bone morphogenetic protein 6 | 3.46 | down | 0.02532 |
| AA092716_at | AA092716 | 198 | HLA-B associated transcript-3 | 13.97 | down | 0.00009 |
| AA093923_at | AA093923 | 200 | EST | 3.82 | down | 0.03924 |
| AA094507_s_at | AA094507 | 201 | EST | 3.52 | down | 0.04783 |
| AA094999_at | AA094999 | 204 | zinc finger protein 216 | 5.12 | down | 0.0257 |
| rc_AA099225_at | AA099225 | 206 | EST | 7.33 | down | 0.00062 |
| AA099391_s_at | AA099391 | 207 | myosin, light polypeptide kinase | 9.07 | down | 0.00003 |
| rc_AA099589_s_at | AA099589 | 210 | GDP dissociation inhibitor 2 | 3.7 | down | 0.04069 |
| rc_AA101055_s_at | AA101055 | 213 | leptin receptor | 3.14 | down | 0.0071 |
| rc_AA101235_at | AA101235 | 214 | EST | 8.46 | down | 0.00822 |
| rc_AA101632_at | AA101632 | 217 | EST | 4.19 | down | 0.00023 |
| rc_AA112101_f_at | AA112101 | 222 | EST | 8.5 | down | 0.00004 |
| rc_AA112209_s_at | AA112209 | 223 | acyl-Coenzyme A dehydrogenase, long chain UDP-N-acetylglucosamine pyrophosphorylase 1; Sperm associated antigen 2 | 3.37 | down | 0.00084 |
| AA114949_at | AA114949 | 228 | | 5.12 | down | 0.01028 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA121140_at | AA121140 | 235 | EST | 3.33 | down | 0.00058 |
| rc_AA122345_f_at | AA122345 | 238 | glutamate dehydrogenase 1 | 16.53 | down | 0.00004 |
| rc_AA125831_t_at | AA125831 | 241 | myosin, light polypeptide kinase | 8.18 | down | 0.00039 |
| rc_AA125856_at | AA125856 | 242 | EST | 3.17 | down | 0.01545 |
| rc_AA125861_at | AA125861 | 243 | EST | 3.69 | down | 0.01547 |
| rc_AA126059_at | AA126059 | 246 | EST | 3.08 | down | 0.00706 |
| rc_AA126722_s_at | AA126722 | 251 | O-6-methylguanine-DNA methyltransferase | 8.26 | down | 0.002 |
| rc_AA127444_at | AA127444 | 252 | EST | 3.56 | down | 0.0291 |
| rc_AA127514_at | AA127514 | 253 | EST | 3.4 | down | 0.00045 |
| rc_AA133215_at | AA133215 | 277 | calcitonin receptor-like receptor activity modifying | 4.55 | down | 0.02092 |
| rc_AA133296_at | AA133296 | 278 | EST | 4.23 | down | 0.00041 |
| rc_AA133439_at | AA133439 | 279 | EST | 4.07 | down | 0.00022 |
| rc_AA134549_at | AA134549 | 288 | EST | 3.36 | down | 0.03438 |
| rc_AA135558_s_at | AA135558 | 293 | peptidase D | 4.17 | down | 0.0068 |
| rc_AA135958_at | AA135958 | 296 | EST | 4.02 | down | 0.00012 |
| rc_AA136079_at | AA136079 | 297 | EST | 4.26 | down | 0.0057 |
| rc_AA142849_at | AA142849 | 306 | EST | 7.59 | down | 0.00804 |
| AA143019_at | AA143019 | 309 | EST | 6.75 | down | 0.00109 |
| rc_aa147646_s_at | AA147646 | 317 | DKFZP586A0522 protein | 21.82 | down | 0 |
| rc_AA148480_s_at | AA148480 | 318 | flavin containing monooxygenase 5 | 19.64 | down | 0 |
| rc_AA148923_at | AA148923 | 321 | decidual protein induced by progesterone | 13.2 | down | 0.00257 |
| rc_AA149253_at | AA149253 | 323 | EST | 5.12 | down | 0.00863 |
| rc_AA150776_at | AA150776 | 330 | EST | 10.45 | down | 0.00015 |
| rc_AA150891_at | AA150891 | 331 | EST | 4.22 | down | 0.01692 |
| rc_AA151210_at | AA151210 | 333 | EST | 4.61 | down | 0.00008 |
| rc_AA151676_at | AA151676 | 337 | peptidyl arginine deiminase, type II | 4.01 | down | 0.00911 |
| rc_AA156336_at | AA156336 | 341 | nuclear receptor co-repressor 1 | 3.69 | down | 0.01276 |
| | | | 4-nitrophenylphosphatase domain and non- | | | |
| rc_AA156565_at | AA156565 | 344 | neuronal SNAP25-like 1 | 15.01 | down | 0.01387 |
| rc_AA157112_at | AA157112 | 345 | EST | 3.94 | down | 0.02571 |
| AA157520_at | AA157520 | 347 | EST | 3.18 | down | 0.00516 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Atfy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA157799_at | AA157799 | 348 | aldo-keto reductase family 7, member A2 | 5.96 | down | 0 |
| rc_AA164586_s_at | AA164586 | 359 | (afatoxin aldehyde reductase) | 5.8 | down | 0.00182 |
| rc_AA167565_at | AA167565 | 362 | estrogen receptor 1 | 8.08 | down | 0.00046 |
| rc_AA171694_at | AA171694 | 366 | EST | 21.23 | down | 0.00179 |
| rc_AA172372_at | AA172372 | 370 | ceruloplasmin (ferroxidase) | 6.48 | down | 0.00344 |
| rc_AA176233_at | AA176233 | 376 | EST | 11.44 | down | 0.01856 |
| rc_AA179004_at | AA179004 | 377 | EST | 14.34 | down | 0.00008 |
| rc_AA179387_at | AA179387 | 379 | DKFZP434N126 protein | 3.7 | down | 0.01588 |
| rc_AA180356_at | AA180356 | 382 | EST | 3.16 | down | 0.00917 |
| rc_AA182030_at | AA182030 | 387 | EST | 8.32 | down | 0.00018 |
| rc_AA182568_at | AA182568 | 388 | STAT induced STAT inhibitor-2 | 10.92 | down | 0.00099 |
| AA188921_at | AA188921 | 393 | similar to Caenorhabditis elegans protein | 4.05 | down | 0.004 |
| rc_AA190816_at | AA190816 | 395 | EST | 4.1 | down | 0.00037 |
| rc_AA191014_at | AA191014 | 396 | EST | 5.07 | down | 0.01455 |
| rc_AA191310_s_at | AA191310 | 397 | protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform | 7.28 | down | 0 |
| rc_AA191488_s_at | AA191488 | 398 | solute carrier family 31 (copper transporters), ceruloplasmin (ferroxidase) | 3.19 | down | 0.00013 |
| rc_AA191647_at | AA191647 | 399 | Arg/Abl-interacting protein ArgBP2 | 4.05 | down | 0.00029 |
| rc_AA193204_at | AA193204 | 402 | EST | 8.98 | down | 0.00861 |
| rc_AA193223_at | AA193223 | 403 | EST | 4.2 | down | 0.02416 |
| AA193297_at | AA193297 | 404 | EST | 4.37 | down | 0.04676 |
| rc_AA194075_f_at | AA194075 | 406 | nuclear receptor coactivator 4 | 4.69 | down | 0.00862 |
| AA194146_at | AA194146 | 407 | EST | 3.53 | down | 0.00352 |
| rc_AA194833_at | AA194833 | 411 | claudin 1 | 11.45 | down | 0.00034 |
| rc_AA194997_s_at | AA194997 | 412 | EST | 16.12 | down | 0.00103 |
| rc_AA195656_at | AA195656 | 418 | KIAA0977 protein | 15.29 | down | 0.00817 |
| rc_AA195657_at | AA195657 | 419 | EST | 6.44 | down | 0.00016 |
| rc_AA196287_at | AA196287 | 420 | EST | 15.07 | down | 0.00001 |
| rc_AA197311_s_at | AA197311 | 422 | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor | 6.07 | down | 0.00053 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| AA203222_at | AA203222 | 424 | FERM, RhoGEF (ARHGEF) and pleckstrin | 4.21 | down | 0.00745 |
| rc_AA205724_at | AA205724 | 426 | domain protein 1 (chondrocyte-derived) | 6.73 | down | 0.00027 |
| rc_AA207123_at | AA207123 | 430 | EST | 3.16 | down | 0.00328 |
| rc_AA210850_at | AA210850 | 431 | immunoglobulin superfamily, member 3 | 4.97 | down | 0.00735 |
| rc_AA211388_at | AA211388 | 433 | EST | 4.56 | down | 0.02703 |
| rc_AA214542_at | AA214542 | 438 | EST | 4.43 | down | 0.00601 |
| rc_AA215585_s_at | AA215585 | 442 | nudix (nucleoside diphosphate linked moiety X)- | 3 | down | 0.03027 |
| AA215919_at | AA215919 | 443 | F-box protein 7 | 6.62 | down | 0.00921 |
| rc_AA218727_at | AA218727 | 445 | EST | 3.47 | down | 0.00125 |
| rc_AA219039_at | AA219039 | 446 | EST | 5.76 | down | 0.00053 |
| rc_AA219304_s_at | AA219304 | 447 | alpha-2-macroglobulin | 21.97 | down | 0.00011 |
| rc_AA219653_at | AA219653 | 448 | EST | 4.08 | down | 0.00607 |
| rc_AA223335_s_at | AA223335 | 449 | propionyl Coenzyme A carboxylase, beta | 5.49 | down | 0.02761 |
| rc_AA223902_at | AA223902 | 450 | EST | 9.91 | down | 0.00003 |
| rc_AA227452_at | AA227452 | 455 | EST | 4.7 | down | 0.02345 |
| rc_AA227480_s_at | AA227480 | 456 | pim-2 oncogene | 3.31 | down | 0.02413 |
| rc_AA227901_at | AA227901 | 459 | SEC24 (S. cerevisiae) related gene family, | 3.18 | down | 0.00397 |
| rc_AA228119_at | AA228119 | 462 | pre-B-cell colony-enhancing factor | 4.77 | down | 0.00031 |
| rc_AA232114_s_at | AA232114 | 463 | epoxide hydrolase 2, cytoplasmic | 24.34 | down | 0.00007 |
| rc_AA233152_at | AA233152 | 467 | EST | 12.95 | down | 0 |
| rc_AA233347_at | AA233347 | 470 | zinc finger protein 216 | 5.9 | down | 0.0041 |
| rc_AA233369_at | AA233369 | 471 | histidine ammonia-lyase | 9.06 | down | 0.0008 |
| rc_AA233763_at | AA233763 | 472 | EST | 4.61 | down | 0.00004 |
| rc_AA233837_at | AA233837 | 474 | EST | 4.79 | down | 0.0034 |
| rc_AA234095_at | AA234095 | 478 | EST | 8.08 | down | 0.00394 |
| rc_AA234527_s_at | AA234527 | 483 | nuclear receptor subfamily 3, group C, member 1 | 6.19 | down | 0.00864 |
| rc_AA234561_at | AA234561 | 485 | EST | 3.88 | down | 0.02058 |
| AA234634_f_at | AA234634 | 486 | CCAAT/enhancer binding protein (C/EBP), delta | 7.48 | down | 0.03318 |
| AA234817_at | AA234817 | 490 | EST | 6.22 | down | 0.00099 |
| rc_AA234831_at | AA234831 | 491 | EST | 3.42 | down | 0.00206 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA234916_at | AA234916 | 492 | EST | 3.2 | down | 0.00799 |
| rc_AA235233_at | AA235233 | 493 | EST | 6.59 | down | 0.00755 |
| rc_AA235288_at | AA235288 | 494 | PTPL1-associated RhoGAP 1 | 3.7 | down | 0.00643 |
| rc_AA235310_at | AA235310 | 496 | EST | 37.86 | down | 0.00091 |
| rc_AA235507_at | AA235507 | 498 | golgi autoantigen, golgin subfamily a, 5 | 3.28 | down | 0.00249 |
| rc_AA235618_f_at | AA235618 | 499 | EST | 3.43 | down | 0.02127 |
| rc_AA235765_s_at | AA235765 | 501 | KIAA0214 gene product | 3.59 | down | 0.01148 |
| rc_AA235811_at | AA235811 | 502 | EST | 3.64 | down | 0.01272 |
| rc_AA235873_s_at | AA235873 | 505 | H factor (complement)-like 1, H factor 1 | 9.98 | down | 0.01667 |
| rc_AA236230_at | AA236230 | 508 | EST | 5.28 | down | 0.01517 |
| rc_AA236365_s_at | AA236365 | 509 | 3-phosphoglycerate dehydrogenase | 10.23 | down | 0.00562 |
| rc_AA236401_at | AA236401 | 510 | EST | 16.71 | down | 0.00088 |
| rc_AA236455_r_at | AA236455 | 512 | EST | 15.71 | down | 0.00286 |
| rc_AA236455_s_at | AA236455 | 512 | EST | 11.35 | down | 0.02859 |
| rc_AA236796_s_at | AA236796 | 517 | folliculin | 8.74 | down | 0.00862 |
| rc_AA236942_at | AA236942 | 519 | EST | 3.18 | down | 0 |
| rc_AA236982_at | AA236982 | 520 | sterol carrier protein 2 | 5.56 | down | 0.01542 |
| rc_AA242766_at | AA242766 | 523 | EST | 3.58 | down | 0.0151 |
| rc_AA243495_at | AA243495 | 528 | lectin, mannose-binding, 1 | 4.23 | down | 0.00179 |
| rc_AA243582_at | AA243582 | 529 | hemoglobin, gamma A | 7.15 | down | 0.0021 |
| rc_AA243595_s_at | AA243595 | 530 | EST | 3.11 | down | 0.008 |
| AA247453_at | AA247453 | 533 | EST | 3.09 | down | 0.0015 |
| rc_AA250744_at | AA250744 | 536 | EST | 3.39 | down | 0.01137 |
| rc_AA250775_at | AA250775 | 537 | EST | 4.52 | down | 0.01752 |
| rc_AA251114_at | AA251114 | 539 | prostate cancer overexpressed gene 1 | 6.6 | down | 0.00039 |
| rc_AA251837_at | AA251837 | 547 | EST | 3.87 | down | 0.00782 |
| rc_AA252289_at | AA252289 | 552 | quinolate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) | 5.66 | down | 0.01389 |
| rc_AA252365_at | AA252365 | 554 | EST | 3.9 | down | 0.01796 |
| rc_AA253043_at | AA253043 | 559 | DKFZP58611419 protein | 3.89 | down | 0.00145 |
| AA253129_at | AA253129 | 560 | F-box protein FBL11 | 6.47 | down | 0.00001 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|----------------------------|-------------|-----------|---------|
| rc_AA253216_at | AA253216 | 561 | EST | 28.18 | down | 0.00141 |
| rc_AA253369_s_at | AA253369 | 563 | EST | 15.59 | down | 0.00091 |
| rc_AA253455_s_at | AA253455 | 565 | EST | 3.05 | down | 0.00533 |
| rc_AA253459_at | AA253459 | 566 | EST | 4.51 | down | 0.00419 |
| rc_AA255546_at | AA255546 | 569 | EST | 4 | down | 0.00301 |
| rc_AA255624_at | AA255624 | 571 | EST | 4.06 | down | 0.00069 |
| rc_AA255878_at | AA255878 | 572 | KIAA0767 protein | 3.96 | down | 0.00592 |
| rc_AA255903_at | AA255903 | 573 | CD39-like 4 | 5.67 | down | 0.01687 |
| rc_AA256171_at | AA256171 | 575 | EST | 7.34 | down | 0.04562 |
| rc_AA256341_at | AA256341 | 578 | EST | 7.37 | down | 0.00091 |
| rc_AA256367_s_at | AA256367 | 579 | paraoxonase 3 | 70.33 | down | 0.00192 |
| rc_AA256666_at | AA256666 | 583 | EST | 4.63 | down | 0.0018 |
| rc_AA257057_s_at | AA257057 | 586 | EST | 8.11 | down | 0.00379 |
| rc_AA258308_at | AA258308 | 590 | EST | 5.4 | down | 0.00023 |
| rc_AA258323_at | AA258323 | 591 | EST | 4.31 | down | 0.00046 |
| rc_AA258350_at | AA258350 | 592 | EST | 5.08 | down | 0.00035 |
| rc_AA258353_at | AA258353 | 593 | EST | 5.28 | down | 0.00193 |
| rc_AA258567_at | AA258567 | 597 | EST | 6.92 | down | 0.00096 |
| rc_AA258613_at | AA258613 | 598 | EST | 4.31 | down | 0.0344 |
| rc_AA258813_at | AA258813 | 600 | EST | 4.63 | down | 0.02395 |
| rc_AA259064_at | AA259064 | 602 | EST | 13.15 | down | 0.00001 |
| rc_AA261954_at | AA261954 | 604 | EST | 7.69 | down | 0.00334 |
| rc_AA262033_s_at | AA262033 | 606 | EST | 4.41 | down | 0.00054 |
| rc_AA262349_at | AA262349 | 607 | EST | 3.78 | down | 0.00043 |
| rc_AA262766_at | AA262766 | 609 | EST | 5.66 | down | 0.03832 |
| rc_AA279112_at | AA279112 | 622 | EST | 3.42 | down | 0.01444 |
| rc_AA279533_at | AA279533 | 627 | EST | 5.01 | down | 0.04448 |
| AA279550_at | AA279550 | 628 | Kruppel-like factor | 4.06 | down | 0.00957 |
| rc_AA279676_s_at | AA279676 | 630 | deoxyribonuclease I-like 3 | 23.35 | down | 0.00001 |
| rc_AA279802_at | AA279802 | 631 | EST | 3.65 | down | 0.03366 |
| rc_AA279937_at | AA279937 | 634 | EST | 3.38 | down | 0.02719 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Atfy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA280130_at | AA280130 | 636 | EST | 4.12 | down | 0.00114 |
| rc_AA280413_s_at | AA280413 | 638 | spleen focus forming virus (SFFV) proviral | 4.46 | down | 0.02062 |
| rc_AA280791_at | AA280791 | 640 | integration oncogene spi1 | 3.11 | down | 0.03339 |
| rc_AA281440_at | AA281440 | 644 | eukaryotic translation initiation factor 5 | 6.43 | down | 0.01246 |
| rc_AA281545_at | AA281545 | 645 | EST | 3.64 | down | 0.00002 |
| rc_AA281591_at | AA281591 | 646 | EST | 3.23 | down | 0.00895 |
| AA281677_at | AA281677 | 648 | DKFZP564M2423 protein | 3.95 | down | 0.03606 |
| rc_AA281770_at | AA281770 | 649 | seven in absentia (Drosophila) homolog 1 | 3.96 | down | 0.00094 |
| rc_AA281796_at | AA281796 | 650 | mannose-P-dolichol utilization defect 1 | 3.3 | down | 0.04108 |
| rc_AA281930_at | AA281930 | 651 | core-binding factor, runt domain, alpha subunit 2; | 3.27 | down | 0.02329 |
| rc_AA282061_at | AA282061 | 652 | translocated to, 3 | 8.95 | down | 0.01033 |
| rc_AA282089_at | AA282089 | 653 | KIAA0962 protein | 4.93 | down | 0.00108 |
| rc_AA282179_at | AA282179 | 655 | EST | 3.09 | down | 0.01693 |
| rc_AA282238_at | AA282238 | 656 | EST | 3.47 | down | 0.00677 |
| rc_AA282516_at | AA282516 | 660 | 7-dehydrocholesterol reductase | 7.67 | down | 0.0008 |
| rc_AA282886_at | AA282886 | 663 | EST | 3.57 | down | 0.00049 |
| rc_AA282971_at | AA282971 | 665 | EST | 4.37 | down | 0.03822 |
| rc_AA283758_at | AA283758 | 670 | EST | 3.67 | down | 0.04293 |
| AA284558_at | AA284558 | 674 | Nck, Ash and phospholipase C binding protein | 3.09 | down | 0.00027 |
| rc_aa284721_s_at | AA284721 | 677 | EST | 3.34 | down | 0.03296 |
| rc_AA284795_at | AA284795 | 678 | phosphatidylethanolamine N-methyltransferase | 10.03 | down | 0.00019 |
| rc_AA285053_at | AA285053 | 681 | EST | 6.95 | down | 0.00125 |
| rc_AA287122_at | AA287122 | 686 | EST | 3.66 | down | 0.00161 |
| rc_AA287550_f_at | AA287550 | 689 | DKFZP434C171 protein | 3.53 | down | 0.00217 |
| rc_AA287566_at | AA287566 | 690 | KIAA0187 gene product | 9.07 | down | 0.00013 |
| rc_AA291323_at | AA291323 | 699 | BCL2-interacting killer (apoptosis-inducing) | 9.15 | down | 0.00514 |
| rc_AA291749_s_at | AA291749 | 703 | estrogen receptor 1 | 4.78 | down | 0.00059 |
| rc_aa292086_s_at | AA292086 | 705 | EST | 5 | down | 0.00161 |
| AA292158_s_at | AA292158 | 706 | EST | 21.79 | down | 0.00031 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA292328_at | AA292328 | 707 | activating transcription factor 5 | 17.51 | down | 0.00689 |
| rc_AA292711_at | AA292711 | 711 | EST | 3 | down | 0.01053 |
| rc_AA292773_s_at | AA292773 | 713 | collagen, type XVIII, alpha 1 | 7.44 | down | 0.00158 |
| rc_AA293327_at | AA293327 | 716 | isocitrate dehydrogenase 1 (NADP+), soluble | 7.04 | down | 0.04377 |
| rc_AA293485_at | AA293485 | 718 | EST | 3.36 | down | 0.02799 |
| AA298180_at | AA298180 | 726 | EST | 3.11 | down | 0.00747 |
| rc_AA299632_at | AA299632 | 728 | EST | 4.23 | down | 0.00371 |
| rc_AA312946_s_at | AA312946 | 731 | EST | 9.21 | down | 0.00106 |
| AA314457_at | AA314457 | 733 | synaptonemal complex protein 3 | 4.86 | down | 0.0013 |
| rc_AA338512_at | AA338512 | 742 | EST | 3.05 | down | 0.03427 |
| rc_AA342301_at | AA342301 | 746 | EST | 3.89 | down | 0.00038 |
| rc_AA342337_at | AA342337 | 747 | EST | 3.87 | down | 0.0069 |
| rc_AA342446_s_at | AA342446 | 748 | insulin receptor | 6.83 | down | 0.00412 |
| rc_AA342771_at | AA342771 | 749 | EST | 5.33 | down | 0.00331 |
| rc_AA343142_at | AA343142 | 751 | EST | 20.87 | down | 0.00003 |
| rc_AA344866_s_at | AA344866 | 752 | complement component 8, gamma polypeptide | 7.28 | down | 0.00206 |
| rc_AA347674_at | AA347674 | 753 | EST | 10.59 | down | 0.03716 |
| rc_AA347717_at | AA347717 | 754 | EST | 5.25 | down | 0.00207 |
| rc_AA348284_at | AA348284 | 755 | EST | 4.54 | down | 0.00759 |
| rc_AA348466_s_at | AA348466 | 756 | regulator of G-protein signalling 5 | 3.2 | down | 0.00571 |
| rc_AA348485_at | AA348485 | 757 | KIAA0438 gene product | 4.01 | down | 0.04563 |
| | | | fatty-acid-Coenzyme A ligase, long-chain 1, fatty- | | | |
| rc_AA348922_s_at | AA348922 | 758 | acid-Coenzyme A ligase, long-chain 2 | 64.27 | down | 0.00002 |
| rc_AA349836_at | AA349836 | 760 | EST | 3.01 | down | 0.00911 |
| | | | KIAA0382 protein; leukemia-associated rho | | | |
| rc_AA370359_s_at | AA370359 | 767 | guanine nucleotide exchange factor (GEF) | 4.82 | down | 0.01077 |
| AA376875_at | AA376875 | 770 | monoamine oxidase A | 3.8 | down | 0.02746 |
| rc_AA377087_at | AA377087 | 771 | EST | 16.75 | down | 0.00002 |
| rc_AA381125_at | AA381125 | 772 | EST | 15.48 | down | 0 |
| rc_AA382975_f_at | AA382975 | 773 | EST | 3.7 | down | 0.00131 |
| rc_AA393825_at | AA393825 | 776 | EST | 3.62 | down | 0.0065 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| AA393961_at | AA393961 | 777 | EST | 3.77 | down | 0.01029 |
| AA397841_at | AA397841 | 780 | EST | 8.21 | down | 0 |
| rc_AA397914_at | AA397914 | 783 | EST | 3.16 | down | 0.00336 |
| rc_AA398102_at | AA398102 | 786 | KIAA0429 gene product | 6.22 | down | 0.00396 |
| rc_AA398124_s_at | AA398124 | 787 | growth factor receptor-bound protein 14 | 7.82 | down | 0.00009 |
| rc_AA398221_at | AA398221 | 790 | calcium/calmodulin-dependent protein kinase | 3.78 | down | 0.00019 |
| rc_AA398257_at | AA398257 | 791 | 7-dehydrocholesterol reductase | 4.43 | down | 0.04169 |
| rc_AA398280_at | AA398280 | 792 | EST | 12.43 | down | 0.00134 |
| rc_AA398386_at | AA398386 | 793 | EST | 5.71 | down | 0.00007 |
| rc_AA398422_i_at | AA398422 | 794 | EST | 3.94 | down | 0.00388 |
| rc_AA398423_at | AA398423 | 795 | EST | 8.26 | down | 0.00063 |
| rc_AA398445_at | AA398445 | 796 | EST | 4.28 | down | 0.01764 |
| rc_AA398892_at | AA398892 | 800 | similar to yeast BET3 (S. cerevisiae) | 7.43 | down | 0.00038 |
| rc_AA400030_at | AA400030 | 806 | EST | 3.98 | down | 0.00088 |
| rc_AA400246_at | AA400246 | 810 | mitogen-activated protein kinase-activated | 3.09 | down | 0.00476 |
| rc_AA400251_at | AA400251 | 811 | EST | 4.07 | down | 0.00032 |
| rc_AA400258_at | AA400258 | 812 | EST | 11.89 | down | 0.00478 |
| rc_AA400259_at | AA400259 | 813 | EST | 3.65 | down | 0.00476 |
| rc_AA400471_at | AA400471 | 816 | EST | 5.45 | down | 0.0056 |
| rc_AA400780_at | AA400780 | 818 | EST | 3.5 | down | 0.00107 |
| rc_AA400831_at | AA400831 | 819 | EST | 3.49 | down | 0.00105 |
| rc_AA400834_f_at | AA400834 | 820 | EST | 4.73 | down | 0.01523 |
| rc_AA400864_at | AA400864 | 821 | EST | 7.51 | down | 0.02237 |
| rc_AA400915_at | AA400915 | 823 | EST | 9.84 | down | 0.00351 |
| rc_AA400934_at | AA400934 | 824 | EST | 4.98 | down | 0.02013 |
| rc_AA400979_at | AA400979 | 825 | calcitonin receptor-like receptor activity modifying | 6.65 | down | 0.01051 |
| rc_AA401151_at | AA401151 | 827 | lysozyme (renal amyloidosis) | 3.01 | down | 0.0051 |
| rc_AA401343_at | AA401343 | 828 | EST | 3.11 | down | 0.01929 |
| rc_AA401376_at | AA401376 | 829 | EST | 3.97 | down | 0.00797 |
| rc_AA401562_s_at | AA401562 | 830 | EST | 50.45 | down | 0.00301 |
| AA402006_at | AA402006 | 834 | EST | 4.19 | down | 0.00094 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Atfy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| AA402095_s_at | AA402095 | 835 | EST | 3.12 | down | 0.01412 |
| rc_AA402224_at | AA402224 | 836 | growth arrest and DNA-damage-inducible, | 14.41 | down | 0.00012 |
| rc_AA402656_at | AA402656 | 841 | EST | 12.05 | down | 0.00001 |
| rc_AA402799_at | AA402799 | 842 | EST | 11.81 | down | 0.00031 |
| AA404252_at | AA404252 | 848 | lectin, mannose-binding, 1 | 16.15 | down | 0.00001 |
| rc_AA404352_at | AA404352 | 850 | EST | 7 | down | 0.00059 |
| rc_AA404500_at | AA404500 | 852 | EST | 4.16 | down | 0.01375 |
| rc_AA405819_at | AA405819 | 865 | KIAA0668 protein | 8.59 | down | 0.02034 |
| rc_AA405832_at | AA405832 | 866 | EST | 12.24 | down | 0.00441 |
| rc_AA405907_at | AA405907 | 867 | EST | 3.12 | down | 0 |
| rc_aa406125_s_at | AA406125 | 868 | EST | 4.95 | down | 0.01027 |
| rc_AA406126_at | AA406126 | 869 | EST | 8.43 | down | 0.00569 |
| rc_AA406231_s_at | AA406231 | 873 | KIAA0381 protein | 4.46 | down | 0.04049 |
| AA406435_at | AA406435 | 877 | EST | 3.24 | down | 0.00941 |
| rc_AA410181_at | AA410181 | 881 | EST | 3 | down | 0.00268 |
| rc_AA410255_at | AA410255 | 882 | EST | 7.56 | down | 0.00043 |
| rc_AA410507_at | AA410507 | 884 | EST | 3.73 | down | 0.01703 |
| rc_AA410523_at | AA410523 | 886 | EST | 6.37 | down | 0.03506 |
| rc_AA411764_at | AA411764 | 891 | similar to APOBEC1 | 4 | down | 0.01491 |
| rc_AA412034_at | AA412034 | 894 | EST | 3.09 | down | 0.02309 |
| rc_AA412063_at | AA412063 | 895 | EST | 8.26 | down | 0.00001 |
| rc_AA412184_at | AA412184 | 898 | EST | 3.08 | down | 0.00012 |
| rc_AA412481_s_at | AA412481 | 902 | EST | 8.07 | down | 0.00014 |
| rc_AA416723_at | AA416723 | 906 | EST | 3.57 | down | 0.01042 |
| rc_AA416740_at | AA416740 | 907 | EST | 3.08 | down | 0.01592 |
| rc_AA416873_at | AA416873 | 908 | EST | 7.82 | down | 0.00005 |
| rc_AA416890_s_at | AA416890 | 909 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) | 6.6 | down | 0.00112 |
| rc_AA416936_at | AA416936 | 910 | 5-methyltetrahydrofolate-homocysteine methyltransferase reductase | 4.98 | down | 0.00632 |
| rc_AA417046_at | AA417046 | 915 | fatty-acid-Coenzyme A ligase, very long-chain 1 | 44 | down | 0 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Atfy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA417078_at | AA417078 | 916 | EST | 4.1 | down | 0.00414 |
| rc_AA417373_at | AA417373 | 917 | EST | 4.8 | down | 0.01342 |
| rc_AA417375_at | AA417375 | 918 | EST | 4.21 | down | 0.00231 |
| AA418098_at | AA418098 | 920 | cAMP responsive element binding protein-like 2 | 3.18 | down | 0.03824 |
| rc_AA418907_s_at | AA418907 | 922 | cytochrome P450, subfamily I (aromatic | | | |
| AA419507_at | AA419507 | 924 | compound-inducible), polypeptide 1 | 4.05 | down | 0.04276 |
| rc_AA419608_at | AA419608 | 925 | EST | 5.58 | down | 0.00578 |
| rc_AA419622_at | AA419622 | 926 | EST | 9.19 | down | 0.00005 |
| rc_AA421049_at | AA421049 | 927 | activating transcription factor 5 | 4.62 | down | 0.00386 |
| rc_AA421052_at | AA421052 | 929 | branched chain alpha-ketoacid dehydrogenase | 44.41 | down | 0.00179 |
| rc_AA421244_s_at | AA421244 | 932 | SH3-domain binding protein 5 (BTK-associated) | 3.52 | down | 0.00869 |
| rc_AA421561_at | AA421561 | 933 | insulin-like growth factor 2 (somatomedin A) | 4.32 | down | 0.007 |
| AA424307_at | AA424307 | 944 | EST | 9.98 | down | 0.00007 |
| rc_AA424672_s_at | AA424672 | 946 | dermatopontin | 5.73 | down | 0.0074 |
| rc_AA424798_at | AA424798 | 947 | EST | 4.69 | down | 0.00843 |
| rc_AA424813_at | AA424813 | 948 | EST | 17.45 | down | 0.00352 |
| rc_AA425294_at | AA425294 | 952 | EST | 5.77 | down | 0.00503 |
| rc_AA425309_at | AA425309 | 953 | nuclear factor I/B | 10.61 | down | 0.00083 |
| rc_AA425782_at | AA425782 | 956 | KIAA0874 protein | 4.9 | down | 0.00466 |
| rc_AA425836_at | AA425836 | 957 | EST | 5.52 | down | 0.03433 |
| AA426156_at | AA426156 | 959 | EST | 4.55 | down | 0.00035 |
| AA426168_at | AA426168 | 960 | KIAA0805 protein | 3.67 | down | 0.00153 |
| AA426304_s_at | AA426304 | 962 | EST | 3.73 | down | 0.01477 |
| rc_AA426330_at | AA426330 | 963 | N-acylsphingosine amidohydrolase (acid | 6.61 | down | 0.01092 |
| rc_AA426468_at | AA426468 | 966 | EST | 4.24 | down | 0.00668 |
| rc_AA426609_at | AA426609 | 968 | EST | 3.38 | down | 0.0099 |
| rc_AA427778_at | AA427778 | 978 | EST | 6.28 | down | 0.01233 |
| AA427783_at | AA427783 | 979 | EST | 3.57 | down | 0.00368 |
| rc_AA427819_at | AA427819 | 980 | midline 2 | 4.37 | down | 0.0004 |
| AA428006_at | AA428006 | 984 | DKFZP564B167 protein | 3.44 | down | 0.00063 |
| | | | | 3.71 | down | 0.02325 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA428150_at | AA428150 | 985 | EST | 5.24 | down | 0.00167 |
| rc_AA428325_at | AA428325 | 988 | EST | 8.36 | down | 0.00002 |
| rc_AA428567_at | AA428567 | 989 | EST | 3.99 | down | 0.00788 |
| rc_AA428607_at | AA428607 | 990 | ribosomal protein S5 pseudogene 1 | 4.21 | down | 0.04305 |
| rc_AA428863_at | AA428863 | 991 | EST | 3.5 | down | 0.01726 |
| rc_AA428900_at | AA428900 | 992 | EST | 7.01 | down | 0.00037 |
| rc_AA429038_at | AA429038 | 995 | EST | 3.29 | down | 0.00927 |
| rc_AA429478_at | AA429478 | 998 | EST | 3.41 | down | 0.02599 |
| rc_AA429904_at | AA429904 | 1005 | EST | 7.26 | down | 0.00524 |
| AA430011_at | AA430011 | 1006 | EST | 8.35 | down | 0.00729 |
| rc_AA430026_at | AA430026 | 1007 | EST | 3.31 | down | 0.00786 |
| rc_AA430028_at | AA430028 | 1008 | EST | 9.14 | down | 0.00246 |
| rc_AA430044_at | AA430044 | 1010 | EST | 7.78 | down | 0.00124 |
| rc_AA430047_at | AA430047 | 1011 | EST | 3.44 | down | 0.0016 |
| rc_AA430108_at | AA430108 | 1013 | EST | 3.8 | down | 0.04484 |
| rc_AA430666_at | AA430666 | 1016 | EST | 5.12 | down | 0.00377 |
| rc_AA431337_at | AA431337 | 1020 | EST | 6.26 | down | 0.00053 |
| rc_AA431462_at | AA431462 | 1022 | EST | 4.45 | down | 0.00956 |
| rc_AA431480_s_at | AA431480 | 1023 | EST | 4.3 | down | 0.00876 |
| rc_AA431773_at | AA431773 | 1026 | EST | 7.61 | down | 0.00063 |
| rc_AA432168_at | AA432168 | 1031 | S-adenosylhomocysteine hydrolase-like 1 | 4.71 | down | 0.01377 |
| rc_AA433946_at | AA433946 | 1033 | EST | 43.74 | down | 0.00005 |
| rc_AA435591_at | AA435591 | 1038 | kinesin family member 3B | 3.5 | down | 0.0001 |
| rc_AA435753_at | AA435753 | 1045 | EST | 4.71 | down | 0.00078 |
| rc_AA435777_f_at | AA435777 | 1047 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 7.48 | down | 0.00613 |
| rc_AA435824_at | AA435824 | 1048 | EST | 3.93 | down | 0.02764 |
| rc_AA435985_at | AA435985 | 1049 | EST | 17.7 | down | 0 |
| rc_AA436489_at | AA436489 | 1053 | EST | 7.34 | down | 0.001 |
| rc_AA436560_at | AA436560 | 1055 | claudin 1 | 11.41 | down | 0.00756 |
| rc_AA436690_at | AA436690 | 1057 | EST | 4.58 | down | 0.00948 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA436880_at | AA436880 | 1058 | EST | 3.22 | down | 0.00699 |
| AA436926_at | AA436926 | 1059 | EST | 5.5 | down | 0.00984 |
| rc_AA437235_s_at | AA437235 | 1060 | EST | 7.15 | down | 0.01455 |
| rc_AA437265_s_at | AA437265 | 1061 | EST | 4.39 | down | 0.00826 |
| rc_AA437295_at | AA437295 | 1062 | ribosomal protein L7a | 4.35 | down | 0.00347 |
| rc_AA441791_at | AA441791 | 1065 | EST | 3.58 | down | 0.00357 |
| AA442334_at | AA442334 | 1069 | EST | 7.15 | down | 0.00018 |
| AA442342_at | AA442342 | 1070 | EST | 5.62 | down | 0.00052 |
| rc_AA443272_at | AA443272 | 1074 | EST | 7.68 | down | 0.00869 |
| rc_AA443658_at | AA443658 | 1079 | transmembrane 7 superfamily member 2 | 9.06 | down | 0.00048 |
| rc_AA443756_at | AA443756 | 1080 | EST | 5.05 | down | 0.00341 |
| rc_AA443822_at | AA443822 | 1082 | EST | 5.46 | down | 0.02538 |
| rc_AA443934_at | AA443934 | 1083 | GTP-binding protein Rho7 | 3.09 | down | 0.00214 |
| rc_AA443936_s_at | AA443936 | 1084 | EST | 22.96 | down | 0.00627 |
| rc_AA443993_at | AA443993 | 1086 | EST | 3.21 | down | 0.02948 |
| rc_AA446342_at | AA446342 | 1088 | seven in absentia (Drosophila) homolog 1 | 4.84 | down | 0.00015 |
| rc_AA446587_at | AA446587 | 1091 | EST | 5.8 | down | 0.00012 |
| rc_AA446651_at | AA446651 | 1093 | EST | 3.14 | down | 0.01902 |
| rc_AA446666_at | AA446666 | 1094 | EST | 4.03 | down | 0.02369 |
| rc_AA447549_at | AA447549 | 1101 | UDP-N-acteylglucosamine pyrophosphorylase 1; | 6.37 | down | 0.02815 |
| rc_AA447617_at | AA447617 | 1103 | Sperm associated antigen 2 | 3.26 | down | 0.04687 |
| rc_AA447740_at | AA447740 | 1106 | EST | 3.22 | down | 0.02518 |
| rc_AA447971_at | AA447971 | 1110 | EST | 8.08 | down | 0.00035 |
| rc_AA447977_s_at | AA447977 | 1111 | EST | 3.84 | down | 0.00045 |
| rc_AA448002_at | AA448002 | 1113 | putative type-II membrane protein | 10.05 | down | 0 |
| rc_AA448282_at | AA448282 | 1115 | EST | 3.87 | down | 0.00217 |
| rc_AA448300_at | AA448300 | 1116 | FXD domain-containing ion transport regulator 1 | 24.97 | down | 0.00001 |
| rc_AA449267_at | AA449267 | 1120 | (phospholemman) | 16.44 | down | 0.00926 |
| rc_AA449297_at | AA449297 | 1121 | EST | 3.78 | down | 0.00039 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA449306_at | AA449306 | 1122 | EST | 5.01 | down | 0.0006 |
| rc_AA449327_at | AA449327 | 1123 | EST | 4.77 | down | 0.01248 |
| rc_AA449448_at | AA449448 | 1125 | EST | 3.97 | down | 0.00103 |
| rc_AA450114_at | AA450114 | 1131 | EST | 4.96 | down | 0.01238 |
| rc_AA450127_at | AA450127 | 1132 | growth arrest and DNA-damage-inducible, beta | 7.98 | down | 0.00078 |
| rc_AA450281_at | AA450281 | 1134 | EST | 5.55 | down | 0.00004 |
| rc_AA451836_at | AA451836 | 1137 | EST | 4.9 | down | 0.01412 |
| rc_AA451911_at | AA451911 | 1139 | EST | 3.44 | down | 0.00221 |
| rc_AA452158_at | AA452158 | 1141 | ras homolog gene family, member B | 28.96 | down | 0.00064 |
| AA452454_at | AA452454 | 1144 | EST | 4.45 | down | 0.00179 |
| rc_AA452549_at | AA452549 | 1146 | platelet-derived growth factor receptor, alpha | 3.3 | down | 0.04155 |
| rc_AA452559_s_at | AA452559 | 1147 | EST | 4.35 | down | 0.00804 |
| rc_aa452598_s_at | AA452598 | 1148 | genethonin 1 | 5.49 | down | 0.00163 |
| rc_AA452855_at | AA452855 | 1150 | lectin, mannose-binding, 1 | 9.88 | down | 0.00428 |
| rc_AA452860_at | AA452860 | 1151 | EST | 3.99 | down | 0.00831 |
| rc_AA452915_at | AA452915 | 1152 | EST | 3.13 | down | 0.00561 |
| rc_AA453770_s_at | AA453770 | 1157 | EST | 6.04 | down | 0.00524 |
| AA453917_at | AA453917 | 1159 | EST | 3.3 | down | 0.01896 |
| rc_AA453988_at | AA453988 | 1160 | methionine adenosyltransferase I, alpha | 54.29 | down | 0.00381 |
| rc_AA454086_f_at | AA454086 | 1161 | UDP-glucose dehydrogenase | 4.29 | down | 0.00981 |
| rc_AA454159_at | AA454159 | 1162 | EST | 10.81 | down | 0.00132 |
| rc_AA454170_at | AA454170 | 1163 | EST | 3.11 | down | 0.03 |
| rc_AA454177_i_at | AA454177 | 1164 | EST | 10.3 | down | 0.0008 |
| rc_AA454184_at | AA454184 | 1165 | EST | 3.96 | down | 0.04605 |
| rc_AA454733_s_at | AA454733 | 1169 | EST | 5.61 | down | 0.01182 |
| rc_AA455097_i_at | AA455097 | 1172 | EST | 6.03 | down | 0.00419 |
| rc_AA455367_at | AA455367 | 1176 | DKFZP586F1018 protein | 3.73 | down | 0.00202 |
| AA455403_at | AA455403 | 1177 | EST | 15.46 | down | 0.01547 |
| rc_AA455865_at | AA455865 | 1180 | phosphatidylinositol glycan, class B | 5.41 | down | 0.00004 |
| rc_AA455896_s_at | AA455896 | 1181 | glypican 1 | 3.46 | down | 0.00887 |
| rc_AA455962_at | AA455962 | 1182 | EST | 3.1 | down | 0.03905 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA455987_at | AA455987 | 1183 | EST | 5.36 | down | 0.00029 |
| rc_AA455988_at | AA455988 | 1184 | butyrobetaine (gamma), 2-oxoglutarate | 15.54 | down | 0.00001 |
| rc_AA456055_at | AA456055 | 1185 | dioxygenase (gamma-butyrobetaine hydroxylase) | 5.16 | down | 0.00158 |
| rc_AA456147_at | AA456147 | 1188 | EST | 4.23 | down | 0.00088 |
| rc_AA456289_at | AA456289 | 1189 | general transcription factor IIIA | 15.31 | down | 0.00004 |
| rc_AA456311_s_at | AA456311 | 1190 | EST | 46.81 | down | 0.001 |
| rc_AA456326_at | AA456326 | 1191 | EST | 3.35 | down | 0.00489 |
| rc_AA456589_at | AA456589 | 1194 | EST | 4.23 | down | 0.00102 |
| AA456687_at | AA456687 | 1197 | EST | 3.08 | down | 0.01189 |
| rc_AA457377_at | AA457377 | 1201 | EST | 3.1 | down | 0.00549 |
| rc_AA458652_at | AA458652 | 1202 | EST | 8.26 | down | 0.00001 |
| rc_AA458923_at | AA458923 | 1207 | EST | 3.36 | down | 0.00421 |
| rc_AA458946_at | AA458946 | 1209 | EST | 15.88 | down | 0.00004 |
| rc_AA459256_at | AA459256 | 1212 | lectin, mannose-binding, 1 | 3.01 | down | 0.00094 |
| rc_AA459293_at | AA459293 | 1213 | EST | 3.2 | down | 0.0001 |
| rc_AA459389_at | AA459389 | 1216 | tyrosylprotein sulfotransferase 2 | 3.72 | down | 0.02252 |
| rc_AA459420_at | AA459420 | 1217 | EST | 7.25 | down | 0.0214 |
| rc_AA459668_at | AA459668 | 1219 | 3-hydroxyisobutyryl-Coenzyme A hydrolase | 7.62 | down | 0.00225 |
| rc_aa459690_s_at | AA459690 | 1221 | EST | 9.18 | down | 0.00732 |
| rc_AA460012_at | AA460012 | 1224 | solute carrier family 22 (extraneuronal | 4.27 | down | 0.04975 |
| AA460047_at | AA460047 | 1226 | monoamine transporter), member 3 | 3.33 | down | 0.04011 |
| AA460128_at | AA460128 | 1227 | EST | 3.28 | down | 0.01299 |
| rc_AA460449_at | AA460449 | 1228 | similar to S. pombe dim1+ | 7.77 | down | 0.00011 |
| rc_AA460661_at | AA460661 | 1229 | EST | 7.02 | down | 0.00053 |
| rc_AA460916_at | AA460916 | 1233 | EST | 3.69 | down | 0.04841 |
| rc_AA461057_at | AA461057 | 1234 | nuclear localization signal deleted in | 5.22 | down | 0.00051 |
| rc_AA461303_at | AA461303 | 1238 | DKFZP586D1519 protein | 4.77 | down | 0.0438 |
| rc_AA461444_at | AA461444 | 1239 | EST | 11.56 | down | 0.00167 |
| rc_AA461458_at | AA461458 | 1241 | EST | 3.37 | down | 0.02427 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA463194_s_at | AA463194 | 1244 | KIAA1037 protein | 4.92 | down | 0.01866 |
| rc_AA463195_at | AA463195 | 1245 | EST | 3.41 | down | 0.00413 |
| AA463311_at | AA463311 | 1248 | EST | 3.71 | down | 0.04902 |
| rc_AA463729_at | AA463729 | 1250 | EST | 4.07 | down | 0.00676 |
| rc_AA463876_at | AA463876 | 1252 | EST | 3.31 | down | 0.00109 |
| rc_AA463946_at | AA463946 | 1254 | pigment epithelium-derived factor | 3.38 | down | 0.0018 |
| rc_AA464188_s_at | AA464188 | 1256 | EST | 4.82 | down | 0.03208 |
| rc_AA464603_at | AA464603 | 1260 | EST | 3.26 | down | 0.0007 |
| rc_AA465240_at | AA465240 | 1270 | EST | 4.03 | down | 0.0046 |
| rc_AA470153_at | AA470153 | 1275 | solute carrier family 21 (organic anion | 13.26 | down | 0.00315 |
| rc_AA476324_s_at | AA476324 | 1281 | EST | 55.22 | down | 0.00132 |
| rc_AA476346_at | AA476346 | 1283 | EST | 3.12 | down | 0.01067 |
| rc_AA476352_at | AA476352 | 1284 | EST | 3.41 | down | 0.02233 |
| rc_AA477119_at | AA477119 | 1289 | EST | 3.13 | down | 0.0338 |
| AA477919_at | AA477919 | 1293 | EST | 4.69 | down | 0.00141 |
| AA477978_s_at | AA477978 | 1294 | short-chain dehydrogenase/reductase 1 | 8.53 | down | 0.01651 |
| rc_AA478416_at | AA478416 | 1300 | EST | 4.04 | down | 0.00078 |
| rc_AA478441_at | AA478441 | 1302 | cathepsin F | 5.07 | down | 0.00752 |
| AA479132_at | AA479132 | 1309 | EST | 3.12 | down | 0.00876 |
| rc_AA479148_at | AA479148 | 1311 | EST | 38.05 | down | 0 |
| rc_AA479488_at | AA479488 | 1313 | S-adenosylhomocysteine hydrolase-like 1 | 4 | down | 0.0269 |
| rc_AA479498_at | AA479498 | 1314 | EST | 5.78 | down | 0.01489 |
| rc_AA479885_at | AA479885 | 1318 | KIAA0843 protein | 15.57 | down | 0.00024 |
| rc_AA479968_s_at | AA479968 | 1321 | arylsulfatase A | 9.01 | down | 0.00224 |
| rc_AA480975_at | AA480975 | 1322 | EST | 8.95 | down | 0.00259 |
| rc_AA480991_s_at | AA480991 | 1323 | EST | 8.59 | down | 0.00156 |
| rc_AA481432_s_at | AA481432 | 1328 | fibronectin 1 | 7.76 | down | 0.0061 |
| rc_AA481526_at | AA481526 | 1329 | EST | 3.73 | down | 0.00002 |
| AA481670_at | AA481670 | 1330 | retinal short-chain dehydrogenase/reductase | 6.2 | down | 0.0078 |
| rc_AA482594_at | AA482594 | 1337 | EST | 5.42 | down | 0.00387 |
| rc_AA485089_at | AA485089 | 1341 | EST | 5.46 | down | 0.00044 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA485326_at | AA485326 | 1342 | ATP-binding cassette, sub-family D (ALD), | 3.08 | down | 0.00415 |
| rc_AA485413_at | AA485413 | 1344 | EST | 4.54 | down | 0.00137 |
| rc_AA486410_at | AA486410 | 1348 | aldehyde dehydrogenase 5 family, member A1 | 8.08 | down | 0.00485 |
| AA486511_at | AA486511 | 1349 | (succinate-semialdehyde dehydrogenase) | 22.21 | down | 0.00113 |
| rc_AA486567_at | AA486567 | 1350 | EST | 5 | down | 0.00002 |
| rc_AA487161_at | AA487161 | 1353 | ubiquitin 2 | 3.13 | down | 0.00023 |
| rc_AA487503_at | AA487503 | 1356 | EST | 8.85 | down | 0.00012 |
| rc_AA487606_at | AA487606 | 1358 | EST | 3.05 | down | 0.00291 |
| rc_AA488843_at | AA488843 | 1362 | cornichon-like | 8.58 | down | 0.02131 |
| rc_AA489061_at | AA489061 | 1367 | EST | 3.49 | down | 0.00223 |
| rc_AA489629_at | AA489629 | 1369 | EST | 8.08 | down | 0.00109 |
| rc_AA489636_at | AA489636 | 1370 | EST | 10.7 | down | 0 |
| rc_AA489798_at | AA489798 | 1373 | hypothetical protein, estradiol-induced | 8.75 | down | 0.00544 |
| rc_AA490159_at | AA490159 | 1374 | glucose-6-phosphatase, transport (glucose-6- | 5.44 | down | 0 |
| rc_AA490214_at | AA490214 | 1376 | EST | 3.12 | down | 0.02382 |
| rc_AA490620_at | AA490620 | 1378 | EST | 4.77 | down | 0.00201 |
| rc_AA490670_at | AA490670 | 1379 | EST | 9.96 | down | 0.00454 |
| AA490775_at | AA490775 | 1380 | UDP-N-acetylglucosamine-2-epimerase/N- | | | |
| rc_AA490882_s_at | AA490882 | 1381 | acetylmannosamine kinase | 5.34 | down | 0.00118 |
| rc_AA490890_at | AA490890 | 1382 | EST | 3.29 | down | 0.00319 |
| rc_AA491000_at | AA491000 | 1385 | EST | 3.02 | down | 0.00007 |
| rc_AA491001_i_at | AA491001 | 1386 | EST | 4.23 | down | 0.02305 |
| rc_AA491001_f_at | AA491001 | 1386 | EST | 8.52 | down | 0.01118 |
| AA495758_s_at | AA495758 | 1391 | EST | 3.73 | down | 0.01957 |
| rc_AA495820_at | AA495820 | 1393 | EST | 3.94 | down | 0.00772 |
| rc_AA496053_at | AA496053 | 1396 | EST | 3.98 | down | 0.00218 |
| AA496423_at | AA496423 | 1399 | WW domain binding protein 2 | 3.28 | down | 0.00095 |
| rc_AA496914_at | AA496914 | 1401 | v-maf musculoaponeurotic fibrosarcoma (avian) | 3.52 | down | 0.01314 |
| rc_AA497052_at | AA497052 | 1408 | DKFZP727G051 protein | 3.48 | down | 0.00361 |
| | | | | 7.28 | down | 0.01745 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA504492_at | AA504492 | 1414 | tubulin, alpha, ubiquitous | 4.21 | down | 0.00752 |
| AA505198_at | AA505198 | 1419 | EST | 3.41 | down | 0.0343 |
| rc_AA521290_at | AA521290 | 1421 | EST | 4.53 | down | 0.0148 |
| rc_AA521292_at | AA521292 | 1422 | EST | 8.58 | down | 0.00064 |
| rc_AA521306_at | AA521306 | 1423 | EST | 4.27 | down | 0.00567 |
| rc_AA598417_at | AA598417 | 1426 | UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase | 8.56 | down | 0.01638 |
| rc_AA598419_s_at | AA598419 | 1427 | translational inhibitor protein p14.5 | 23.6 | down | 0.00036 |
| rc_AA598675_at | AA598675 | 1433 | EST | 3.25 | down | 0.03934 |
| rc_AA598679_at | AA598679 | 1434 | EST | 5.37 | down | 0.00467 |
| rc_AA598746_at | AA598746 | 1437 | EST | 3.8 | down | 0.02667 |
| rc_AA598926_at | AA598926 | 1441 | EST | 3.7 | down | 0.00432 |
| rc_AA599211_at | AA599211 | 1445 | short-chain dehydrogenase/reductase 1 | 7.85 | down | 0.00911 |
| rc_AA599234_s_at | AA599234 | 1447 | murine leukemia viral (bmi-1) oncogene homolog | 3.9 | down | 0.0068 |
| rc_AA599472_at | AA599472 | 1451 | succinate-CoA ligase, GDP-forming, beta subunit | 5.07 | down | 0.00447 |
| rc_AA599526_at | AA599526 | 1453 | cartilage associated protein | 3.02 | down | 0.00043 |
| rc_AA599814_at | AA599814 | 1456 | EST | 12.37 | down | 0.00002 |
| rc_AA599937_s_at | AA599937 | 1458 | insulin-like growth factor-binding protein 4 | 26.92 | down | 0.00094 |
| rc_AA599954_at | AA599954 | 1459 | cell cycle progression 8 protein | 3.15 | down | 0.00021 |
| rc_AA608546_at | AA608546 | 1463 | EST | 12.52 | down | 0.00003 |
| rc_AA608671_at | AA608671 | 1466 | EST | 3.14 | down | 0.04543 |
| rc_AA608729_at | AA608729 | 1468 | EST | 3.89 | down | 0.01757 |
| rc_AA608751_i_at | AA608751 | 1469 | EST | 5.76 | down | 0.01404 |
| rc_AA608802_at | AA608802 | 1470 | EST | 6.95 | down | 0.00263 |
| rc_AA608807_s_at | AA608807 | 1471 | inhibin, beta B (activin AB beta polypeptide) | 4.05 | down | 0.00568 |
| rc_AA608837_at | AA608837 | 1472 | EST | 6.2 | down | 0.00006 |
| rc_AA609011_at | AA609011 | 1476 | EST | 3.94 | down | 0.0313 |
| rc_AA609164_at | AA609164 | 1480 | cytochrome b-561 | 6.8 | down | 0.02298 |
| rc_AA609316_at | AA609316 | 1481 | EGF-like-domain, multiple 5 | 7.97 | down | 0.00011 |
| rc_AA609519_at | AA609519 | 1482 | EST | 8.13 | down | 0.00009 |
| rc_AA609537_s_at | AA609537 | 1483 | hepatic leukemia factor | 8.76 | down | 0.00018 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA609572_at | AA609572 | 1484 | EST | 3.02 | down | 0.01534 |
| rc_AA609574_at | AA609574 | 1485 | EST | 5.03 | down | 0 |
| rc_AA609576_at | AA609576 | 1486 | EST | 3.1 | down | 0.00266 |
| rc_AA609773_at | AA609773 | 1489 | EST | 6.09 | down | 0.01103 |
| rc_AA609774_at | AA609774 | 1490 | EST | 4.02 | down | 0.00424 |
| rc_AA609934_at | AA609934 | 1493 | EST | 6.84 | down | 0.00048 |
| rc_AA609996_at | AA609996 | 1495 | EST | 3.93 | down | 0.00988 |
| rc_AA620343_at | AA620343 | 1500 | EST | 5.04 | down | 0.00407 |
| rc_AA620556_at | AA620556 | 1505 | EST | 32.4 | down | 0.00353 |
| rc_AA620667_s_at | AA620667 | 1506 | protein tyrosine phosphatase type IVA, member 1 | 5.92 | down | 0.00206 |
| rc_AA620830_at | AA620830 | 1509 | DKFZP564I122 protein | 3.42 | down | 0.02421 |
| rc_AA621131_at | AA621131 | 1513 | EST | 35.37 | down | 0 |
| rc_AA621192_at | AA621192 | 1515 | EST | 5.39 | down | 0.0016 |
| rc_AA621209_at | AA621209 | 1516 | similar to Caenorhabditis elegans protein | 6.34 | down | 0.00144 |
| rc_AA621235_at | AA621235 | 1517 | EST | 3.44 | down | 0.0021 |
| rc_AA621274_i_at | AA621274 | 1519 | EST | 7.43 | down | 0.00065 |
| rc_AA621430_at | AA621430 | 1525 | doublecortin; lissencephaly, X-linked | 3.09 | down | 0.00024 |
| rc_AA621796_at | AA621796 | 1531 | kinesin family member 3B | 4.44 | down | 0.00032 |
| AB002311_at | AB002311 | 1535 | PDZ domain containing guanine nucleotide | | | |
| AB002328_at | AB002328 | 1536 | exchange factor(GEF)1; RA(Ras/Rap1A- | 4.21 | down | 0.00476 |
| AF000573_ma1_at | AF000573 | 1543 | calcineurin binding protein 1 | 5.55 | down | 0.00016 |
| AF005039_at | AF005039 | 1548 | homogenisate 1,2-dioxygenase (homogenisate | 13.76 | down | 0.00002 |
| | | | secretory carrier membrane protein 3 | 3.42 | down | 0.04953 |
| | | | solute carrier family 4, sodium bicarbonate | | | |
| AF007216_at | AF007216 | 1550 | cotransporter, member 4 | 5.79 | down | 0.00005 |
| C01257_at | C01257 | 1554 | EST | 5.35 | down | 0.00608 |
| C01286_s_at | C01286 | 1555 | integral membrane protein 2B | 4.11 | down | 0.00292 |
| C01409_s_at | C01409 | 1556 | EST | 4.41 | down | 0.01725 |
| C01686_at | C01686 | 1557 | EST | 3.01 | down | 0.00048 |
| C02099_s_at | C02099 | 1560 | CGI-131 protein | 5.85 | down | 0.02377 |
| C02460_at | C02460 | 1562 | EST | 3.64 | down | 0.02705 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_C14963_s_at | C14963 | 1572 | nicotinamide nucleotide transhydrogenase | 3.9 | down | 0.0044 |
| C15871_at | C15871 | 1575 | EST | 3.26 | down | 0.0046 |
| C16420_s_at | C16420 | 1576 | EST | 5.95 | down | 0.00119 |
| rc_C20653_at | C20653 | 1578 | EST | 10.59 | down | 0.00001 |
| rc_C20810_at | C20810 | 1579 | EST | 5.17 | down | 0.00614 |
| rc_C20911_at | C20911 | 1580 | antithrombin III | 6.56 | down | 0.00175 |
| rc_C20974_at | C20974 | 1581 | Vanin 1 | 6.66 | down | 0.00272 |
| rc_C21130_at | C21130 | 1583 | EST | 8.79 | down | 0.00008 |
| rc_C21238_at | C21238 | 1584 | EST | 4.54 | down | 0.02074 |
| D00003_s_at | D00003 | 1586 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3 | 22.05 | down | 0.00059 |
| D00003_at | D00003 | 1586 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3 | 9.46 | down | 0.00001 |
| D00097_s_at | D00097 | 1588 | amyloid P component, serum | 16.72 | down | 0.00098 |
| D00408_s_at | D00408 | 1589 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3, cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 7 | 11.1 | down | 0 |
| D00632_at | D00632 | 1591 | 5, cytochrome P450, subfamily IIIA, polypeptide 7 | 6.55 | down | 0.00121 |
| D00723_at | D00723 | 1592 | glutathione peroxidase 3 (plasma) | 4.18 | down | 0.00543 |
| D10040_at | D10040 | 1593 | glycine cleavage system protein H (aminomethyl fatty-acid-Coenzyme A ligase, long-chain 2 | 20.51 | down | 0 |
| D10511_at | D10511 | 1594 | acetyl-Coenzyme A acetyltransferase 1 | 10.68 | down | 0.0002 |
| rc_D11756_f_at | D11756 | 1596 | (acetoacetyl Coenzyme A thiolase) | 5.49 | down | 0.01272 |
| rc_D11802_at | D11802 | 1597 | angiotensinogen | 5.65 | down | 0.00009 |
| rc_D11835_at | D11835 | 1598 | low density lipoprotein receptor (familial | 21.76 | down | 0.00307 |
| rc_D11881_at | D11881 | 1599 | KIAA0962 protein | 4.37 | down | 0.01627 |
| D12485_at | D12485 | 1600 | phosphodiesterase 1/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen) | 4.57 | down | 0.00008 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P Value |
|--------------|---------|--------|---|-------------|-----------|---------|
| D12620_s_at | D12620 | 1601 | cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) | 35.09 | down | 0.00015 |
| D12620_s_at | D12620 | 1601 | cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) | 13.45 | down | 0 |
| D13243_s_at | D13243 | 1602 | pyruvate kinase, liver and RBC | 20.22 | down | 0 |
| D13643_at | D13643 | 1609 | KIAA0018 gene product | 10.84 | down | 0.00058 |
| D13705_s_at | D13705 | 1610 | cytochrome P450, subfamily IVA, polypeptide 11 | 3.7 | down | 0.00038 |
| D13814_s_at | D13814 | 1611 | angiotensin receptor 1, angiotensin receptor 1B | 3.12 | down | 0.00101 |
| D14012_s_at | D14012 | 1612 | HGF activator | 12.75 | down | 0.0035 |
| D14664_at | D14664 | 1616 | KIAA0022 gene product | 8.98 | down | 0.00011 |
| D14695_at | D14695 | 1618 | KIAA0025 gene product; MMS-inducible gene acetyl-Coenzyme A acyltransferase 2 | 6.48 | down | 0 |
| D16294_at | D16294 | 1619 | (mitochondrial 3-oxoacyl-Coenzyme A thiolase) | 4.81 | down | 0.03921 |
| D16350_at | D16350 | 1620 | SA (rat hypertension-associated) homolog hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit histidine ammonia-lyase | 3.83 | down | 0.00117 |
| D16481_at | D16481 | 1621 | histidine ammonia-lyase | 3.18 | down | 0.00695 |
| D16626_at | D16626 | 1622 | histidine ammonia-lyase | 22.66 | down | 0 |
| D16626_at | D16626 | 1622 | histidine ammonia-lyase | 9.25 | down | 0.00025 |
| rc_D20350_at | D20350 | 1624 | EST | 13.97 | down | 0.00057 |
| D31117_at | D31117 | 1640 | ribosome binding protein 1 (dog 180kD homolog) | 5.3 | down | 0.02749 |
| D31225_at | D31225 | 1641 | EST | 3.17 | down | 0.01073 |
| D31289_at | D31289 | 1642 | EST | 4.16 | down | 0.02166 |
| D31381_at | D31381 | 1644 | dynein, axonemal, light polypeptide 4 | 4.97 | down | 0.01806 |
| D31628_s_at | D31628 | 1646 | 4-hydroxyphenylpyruvate dioxygenase | 50.48 | down | 0.00002 |
| D31716_at | D31716 | 1647 | basic transcription element binding protein 1 | 5.35 | down | 0.00086 |
| D31815_at | D31815 | 1648 | regucalcin (senescence marker protein-30) | 10.55 | down | 0.00037 |
| D31887_at | D31887 | 1649 | KIAA0062 protein | 4.26 | down | 0.00101 |
| D37931_at | D37931 | 1650 | ribonuclease, RNase A family, 4 | 5.81 | down | 0.00836 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| D38535_at | D38535 | 1654 | inter-alpha (globulin) inhibitor H4 (plasma | 13.2 | down | 0.01165 |
| rc_D45529_at | D45529 | 1662 | Kallikrein-sensitive glycoprotein) | 3.82 | down | 0.00193 |
| rc_D45556_at | D45556 | 1663 | EST | 4.83 | down | 0.01044 |
| rc_D45714_at | D45714 | 1664 | EST | 5.64 | down | 0.00384 |
| D49357_at | D49357 | 1665 | methionine adenosyltransferase I, alpha | 11.28 | down | 0.00331 |
| D49387_at | D49387 | 1666 | NADP dependent leukotriene b4 12- | 8.17 | down | 0.00972 |
| D49742_at | D49742 | 1668 | hyaluronan-binding protein 2 | 18.13 | down | 0.00012 |
| rc_D51199_at | D51199 | 1677 | EST | 5.05 | down | 0.00192 |
| rc_D51279_s_at | D51279 | 1679 | ovarian granulosa cell protein (13kD) | 5.88 | down | 0.01271 |
| rc_D52097_s_at | D52097 | 1682 | prostatic binding protein | 8.1 | down | 0.00141 |
| D57823_at | D57823 | 1690 | Sec23 (S. cerevisiae) homolog A | 4.43 | down | 0 |
| D58231_s_at | D58231 | 1692 | ubiquitin-like 3 | 3.07 | down | 0.0002 |
| rc_D59344_s_at | D59344 | 1695 | EST | 3.34 | down | 0.01337 |
| rc_D59554_f_at | D59554 | 1698 | EST | 6.7 | down | 0 |
| rc_D59714_s_at | D59714 | 1700 | mitogen inducible 2 | 17.62 | down | 0.00014 |
| rc_D60670_at | D60670 | 1702 | EST | 3.73 | down | 0.00382 |
| rc_D60769_s_at | D60769 | 1703 | KIAA0096 protein | 4.31 | down | 0.00142 |
| rc_D60856_f_at | D60856 | 1705 | UDP-glucose dehydrogenase | 6.45 | down | 0.01222 |
| D61991_at | D61991 | 1706 | EST | 4.84 | down | 0.00005 |
| D62103_s_at | D62103 | 1707 | EST | 4.11 | down | 0.0263 |
| rc_D62518_at | D62518 | 1708 | EST | 17.49 | down | 0.00017 |
| D63160_at | D63160 | 1709 | ficolin (collagen/fibrinogen domain-containing | 4.01 | down | 0.00391 |
| D78011_at | D78011 | 1717 | dihydropyrimidinase | 21.37 | down | 0.00003 |
| D79276_at | D79276 | 1722 | succinate-CoA ligase, GDP-forming, beta subunit | 6.8 | down | 0.00047 |
| D79687_at | D79687 | 1723 | KIAA1053 protein | 5.06 | down | 0.00047 |
| rc_D80050_at | D80050 | 1726 | EST | 4.64 | down | 0.01001 |
| rc_D80217_f_at | D80217 | 1727 | H91620p protein | 3.61 | down | 0.01973 |
| rc_D80218_f_at | D80218 | 1728 | brain acid-soluble protein 1 | 3.83 | down | 0.0137 |
| rc_D80312_f_at | D80312 | 1730 | EST | 3.74 | down | 0.01909 |
| rc_D80408_at | D80408 | 1731 | EST | 3.36 | down | 0.00102 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_D80905_at | D80905 | 1735 | EST | 3.59 | down | 0.0007 |
| D82061_at | D82061 | 1741 | Ke6 gene, mouse, human homolog of | 6.1 | down | 0.00104 |
| D82422_at | D82422 | 1745 | ferroportin 1; iron regulated gene 1 | 6.01 | down | 0.02351 |
| D85181_at | D85181 | 1750 | sterol-C5-desaturase (fungal ERG3, delta-5- | 9.56 | down | 0.00005 |
| D86062_s_at | D86062 | 1752 | ES1 (zebrafish) protein, human homolog of | 3.63 | down | 0.0001 |
| D87075_at | D87075 | 1760 | solute carrier family 23 (nucleobase transporters), | 4.15 | down | 0.00067 |
| D87436_at | D87436 | 1761 | KIAA0249 gene product | 5.49 | down | 0.00333 |
| D87449_at | D87449 | 1762 | KIAA0260 protein | 4.58 | down | 0.00026 |
| D87466_at | D87466 | 1763 | KIAA0276 protein | 4.83 | down | 0.0007 |
| D90042_at | D90042 | 1767 | N-acetyltransferase 2 (arylamine N- | 7.06 | down | 0 |
| D90282_at | D90282 | 1769 | carbamoyl-phosphate synthetase 1, mitochondrial | 27.29 | down | 0.00002 |
| rc_F02028_at | F02028 | 1774 | EST | 23.48 | down | 0.00465 |
| rc_F02094_at | F02094 | 1775 | ecotropic viral integration site 5 | 3.41 | down | 0.00495 |
| rc_F02245_at | F02245 | 1776 | monoamine oxidase A | 3.9 | down | 0.02943 |
| rc_F02345_at | F02345 | 1779 | EST | 3.9 | down | 0.0033 |
| rc_F03200_at | F03200 | 1783 | EST | 3.75 | down | 0.01805 |
| rc_F03969_at | F03969 | 1785 | matrix metalloproteinase 2 (gelatinase A, 72kD | 7.87 | down | 0.00014 |
| rc_F04335_at | F04335 | 1787 | gelatinase, 72kD type IV collagenase) | 3.16 | down | 0.0058 |
| rc_F04611_at | F04611 | 1792 | EST | 23.96 | down | 0.00018 |
| rc_F04944_s_at | F04944 | 1795 | acyl-Coenzyme A oxidase | 4.01 | down | 0.00242 |
| rc_F08817_at | F08817 | 1796 | EST | 8.29 | down | 0.0077 |
| rc_F08941_at | F08941 | 1798 | EST | 3.48 | down | 0.00428 |
| rc_F09058_at | F09058 | 1799 | EST | 3.6 | down | 0.00595 |
| rc_F09350_at | F09350 | 1801 | EST | 4.79 | down | 0.00088 |
| rc_F09353_at | F09353 | 1802 | solute carrier family 5 (inositol transporters), | 3.3 | down | 0.02841 |
| rc_F09578_at | F09578 | 1804 | core-binding factor, runt domain, alpha subunit 2; | 4.66 | down | 0.04463 |
| rc_F09979_at | F09979 | 1809 | translocated to, 3 | 4.36 | down | 0.02555 |
| rc_F10182_s_at | F10182 | 1812 | EST | 58.92 | down | 0.00837 |
| rc_F10276_s_at | F10276 | 1814 | hepsin (transmembrane protease, serine 1) | 8.13 | down | 0.0001 |
| | | | dual specificity phosphatase 6 | | | |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_F10466_at | F10466 | 1820 | EST | 5.32 | down | 0.02494 |
| rc_F10640_at | F10640 | 1821 | EST | 3.58 | down | 0.00152 |
| rc_F10874_f_at | F10874 | 1823 | EST | 4.19 | down | 0.00025 |
| rc_F10875_at | F10875 | 1824 | EST | 5.09 | down | 0.00004 |
| rc_F13702_at | F13702 | 1826 | EST | 6.01 | down | 0.00064 |
| rc_F13782_s_at | F13782 | 1827 | LIM binding domain 2 | 4.17 | down | 0.00109 |
| rc_H02848_s_at | H02848 | 1831 | TEK tyrosine kinase, endothelial (venous | | | |
| rc_H02855_at | H02855 | 1832 | malformations, multiple cutaneous and mucosal) | 3.47 | down | 0.0089 |
| rc_H03348_at | H03348 | 1833 | EST | 5.96 | down | 0.00458 |
| rc_H03945_at | H03945 | 1835 | claudin 1 | 5.77 | down | 0.0001 |
| rc_H04142_f_at | H04142 | 1836 | EST | 4.94 | down | 0.02603 |
| rc_H04242_at | H04242 | 1837 | EST | 3.57 | down | 0.01906 |
| H04854_at | H04854 | 1842 | RAB5B, member RAS oncogene family | 3.27 | down | 0.04826 |
| rc_H05072_at | H05072 | 1843 | interleukin 1 receptor accessory protein | 6.58 | down | 0.00007 |
| rc_H05974_s_at | H05974 | 1850 | EST | 3.12 | down | 0.01248 |
| rc_H05985_at | H05985 | 1851 | EST | 6.28 | down | 0.00549 |
| rc_H06063_s_at | H06063 | 1852 | hypothetical protein | 6.43 | down | 0.04887 |
| rc_H06144_at | H06144 | 1853 | chondroitin sulfate proteoglycan 3 (neurocan) | 3.15 | down | 0.00599 |
| rc_H06166_at | H06166 | 1854 | EST | 3.1 | down | 0.00745 |
| rc_H06935_s_at | H06935 | 1855 | electron-transferring-flavoprotein dehydrogenase | 3.31 | down | 0.03778 |
| rc_H08054_at | H08054 | 1857 | EST | 6.82 | down | 0.00105 |
| rc_H08102_at | H08102 | 1858 | breast cell glutaminase | 4.2 | down | 0.0009 |
| rc_H09167_at | H09167 | 1860 | KIAA0195 gene product | 27.77 | down | 0.00032 |
| rc_H09353_at | H09353 | 1866 | EST | 3.31 | down | 0.00313 |
| H09364_s_at | H09364 | 1867 | succinate dehydrogenase complex, subunit A, | 23.06 | down | 0.00094 |
| rc_H09594_at | H09594 | 1868 | EST | 5.74 | down | 0.03125 |
| rc_H09959_s_at | H09959 | 1869 | choline kinase | 3.12 | down | 0.00231 |
| H10482_at | H10482 | 1870 | EST | 3.25 | down | 0.00225 |
| rc_H10661_at | H10661 | 1871 | EST | 3.19 | down | 0.01611 |
| | | | | 4.54 | down | 0.00276 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_H10779_s_at | H10779 | 1872 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase | 9.73 | down | 0.00035 |
| rc_H11274_at | H11274 | 1874 | | 4.13 | down | 0.01478 |
| rc_H11739_s_at | H11739 | 1876 | glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein | 10.33 | down | 0.00023 |
| rc_H11746_at | H11746 | 1877 | | 3.92 | down | 0.00012 |
| rc_H12257_at | H12257 | 1879 | EST | 3.19 | down | 0.0069 |
| rc_H12593_at | H12593 | 1880 | zinc-finger protein 265 | 10.72 | down | 0.0056 |
| rc_H13696_at | H13696 | 1882 | EST | 3.48 | down | 0.01796 |
| rc_H14372_s_at | H14372 | 1883 | ATP-binding cassette, sub-family A (ABC1), | 5.16 | down | 0.00012 |
| rc_H16768_at | H16768 | 1887 | EST | 3.72 | down | 0.00688 |
| rc_H18950_at | H18950 | 1892 | EST | 3.85 | down | 0.00162 |
| rc_H18997_at | H18997 | 1893 | F-box protein 21 | 3.87 | down | 0.00611 |
| rc_H19504_f_at | H19504 | 1895 | EST | 3.13 | down | 0.04948 |
| rc_H20543_at | H20543 | 1897 | DKFZP586B1621 protein | 31.03 | down | 0.00074 |
| rc_H25124_at | H25124 | 1903 | EST | 3.65 | down | 0.00004 |
| rc_H25551_at | H25551 | 1904 | EST | 3.54 | down | 0.00366 |
| rc_H25836_at | H25836 | 1905 | tumor necrosis factor (ligand) superfamily, | 3.3 | down | 0.03125 |
| rc_H26417_at | H26417 | 1906 | EST | 3.22 | down | 0.03672 |
| rc_H26763_at | H26763 | 1907 | EST | 3.39 | down | 0.04188 |
| rc_H27330_at | H27330 | 1909 | EST | 3.2 | down | 0.00067 |
| rc_H27442_s_at | H27442 | 1910 | erythrocyte membrane protein band 7.2 | 6.81 | down | 0.00083 |
| rc_H29568_at | H29568 | 1914 | EST | 11.45 | down | 0.00058 |
| rc_H30270_at | H30270 | 1915 | EST | 17.09 | down | 0.00001 |
| rc_H38246_s_at | H38246 | 1917 | EST | 9.25 | down | 0.00157 |
| rc_H39119_at | H39119 | 1919 | EST | 3.06 | down | 0.03349 |
| rc_H40149_at | H40149 | 1921 | KIAA0937 protein | 4.59 | down | 0.00112 |
| rc_H40424_s_at | H40424 | 1922 | butyrate response factor 1 (EGF-response factor | 3.56 | down | 0.04066 |
| rc_H40534_at | H40534 | 1923 | EST | 3.18 | down | 0.01381 |
| rc_H41084_at | H41084 | 1924 | EST | 6.31 | down | 0.0227 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_H41280_at | H41280 | 1925 | EST | 3.68 | down | 0.00455 |
| rc_H42053_s_at | H42053 | 1927 | EST | 3.49 | down | 0.01057 |
| rc_H46001_at | H46001 | 1931 | EST | 5.03 | down | 0.00563 |
| H46990_at | H46990 | 1933 | cytochrome P450, subfamily IIE (ethanol- | 3.2 | down | 0.00095 |
| rc_H47391_at | H47391 | 1935 | EST | 3.1 | down | 0.03807 |
| rc_H47838_at | H47838 | 1936 | carboxypeptidase B2 (plasma) | 16.74 | down | 0.00002 |
| rc_H49415_at | H49415 | 1938 | EST | 3.72 | down | 0.0005 |
| H51340_at | H51340 | 1941 | EST | 3.73 | down | 0.02643 |
| rc_H54285_s_at | H54285 | 1947 | EST | 5.14 | down | 0.00426 |
| rc_H55759_at | H55759 | 1949 | EST | 11.52 | down | 0.00034 |
| rc_H56584_at | H56584 | 1951 | 4-nitrophenylphosphatase domain and non- | | | 0 |
| rc_H57060_s_at | H57060 | 1954 | neuronal SNAP25-like 1 | 9.5 | down | 0.01687 |
| rc_H57166_at | H57166 | 1955 | EST | 30.98 | down | 0.00007 |
| rc_H57816_at | H57816 | 1957 | EST | 60.76 | down | 0.00206 |
| rc_H57850_at | H57850 | 1958 | protein phosphatase 2 (formerly 2A), regulatory | | | |
| rc_H58673_at | H58673 | 1959 | subunit A (PR 65), beta isoform | 3.02 | down | 0.00123 |
| rc_h58692_s_at | H58692 | 1960 | EST | 14.85 | down | 0.00005 |
| rc_H59136_at | H59136 | 1962 | formyltetrahydrofolate dehydrogenase | 81.41 | down | 0 |
| rc_H59141_at | H59141 | 1963 | EST | 8.64 | down | 0.00013 |
| rc_H60595_s_at | H60595 | 1966 | progesterone binding protein | 3.12 | down | 0.00293 |
| H61295_s_at | H61295 | 1968 | CD4 antigen (p55) | 15.8 | down | 0.01078 |
| rc_H62838_at | H62838 | 1971 | EST | 10.71 | down | 0.00925 |
| rc_H63251_at | H63251 | 1972 | KIAA0606 protein; SCN Circadian Oscillatory | 3.09 | down | 0.03201 |
| rc_H65650_at | H65650 | 1976 | EST | 3.27 | down | 0.02455 |
| H66367_at | H66367 | 1977 | EST | 3.88 | down | 0.0083 |
| rc_H66840_at | H66840 | 1978 | EST | 6.68 | down | 0.0001 |
| rc_H67094_at | H67094 | 1979 | EST | 3.67 | down | 0.0143 |
| H67840_at | H67840 | 1980 | EST | 3.24 | down | 0.00075 |
| rc_H68097_at | H68097 | 1982 | EST | 3.1 | down | 0.00528 |
| | | | | 3.83 | down | 0.00797 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| H68953_at | H68953 | 1985 | transferrin | 6.4 | down | 0.00132 |
| rc_H69138_at | H69138 | 1986 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene | 6.76 | down | 0.00142 |
| rc_H69565_at | H69565 | 1987 | EST | 4.11 | down | 0.00002 |
| rc_H70554_at | H70554 | 1989 | EST | 10.99 | down | 0 |
| rc_H71169_at | H71169 | 1992 | putative protein similar to nessy (Drosophila) glucan (1,4-alpha-), branching enzyme 1 | 4 | down | 0.00709 |
| rc_H71861_s_at | H71861 | 1993 | (glycogen branching enzyme, Andersen disease, | 5.97 | down | 0.00007 |
| rc_H73535_s_at | H73535 | 1996 | EST | 6.89 | down | 0.00202 |
| rc_H74317_s_at | H74317 | 1997 | apolipoprotein A-II | 45.09 | down | 0.01982 |
| rc_H77597_f_at | H77597 | 2000 | metallothionein 1H | 16.03 | down | 0.00675 |
| H78628_at | H78628 | 2003 | EST | 4.98 | down | 0.00729 |
| rc_H79820_at | H79820 | 2004 | EST | 3.25 | down | 0.01466 |
| rc_H80901_s_at | H80901 | 2005 | ficolin (collagen/fibrinogen domain-containing) 3 | 50.61 | down | 0.00262 |
| rc_H81070_f_at | H81070 | 2006 | RNA helicase-related protein | 25.74 | down | 0.00126 |
| rc_H82966_s_at | H82966 | 2011 | apolipoprotein B (including Ag(x) antigen) | 3.42 | down | 0.00769 |
| rc_H83109_f_at | H83109 | 2012 | EST | 16.55 | down | 0.00001 |
| rc_H83442_s_at | H83442 | 2013 | catechol-O-methyltransferase | 3.99 | down | 0.00594 |
| rc_H83451_at | H83451 | 2014 | EST | 3.35 | down | 0.00498 |
| rc_H87144_at | H87144 | 2016 | EST | 3.41 | down | 0.00387 |
| rc_H87765_at | H87765 | 2017 | KIAA0626 gene product | 3.86 | down | 0.00131 |
| H88033_s_at | H88033 | 2019 | KIAA0733 protein | 4.42 | down | 0.02032 |
| rc_H88359_s_at | H88359 | 2020 | nuclear factor (erythroid-derived 2)-like 2 | 5.16 | down | 0.01253 |
| rc_H88675_at | H88675 | 2022 | EST | 5.63 | down | 0.00554 |
| rc_H89514_s_at | H89514 | 2023 | protein kinase, cAMP-dependent, catalytic, alpha | 3.44 | down | 0.00435 |
| rc_H89893_at | H89893 | 2025 | EST | 3.17 | down | 0.00658 |
| rc_H89980_at | H89980 | 2026 | protein phosphatase 1, regulatory (inhibitor) | 31.13 | down | 0.00006 |
| rc_H90417_s_at | H90417 | 2028 | EST | 4.17 | down | 0.015 |
| rc_H91325_s_at | H91325 | 2029 | aldolase B, fructose-bisphosphate | 45.85 | down | 0.00505 |
| rc_H91456_s_at | H91456 | 2030 | nuclear receptor subfamily 1, group H, member 4 | 4.9 | down | 0.00255 |
| | | | phosphorylase, glycogen; liver (Hers disease, | | | |
| rc_H91680_s_at | H91680 | 2032 | glycogen storage disease type VI) | 4.15 | down | 0.00746 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_H93053_s_at | H93053 | 2034 | glutamate-cysteine ligase (gamma- | 5.06 | down | 0.01029 |
| H93246_s_at | H93246 | 2035 | glutamylcysteine synthetase), catalytic (72.8kD) | 15.3 | down | 0.00233 |
| rc_H93381_at | H93381 | 2036 | EST | 24.23 | down | 0 |
| rc_H93562_at | H93562 | 2038 | proline synthetase co-transcribed (bacterial | 3.17 | down | 0.00113 |
| | | | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase | | | |
| rc_H94247_s_at | H94247 | 2041 | 2 (mitochondrial) | 9.49 | down | 0.02373 |
| rc_H94475_s_at | H94475 | 2043 | alpha-2-plasmin inhibitor | 40.92 | down | 0.00271 |
| rc_H94648_at | H94648 | 2044 | EST | 4.77 | down | 0.00266 |
| rc_H94666_at | H94666 | 2045 | alpha-1-B glycoprotein | 47.03 | down | 0.01158 |
| rc_H95358_at | H95358 | 2049 | EST | 3.17 | down | 0.00182 |
| rc_H95569_i_at | H95569 | 2051 | DKFZP586A0522 protein | 28.48 | down | 0.00139 |
| rc_H95978_at | H95978 | 2052 | EST | 8.55 | down | 0.00046 |
| rc_H96614_at | H96614 | 2054 | EST | 4.02 | down | 0.01565 |
| rc_H97868_at | H97868 | 2064 | EST | 3.86 | down | 0.00362 |
| rc_H97986_at | H97986 | 2065 | EST | 3.86 | down | 0.01534 |
| rc_H98071_at | H98071 | 2066 | EST | 4.66 | down | 0.03722 |
| rc_H98083_at | H98083 | 2067 | EST | 5.09 | down | 0.00025 |
| rc_H98771_i_at | H98771 | 2069 | BCL2/adenovirus E1B 19kD-interacting protein 3 | 8 | down | 0.0018 |
| rc_H98822_at | H98822 | 2070 | EST | 3.31 | down | 0.00174 |
| rc_H98910_s_at | H98910 | 2071 | EST | 4.38 | down | 0.00548 |
| rc_H98977_at | H98977 | 2073 | EST | 3.57 | down | 0.00298 |
| rc_H99393_s_at | H99393 | 2076 | endothelin receptor type B | 3.43 | down | 0.00093 |
| rc_H99727_at | H99727 | 2080 | adipose differentiation-related protein; adipophilin | 5.83 | down | 0.04346 |
| rc_H99935_s_at | H99935 | 2085 | interleukin 6 signal transducer (gp130, oncostatin | 3.59 | down | 0.00366 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|---------------|---------|--------|---|-------------|-----------|---------|
| J02843_at | J02843 | 2088 | cytochrome P450, subfamily IIE (ethanol- | 22.58 | down | 0.00935 |
| J02888_at | J02888 | 2089 | NAD(P)H menadiene oxidoreductase 2, dioxin- | 3.15 | down | 0.02385 |
| J02943_at | J02943 | 2090 | corticosteroid binding globulin | 18.98 | down | 0.00087 |
| J03242_s_at | J03242 | 2092 | insulin-like growth factor 2 (somatomedin A) | 4.01 | down | 0.00042 |
| J03507_at | J03507 | 2095 | complement component 7 | 3.77 | down | 0.00184 |
| J03764_at | J03764 | 2097 | plasminogen activator inhibitor, type 1 | 5.6 | down | 0.02196 |
| J03805_s_at | J03805 | 2098 | protein phosphatase 2 (formerly 2A), catalytic | 3.87 | down | 0.0116 |
| J03810_at | J03810 | 2099 | subunit, beta isoform | 21.99 | down | 0.00004 |
| J03910_ma1_at | J03910 | 2101 | solute carrier family 2 (facilitated glucose EST | 12.42 | down | 0.01167 |
| J04031_at | J04031 | 2103 | methylenetetrahydrofolate dehydrogenase | 3.4 | down | 0.00786 |
| J04056_at | J04056 | 2104 | (NADP+ dependent), methylenetetrahydrofolate | 5.19 | down | 0.00001 |
| J04080_at | J04080 | 2105 | cyclohydrolase, formyltetrahydrofolate synthetase | 5.48 | down | 0.0239 |
| J04093_s_at | J04093 | 2106 | carboxyl reductase 1 | 18.92 | down | 0 |
| | | | complement component 1, s subcomponent | | | |
| | | | UDP glycosyltransferase 1 | | | |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------|---------|--------|--|-------------|-----------|---------|
| J04093_s_at | J04093 | 2106 | UDP glycosyltransferase 1 | 18.92 | down | 0 |
| J04449_at | J04449 | 2110 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3 | 5.25 | down | 0.01583 |
| J04615_at | J04615 | 2112 | SNRPN upstream reading frame | 3.14 | down | 0.02928 |
| J04621_at | J04621 | 2113 | syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) | 3.38 | down | 0.00275 |
| J04813_s_at | J04813 | 2114 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 5 | 9.67 | down | 0.0107 |
| J05037_at | J05037 | 2116 | serine dehydratase | 16.24 | down | 0.00015 |
| J05158_at | J05158 | 2117 | carboxypeptidase N, polypeptide 2, 83kD | 8.52 | down | 0 |
| J05428_at | J05428 | 2120 | UDP glycosyltransferase 2 family, polypeptide B7 | 16.14 | down | 0.00563 |
| K02100_at | K02100 | 2123 | ornithine carbamoyltransferase | 10.24 | down | 0.00009 |
| K02215_at | K02215 | 2124 | angiotensinogen | 16.51 | down | 0.00006 |
| K02402_at | K02402 | 2125 | coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) | 28.81 | down | 0.00001 |
| K02766_at | K02766 | 2126 | complement component 9 | 21.24 | down | 0 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 69.92 | down | 0 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 50.16 | down | 0 |
| L00190_s_at | L00190 | 2130 | antithrombin III | 42.41 | down | 0.00012 |
| L00352_at | L00352 | 2131 | low density lipoprotein receptor (familial) | 4.19 | down | 0.00352 |
| L00972_at | L00972 | 2133 | cystathionine-beta-synthase | 7.19 | down | 0.00008 |
| L04751_at | L04751 | 2138 | cytochrome P450, subfamily IVA, polypeptide 11 | 36.79 | down | 0.00004 |
| L05144_at | L05144 | 2139 | phosphoenolpyruvate carboxykinase 1 (soluble) | 4.76 | down | 0.02289 |
| L05779_at | L05779 | 2140 | epoxide hydrolase 2, cytoplasmic | 5.35 | down | 0.00006 |
| L07033_at | L07033 | 2144 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) | 3.49 | down | 0 |
| L07077_at | L07077 | 2145 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl | 4.82 | down | 0.00403 |
| L07765_at | L07765 | 2147 | Coenzyme A dehydrogenase | 20.53 | down | 0.00025 |
| | | | carboxylesterase 1 (monocyte/macrophage) | | | |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------|---------|--------|--|-------------|-----------|---------|
| L07956_at | L07956 | 2148 | glucan (1,4-alpha-), branching enzyme 1 | 5.6 | down | 0.00029 |
| L09229_s_at | L09229 | 2150 | (glycogen branching enzyme, Andersen disease, fatty-acid-Coenzyme A ligase, long-chain 1, fatty-acid-Coenzyme A ligase, long-chain 2 | 18.34 | down | 0.00016 |
| L09708_at | L09708 | 2152 | complement component 2 | 3.92 | down | 0.00693 |
| L09717_at | L09717 | 2153 | lysosomal-associated membrane protein 2 | 4.06 | down | 0.00034 |
| L11005_at | L11005 | 2154 | aldehyde oxidase 1 | 16.3 | down | 0.00065 |
| L11244_s_at | L11244 | 2155 | complement component 4-binding protein, beta | 43.33 | down | 0 |
| L11244_s_at | L11244 | 2155 | complement component 4-binding protein, beta | 12.03 | down | 0.0001 |
| L11708_at | L11708 | 2158 | hydroxysteroid (17-beta) dehydrogenase 2 | 5.99 | down | 0.01516 |
| L11931_at | L11931 | 2159 | serine hydroxymethyltransferase 1 (soluble) | 7.27 | down | 0.00041 |
| L12760_s_at | L12760 | 2162 | phosphoenolpyruvate carboxykinase 1 (soluble) | 12.75 | down | 0.00035 |
| L13278_at | L13278 | 2163 | crystallin, zeta (quinone reductase) | 5.83 | down | 0.0034 |
| L15702_at | L15702 | 2165 | B-factor, properdin | 3.7 | down | 0.04693 |
| L16883_s_at | L16883 | 2166 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 | 84.71 | down | 0.00327 |
| L17128_at | L17128 | 2167 | gamma-glutamyl carboxylase | 4.02 | down | 0.00096 |
| L20965_at | L20965 | 2175 | phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) | 3.02 | down | 0.01177 |
| L21893_at | L21893 | 2176 | solute carrier family 10 (sodium/bile acid cotransporter family), member 1 | 13.18 | down | 0.00155 |
| L22548_at | L22548 | 2178 | collagen, type XVIII, alpha 1 | 3.87 | down | 0.0299 |
| L25878_s_at | L25878 | 2183 | epoxide hydrolase 1, microsomal (xenobiotic) | 26.84 | down | 0 |
| L25880_s_at | L25880 | 2184 | epoxide hydrolase 1, microsomal (xenobiotic) | 58.7 | down | 0.00013 |
| L27050_at | L27050 | 2186 | apolipoprotein F | 10.26 | down | 0.00026 |
| L29008_at | L29008 | 2189 | sorbitol dehydrogenase | 3.51 | down | 0.00825 |
| L29433_at | L29433 | 2191 | coagulation factor X | 7.74 | down | 0.00244 |
| L32140_at | L32140 | 2192 | afamin | 17.31 | down | 0.00003 |
| L32179_at | L32179 | 2193 | arylamide deacetylase (esterase) | 23.83 | down | 0 |
| L34081_at | L34081 | 2199 | bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase) | 11.96 | down | 0.00008 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| L35546_at | L35546 | 2203 | glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) | 14.18 | down | 0.00018 |
| L35546_at | L35546 | 2203 | glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) | 5.56 | down | 0.0005 |
| L36033_at | L36033 | 2204 | stromal cell-derived factor 1 | 5.1 | down | 0.00603 |
| L38490_s_at | L38490 | 2207 | ADP-ribosylation factor 4-like | 3.13 | down | 0.01306 |
| L38928_at | L38928 | 2209 | 5,10-methylenetetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) | 10.97 | down | 0.0267 |
| L38928_at | L38928 | 2209 | 5,10-methylenetetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) | 5.17 | down | 0.00726 |
| L40401_at | L40401 | 2211 | putative protein | 6.97 | down | 0.00079 |
| L40401_at | L40401 | 2211 | putative protein | 4.26 | down | 0.00194 |
| L41067_at | L41067 | 2213 | nuclear factor of activated T-cells, cytoplasmic 3 | 4.96 | down | 0.00473 |
| L47726_at | L47726 | 2219 | phenylalanine hydroxylase | 25.63 | down | 0.00019 |
| L48516_at | L48516 | 2220 | paraoxonase 3 | 22.21 | down | 0.00004 |
| L49169_at | L49169 | 2221 | FBJ murine osteosarcoma viral oncogene | 3.4 | down | 0.01193 |
| L76465_at | L76465 | 2224 | hydroxyprostaglandin dehydrogenase 15-(NAD) | 3.56 | down | 0.00688 |
| L76571_at | L76571 | 2226 | nuclear receptor subfamily 0, group B, member 2 | 4.44 | down | 0.00312 |
| L76687_at | L76687 | 2227 | growth factor receptor-bound protein 14 | 5.16 | down | 0.00199 |
| L76927_rna1_at | L76927 | 2228 | galactokinase 1 | 3.66 | down | 0.00999 |
| L77567_s_at | L77567 | 2229 | solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 | 3.14 | down | 0.04095 |
| M10058_at | M10058 | 2230 | asialoglycoprotein receptor 1 | 23.96 | down | 0 |
| M10612_at | M10612 | 2232 | apolipoprotein C-II | 17.13 | down | 0.00746 |
| M10942_at | M10942 | 2233 | metallothionein 1E (functional) | 6.19 | down | 0.00428 |
| M10943_at | M10943 | 2234 | metallothionein 1F (functional) | 3.88 | down | 0 |
| M11025_s_at | M11025 | 2235 | asialoglycoprotein receptor 2 | 17.56 | down | 0.00003 |
| M11313_s_at | M11313 | 2236 | alpha-2-macroglobulin | 10.05 | down | 0.00014 |
| M11321_at | M11321 | 2237 | group-specific component (vitamin D binding | 16.52 | down | 0.01416 |
| M11437_cds1_at | M11437 | 2238 | kininogen | 18.38 | down | 0.00006 |
| M11437_cds2_at | M11437 | 2238 | kininogen | 16.19 | down | 0.02277 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------|---------|--------|--|-------------|-----------|---------|
| M16967_at | M16967 | 2275 | coagulation factor V (proaccelerin, labile factor) | 5.56 | down | 0.00047 |
| M16973_at | M16973 | 2276 | complement component 8, beta polypeptide | 22.75 | down | 0.00001 |
| M16974_s_at | M16974 | 2277 | complement component 8, alpha polypeptide | 49.47 | down | 0.00046 |
| M17262_at | M17262 | 2278 | coagulation factor II (thrombin) | 44.3 | down | 0.00345 |
| M17262_at | M17262 | 2278 | coagulation factor II (thrombin) | 14.24 | down | 0.00028 |
| M17466_at | M17466 | 2279 | coagulation factor XII (Hageman factor) | 9.76 | down | 0.00285 |
| | | | dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, apolipoprotein B (including Ag(x) antigen) | 3.45 | down | 0.00313 |
| M18533_at | M18533 | 2284 | coagulation factor XI (plasma thromboplastin alpha-2-plasmin inhibitor) | 29.37 | down | 0.00137 |
| M19828_s_at | M19828 | 2287 | glutamate dehydrogenase 1 | 6.4 | down | 0.00004 |
| M20218_at | M20218 | 2288 | apolipoprotein C-I | 16.95 | down | 0.00709 |
| M20786_at | M20786 | 2290 | antithrombin III | 17.73 | down | 0.00002 |
| M20867_s_at | M20867 | 2291 | antithrombin III | 3.14 | down | 0.0389 |
| M20902_at | M20902 | 2292 | cytochrome b-5 | 15.82 | down | 0.01027 |
| M21642_at | M21642 | 2294 | EST | 15.23 | down | 0.02088 |
| M21642_s_at | M21642 | 2294 | ATP-binding cassette, sub-family B (MDR/TAP), androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 7.39 | down | 0.02431 |
| M22976_at | M22976 | 2297 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 3.44 | down | 0.00733 |
| M23161_at | M23161 | 2298 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 10.05 | down | 0 |
| M23234_s_at | M23234 | 2299 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 4.6 | down | 0.00005 |
| M23263_at | M23263 | 2300 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 3.35 | down | 0.02551 |
| M23263_at | M23263 | 2300 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | 3.19 | down | 0.04985 |
| M24283_at | M24283 | 2303 | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor | 9.15 | down | 0.01399 |
| M25079_s_at | M25079 | 2305 | hemoglobin, beta | 3.39 | down | 0.004 |
| M25280_at | M25280 | 2306 | selectin L (lymphocyte adhesion molecule 1) | 16.27 | down | 0.00007 |
| M26393_s_at | M26393 | 2309 | acyl-Coenzyme A dehydrogenase, C-2 to C-3 | 4.62 | down | 0.0082 |
| M27492_at | M27492 | 2312 | interleukin 1 receptor, type I | | | |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|-------------|---------|--------|---|-------------|-----------|---------|
| M29194_at | M29194 | 2315 | lipase, hepatic | 12.18 | down | 0.00012 |
| M29873_s_at | M29873 | 2318 | cytochrome P450, subfamily 11B (phenobarbital-) | 56.71 | down | 0.0054 |
| M29874_s_at | M29874 | 2319 | cytochrome P450, subfamily 11B (phenobarbital-) | 18.44 | down | 0.00081 |
| M29971_at | M29971 | 2320 | O-6-methylguanine-DNA methyltransferase | 3.97 | down | 0.00424 |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, plasma | 3.83 | down | 0.0013 |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, plasma | 3.39 | down | 0.00089 |
| M30257_s_at | M30257 | 2322 | vascular cell adhesion molecule 1 | 3.11 | down | 0.00064 |
| M30269_at | M30269 | 2323 | nidogen (enactin) | 3.4 | down | 0.00026 |
| M31169_s_at | M31169 | 2325 | propionyl Coenzyme A carboxylase, beta | 4.65 | down | 0.00467 |
| M31627_at | M31627 | 2330 | X-box binding protein 1 | 6.97 | down | 0.00052 |
| M31667_f_at | M31667 | 2331 | cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2 | 4.38 | down | 0.00078 |
| M31994_at | M31994 | 2332 | aldehyde dehydrogenase 1, soluble | 11.24 | down | 0.01192 |
| M33317_f_at | M33317 | 2338 | cytochrome P450, subfamily 11A (phenobarbital-inducible), polypeptide 7 | 32.63 | down | 0 |
| M33318_r_at | M33318 | 2339 | cytochrome P450, subfamily 11A (phenobarbital-inducible), polypeptide 6 | 3.21 | down | 0.01621 |
| M34276_at | M34276 | 2341 | plasminogen | 24.73 | down | 0.00031 |
| M35410_s_at | M35410 | 2344 | insulin-like growth factor binding protein 2 (36kD) | 6.45 | down | 0.04517 |
| MIP1-B_at | M35590 | 2345 | small inducible cytokine A4 | 5.96 | down | 0.00604 |
| MIP1-B_at | M35590 | 2345 | small inducible cytokine A4 | 4.74 | down | 0.01225 |
| MIP1-B_at | M35590 | 2345 | small inducible cytokine A4 | 4.62 | down | 0.01268 |
| M35878_at | M35878 | 2346 | insulin-like growth factor binding protein 3 | 4.3 | down | 0.0027 |
| M37400_at | M37400 | 2348 | glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) | 8.7 | down | 0.0004 |
| M55150_at | M55150 | 2352 | fumarylacetoacetate | 3.93 | down | 0.00213 |
| M55513_s_at | M55513 | 2354 | potassium voltage-gated channel, shaker-related subfamily, member 5 | 4.81 | down | 0.02141 |
| M55671_at | M55671 | 2355 | protein Z, vitamin K-dependent plasma | 4.74 | down | 0.00078 |
| M57731_s_at | M57731 | 2359 | GRO2 oncogene | 13.87 | down | 0.0123 |
| M58286_s_at | M58286 | 2360 | tumor necrosis factor receptor superfamily, | 8.15 | down | 0.00037 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-----------------|---------|--------|--|-------------|-----------|---------|
| M58569_s_at | M58569 | 2361 | EST | 16.15 | down | 0.00174 |
| M58600_ma1_at | M58600 | 2362 | heparin cofactor II | 39.79 | down | 0.00034 |
| M59499_at | M59499 | 2363 | tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) | 5.92 | down | 0.0005 |
| M59815_at | M59815 | 2364 | complement component 4A | 8.02 | down | 0.00049 |
| M59916_at | M59916 | 2365 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) | 3.36 | down | 0.0038 |
| M60974_s_at | M60974 | 2368 | growth arrest and DNA-damage-inducible, alpha | 3.48 | down | 0.00209 |
| M61853_at | M61853 | 2369 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18 | 7.82 | down | 0.00024 |
| M61854_s_at | M61854 | 2370 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 | 3.3 | down | 0.04185 |
| M61855_at | M61855 | 2371 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 | 38.82 | down | 0.00023 |
| M62403_s_at | M62403 | 2373 | insulin-like growth factor-binding protein 4 | 4.12 | down | 0.00226 |
| M62486_at | M62486 | 2374 | complement component 4-binding protein, alpha | 22.08 | down | 0.00272 |
| M63509_s_at | M63509 | 2376 | glutathione S-transferase M1, glutathione S-transferase M2 (muscle), glutathione S- | 7.06 | down | 0.03887 |
| M63967_at | M63967 | 2378 | aldehyde dehydrogenase 5 | 4.04 | down | 0.00058 |
| M64554_ma1_at | M64554 | 2380 | coagulation factor XIII, B polypeptide | 5.87 | down | 0.00011 |
| M64590_at | M64590 | 2381 | glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein | 6.41 | down | 0.00002 |
| M65131_ma1_at | M65131 | 2384 | methylenetetrahydrofolate dehydrogenase | 7.44 | down | 0.00004 |
| M65134_s_at | M65134 | 2385 | complement component 5 | 12.01 | down | 0.00012 |
| M65292_s_at | M65292 | 2386 | H factor (complement)-like 1, H factor 1 | 7.56 | down | 0.01152 |
| M68516_ma1_at | M68516 | 2387 | protein C inhibitor (plasminogen activator inhibitor | 20.54 | down | 0 |
| M68840_at | M68840 | 2388 | monoamine oxidase A | 3.96 | down | 0.01396 |
| M68895_ma1_at | M68895 | 2390 | alcohol dehydrogenase 6 (class V) | 4.25 | down | 0.00354 |
| M69177_at | M69177 | 2392 | monoamine oxidase B | 11.64 | down | 0.00001 |
| M72885_ma1_s_at | M72885 | 2393 | putative lymphocyte G0/G1 switch gene | 6.5 | down | 0.03461 |
| M74587_ma1_s_at | M74587 | 2394 | insulin-like growth factor binding protein 1 | 11.42 | down | 0.00274 |
| M75106_at | M75106 | 2397 | carboxypeptidase B2 (plasma) | 40.63 | down | 0 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| M76665_at | M76665 | 2398 | hydroxysteroid (11-beta) dehydrogenase 1 | 19.22 | down | 0.00004 |
| M80482_at | M80482 | 2403 | paired basic amino acid cleaving system 4 | 4.26 | down | 0.00041 |
| M81182_s_at | M81182 | 2404 | ATP-binding cassette, sub-family D (ALD), | 3.45 | down | 0.00499 |
| M81349_at | M81349 | 2405 | serum amyloid A4, constitutive | 76.15 | down | 0.00015 |
| M83216_s_at | M83216 | 2407 | caldesmon 1 | 4.27 | down | 0.00037 |
| M83652_s_at | M83652 | 2408 | properdin P factor, complement | 6 | down | 0.00002 |
| M83772_at | M83772 | 2409 | flavin containing monooxygenase 3 | 19.54 | down | 0 |
| M86826_at | M86826 | 2413 | insulin-like growth factor binding protein, acid | 3.75 | down | 0.01157 |
| M86873_s_at | M86873 | 2414 | plasminogen, plasminogen-like | 17.54 | down | 0 |
| | | | SWI/SNF related, matrix associated, actin | | | |
| M88163_at | M88163 | 2416 | dependent regulator of chromatin, subfamily a, | 3.37 | down | 0.00098 |
| M91432_at | M91432 | 2420 | acyl-Coenzyme A dehydrogenase, C-4 to C-12 | 6.74 | down | 0.00008 |
| M92843_s_at | M92843 | 2421 | zinc finger protein homologous to Zfp-36 in | 3.02 | down | 0.04958 |
| M93143_at | M93143 | 2423 | plasminogen-like | 10.06 | down | 0.00098 |
| M93405_at | M93405 | 2424 | methylmalonate-semialdehyde dehydrogenase | 23.06 | down | 0 |
| M94065_s_at | M94065 | 2425 | dihydroorotate dehydrogenase | 11.78 | down | 0.00034 |
| M94065_at | M94065 | 2425 | dihydroorotate dehydrogenase | 6.47 | down | 0.00013 |
| M95585_s_at | M95585 | 2430 | hepatic leukemia factor | 4.2 | down | 0.00212 |
| M95767_at | M95767 | 2432 | chitobiose, di-N-acetyl- | 4.94 | down | 0.00004 |
| | | | glutathione S-transferase M1, glutathione S- | | | |
| M96233_s_at | M96233 | 2433 | transferase M2 (muscle), glutathione S- | 4.23 | down | 0.04227 |
| M96843_at | M96843 | 2435 | EST | 8.42 | down | 0.02394 |
| M96843_at | M96843 | 2435 | EST | 4.08 | down | 0.02912 |
| M99439_at | M99439 | 2438 | transducin-like enhancer of split 4, homolog of | 5.14 | down | 0.00001 |
| rc_N20113_s_at | N20113 | 2439 | EST | 5.24 | down | 0.01346 |
| rc_N21079_at | N21079 | 2441 | nucleolar cysteine-rich protein | 4.1 | down | 0.00028 |
| rc_N21550_at | N21550 | 2444 | EST | 3.08 | down | 0.00006 |
| rc_N21646_at | N21646 | 2446 | EST | 3.79 | down | 0.00079 |
| rc_N22404_at | N22404 | 2450 | EST | 3.99 | down | 0.01152 |
| rc_N22434_at | N22434 | 2451 | EST | 4.37 | down | 0.01725 |
| rc_N22854_s_at | N22854 | 2452 | CASP2 and RIPK1 domain containing adaptor | 3.34 | down | 0.0084 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_N22938_s_at | N22938 | 2453 | serum amyloid A4, constitutive | 35.39 | down | 0.00128 |
| rc_N23665_s_at | N23665 | 2455 | hydroxysteroid (17-beta) dehydrogenase 2 | 9.4 | down | 0.00055 |
| rc_N23730_s_at | N23730 | 2456 | v-fos FBJ murine osteosarcoma viral oncogene | 4.38 | down | 0.04395 |
| rc_N23761_at | N23761 | 2457 | DKFZP586G011 protein | 5.41 | down | 0.00448 |
| N23817_at | N23817 | 2458 | EST | 3.76 | down | 0.00288 |
| rc_N24879_at | N24879 | 2460 | EST | 9.44 | down | 0.00008 |
| rc_N25082_s_at | N25082 | 2463 | amplified in osteosarcoma | 5.19 | down | 0.00895 |
| rc_N25193_at | N25193 | 2464 | EST | 3.13 | down | 0.01955 |
| rc_N25969_s_at | N25969 | 2466 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | 4.32 | down | 0.00304 |
| rc_N26184_at | N26184 | 2467 | MYLE protein | 4.82 | down | 0.00056 |
| rc_N27524_at | N27524 | 2472 | EST | 3.13 | down | 0.00216 |
| rc_N27563_at | N27563 | 2473 | EST | 3.3 | down | 0.00021 |
| N27670_at | N27670 | 2474 | progesterone membrane binding protein | 6.15 | down | 0.00321 |
| rc_N27834_at | N27834 | 2475 | alpha2,3-sialyltransferase | 5.31 | down | 0.00039 |
| rc_N29319_at | N29319 | 2476 | EST | 4.58 | down | 0.00011 |
| rc_N29353_at | N29353 | 2477 | kynurenine 3-monooxygenase (kynurenine 3-solute carrier family 19 (thiamine transporter), EST | 4.78 | down | 0.00019 |
| rc_N30856_at | N30856 | 2485 | EST | 3.71 | down | 0.00393 |
| rc_N31598_at | N31598 | 2488 | serine hydroxymethyltransferase 1 (soluble) | 3.1 | down | 0.00203 |
| rc_N31741_at | N31741 | 2489 | EST | 14.76 | down | 0.00001 |
| rc_N31952_at | N31952 | 2490 | EST | 3.13 | down | 0.01481 |
| rc_N32071_at | N32071 | 2491 | EST | 8.75 | down | 0.00006 |
| rc_N33009_s_at | N33009 | 2492 | apolipoprotein E | 60.54 | down | 0.0093 |
| rc_N34441_at | N34441 | 2496 | EST | 3.07 | down | 0.00186 |
| rc_N34804_at | N34804 | 2497 | DKFZP434J214 protein | 8.08 | down | 0.00028 |
| rc_N36001_at | N36001 | 2504 | EST | 6.16 | down | 0.00222 |
| rc_N36250_at | N36250 | 2506 | cellular repressor of E1A-stimulated genes | 4.06 | down | 0.00776 |
| rc_N39163_at | N39163 | 2509 | metallothionein 1L | 4.3 | down | 0.03917 |
| rc_N39201_at | N39201 | 2510 | protease inhibitor 4 (kallistatin) | 24.91 | down | 0.00253 |
| rc_N40188_at | N40188 | 2513 | EST | 3.72 | down | 0.01771 |
| N40320_at | N40320 | 2514 | EST | 7.56 | down | 0.01584 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_N45232_at | N45232 | 2517 | EST | 3.61 | down | 0.01308 |
| rc_N45307_s_at | N45307 | 2518 | EST | 4.55 | down | 0.00006 |
| rc_N45998_at | N45998 | 2520 | EST | 3.14 | down | 0.00337 |
| rc_N47469_at | N47469 | 2522 | EST | 3.34 | down | 0.00329 |
| rc_N47942_at | N47942 | 2523 | progesterone membrane binding protein | 4.51 | down | 0.00168 |
| rc_N48180_at | N48180 | 2526 | EST | 3.36 | down | 0.00543 |
| rc_N48315_at | N48315 | 2527 | adaptor-related protein complex 2, mu 1 subunit | 5.3 | down | 0.0149 |
| rc_N48602_at | N48602 | 2529 | EST | 3.17 | down | 0.02913 |
| rc_N48674_at | N48674 | 2530 | EST | 4.06 | down | 0.00028 |
| rc_N48787_at | N48787 | 2531 | protease inhibitor 1 (anti-elastase), alpha-1- | 4.4 | down | 0.00292 |
| rc_N49090_at | N49090 | 2533 | EST | 18 | down | 0.00501 |
| rc_N49104_s_at | N49104 | 2534 | nuclear receptor interacting protein 1 | 3.83 | down | 0.00144 |
| rc_N49113_at | N49113 | 2535 | EST | 3.4 | down | 0.00162 |
| rc_N49214_at | N49214 | 2536 | EST | 4.74 | down | 0.00064 |
| rc_N49595_at | N49595 | 2538 | EST | 10.39 | down | 0.00022 |
| rc_N49902_at | N49902 | 2540 | EST | 3.55 | down | 0.00455 |
| rc_N51117_at | N51117 | 2544 | EST | 9.68 | down | 0.00081 |
| rc_N51737_at | N51737 | 2547 | mitogen-activated protein kinase kinase kinase | 3.32 | down | 0.00376 |
| rc_N51773_at | N51773 | 2549 | EST | 16.32 | down | 0.0007 |
| rc_N52271_at | N52271 | 2552 | LIM protein (similar to rat protein kinase C- | 8.06 | down | 0.00011 |
| rc_N52322_at | N52322 | 2553 | EST | 3.27 | down | 0.00933 |
| rc_N52845_at | N52845 | 2554 | EST | 5.53 | down | 0.00088 |
| rc_N52985_at | N52985 | 2555 | nidogen (enactin) | 4.21 | down | 0.01385 |
| rc_N53031_s_at | N53031 | 2556 | UDP glycosyltransferase 2 family, polypeptide B4 | 97.58 | down | 0.00022 |
| rc_N53352_at | N53352 | 2558 | EST | 3.22 | down | 0.00416 |
| rc_N53549_s_at | N53549 | 2559 | cytochrome P450, subfamily IIJ (arachidonic acid | | | |
| rc_N53757_at | N53757 | 2560 | epoxygenase) polypeptide 2 | 4.68 | down | 0.00818 |
| rc_N54053_at | N54053 | 2561 | secreted phosphoprotein 2, 24kD | 3.97 | down | 0.00255 |
| rc_N54311_at | N54311 | 2564 | EST | 60.39 | down | 0.00087 |
| rc_N54399_at | N54399 | 2566 | EST | 4.82 | down | 0.00183 |
| | | | | 3.34 | down | 0.00048 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_N54417_s_at | N54417 | 2567 | fibrinogen, A alpha polypeptide | 99.28 | down | 0.00001 |
| rc_N54429_at | N54429 | 2568 | EST | 57.81 | down | 0.00724 |
| rc_N54511_s_at | N54511 | 2569 | KIAA0265 protein | 3.45 | down | 0.03362 |
| rc_N54604_at | N54604 | 2570 | EST | 3.72 | down | 0.00741 |
| rc_N54792_at | N54792 | 2571 | cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminase) | 3.23 | down | 0.00099 |
| rc_N54950_s_at | N54950 | 2573 | ketohexokinase (fructokinase) | 17.17 | down | 0.00078 |
| N57464_at | N57464 | 2576 | CCAAT/enhancer binding protein (C/EBP), delta | 14.69 | down | 0.00018 |
| rc_N57934_s_at | N57934 | 2577 | formiminotransferase cyclodeaminase | 13.81 | down | 0.00171 |
| rc_N58326_at | N58326 | 2579 | EST | 14.97 | down | 0.00647 |
| rc_N59089_at | N59089 | 2581 | EST | 4.74 | down | 0.00055 |
| rc_N59231_s_at | N59231 | 2582 | pyruvate carboxylase | 3.45 | down | 0.02066 |
| rc_N59283_at | N59283 | 2583 | EST | 4.65 | down | 0.02343 |
| rc_N59474_at | N59474 | 2584 | EST | 6.93 | down | 0.00337 |
| rc_N59532_s_at | N59532 | 2585 | aminomethyltransferase (glycine cleavage | 6.73 | down | 0.00005 |
| rc_N59543_at | N59543 | 2587 | PDZ domain containing 1 | 9.96 | down | 0.00052 |
| rc_N59550_at | N59550 | 2588 | EST | 25.56 | down | 0.00024 |
| rc_N62443_at | N62443 | 2590 | EST | 3.72 | down | 0.01717 |
| rc_N62523_at | N62523 | 2592 | hepatic leukemia factor | 5.02 | down | 0.00087 |
| rc_N62652_s_at | N62652 | 2593 | EST | 5.23 | down | 0.03006 |
| rc_N63391_at | N63391 | 2600 | EST | 7.39 | down | 0.00565 |
| rc_N63688_at | N63688 | 2603 | EST | 3.13 | down | 0.002 |
| rc_N63698_at | N63698 | 2604 | EST | 7.92 | down | 0.00001 |
| rc_N63845_at | N63845 | 2605 | phytanoyl-CoA hydroxylase (Refsum disease) | 25.92 | down | 0.00084 |
| rc_N64017_at | N64017 | 2606 | EST | 5.27 | down | 0.00022 |
| rc_N64036_s_at | N64036 | 2607 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl | | | |
| rc_N64436_at | N64436 | 2609 | Coenzyme A dehydrogenase | 9.99 | down | 0.00125 |
| rc_N64535_at | N64535 | 2610 | EST | 3.51 | down | 0.00441 |
| rc_N65959_at | N65959 | 2612 | EST | 6.19 | down | 0.00106 |
| rc_N66066_at | N66066 | 2613 | EST | 5.43 | down | 0.00044 |
| | | | | 28.35 | down | 0.00055 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_N66130_at | N66130 | 2614 | progesterone membrane binding protein | 3.98 | down | 0.0106 |
| rc_N66422_at | N66422 | 2616 | EST | 4.1 | down | 0.00237 |
| rc_N66763_at | N66763 | 2619 | EST | 3.79 | down | 0.03015 |
| rc_N66857_at | N66857 | 2620 | EST | 15.03 | down | 0.00005 |
| rc_N67009_s_at | N67009 | 2622 | prion protein (p27-30) (Creutzfeld-Jakob disease, | | | |
| rc_N67096_at | N67096 | 2623 | Gerstmann-Strausler-Scheinker syndrome, fatal | 3.55 | down | 0.00956 |
| rc_N67105_at | N67105 | 2624 | EST | 3.23 | down | 0.00446 |
| rc_N67378_at | N67378 | 2626 | KIAA1053 protein | 5.01 | down | 0.00176 |
| rc_N67876_s_at | N67876 | 2628 | insulin-like growth factor 1 (somatomedin C) | 7.14 | down | 0 |
| rc_N67893_at | N67893 | 2629 | EST | 8.89 | down | 0.00042 |
| rc_N68596_s_at | N68596 | 2636 | betaine-homocysteine methyltransferase | 10.48 | down | 0.00341 |
| rc_N68730_at | N68730 | 2637 | EST | 40.99 | down | 0 |
| rc_N68974_at | N68974 | 2640 | EST | 3.88 | down | 0.00091 |
| rc_N68993_at | N68993 | 2641 | EST | 16.44 | down | 0.00087 |
| rc_N69136_at | N69136 | 2645 | EST | 3.06 | down | 0.00867 |
| rc_N69216_at | N69216 | 2646 | EST | 18.53 | down | 0.00366 |
| rc_N69299_at | N69299 | 2649 | EST | 3.4 | down | 0.00497 |
| rc_N70005_at | N70005 | 2653 | EST | 3.63 | down | 0.03776 |
| rc_N70057_s_at | N70057 | 2654 | DNA segment on chromosome 6 (unique) 49 | 3.42 | down | 0.04229 |
| rc_N70305_at | N70305 | 2655 | EST | 5.24 | down | 0.01178 |
| rc_N70358_s_at | N70358 | 2657 | growth hormone receptor | 4.41 | down | 0.00078 |
| rc_N70861_at | N70861 | 2661 | EST | 34.35 | down | 0 |
| rc_N70966_s_at | N70966 | 2663 | solute carrier family 10 (sodium/bile acid | 6.55 | down | 0.00001 |
| rc_N71542_at | N71542 | 2665 | cotransporter family), member 1 | 34.06 | down | 0.0006 |
| rc_N71935_s_at | N71935 | 2667 | kidney- and liver-specific gene | 21.05 | down | 0 |
| rc_N72259_at | N72259 | 2670 | multiple PDZ domain protein | 16.28 | down | 0 |
| rc_N72695_s_at | N72695 | 2671 | cornichon-like | 4.65 | down | 0.0054 |
| rc_N73461_f_at | N73461 | 2673 | EST | 9.18 | down | 0.00069 |
| rc_N73468_s_at | N73468 | 2674 | protein S (alpha) | 4.25 | down | 0.00162 |
| | | | | 4.4 | down | 0.00853 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--|--|-------------|-----------|---------|
| rc_N73543_at | N73543 | 2675 EST | | 17 | down | 0.00003 |
| rc_N73561_at | N73561 | 2676 EST | | 12.96 | down | 0.00011 |
| rc_N73883_at | N73883 | 2682 EST | | 9.35 | down | 0 |
| rc_N73988_at | N73988 | 2683 EST | | 10.27 | down | 0.00083 |
| rc_N74025_at | N74025 | 2685 deiodinase, iodothyronine, type I | | 22.79 | down | 0 |
| rc_N74422_at | N74422 | 2686 EST | | 30.32 | down | 0 |
| rc_N74558_at | N74558 | 2687 EST | | 3.19 | down | 0.00247 |
| rc_N75072_at | N75072 | 2689 EST | | 3.73 | down | 0.00379 |
| N75203_s_at | N75203 | 2691 EST | | 6.15 | down | 0.00181 |
| N75870_s_at | N75870 | 2693 dual specificity phosphatase 1 | | 13.41 | down | 0.00251 |
| rc_N76012_f_at | N76012 | 2694 EST | | 36.71 | down | 0.00598 |
| N77326_at | N77326 | 2696 EST | | 7.51 | down | 0.00542 |
| N77606_at | N77606 | 2697 EST | | 4.22 | down | 0.00119 |
| rc_N78850_s_at | N78850 | 2699 | macrophage stimulating 1 (hepatocyte growth | 13.69 | down | 0.00421 |
| rc_N78902_at | N78902 | 2700 | factor-like),macrophage stimulating, pseudogene | 6.79 | down | 0.0041 |
| rc_N79435_at | N79435 | 2701 | leptin receptor | 3.12 | down | 0.00861 |
| rc_N79778_at | N79778 | 2702 | chromosome 15 open reading frame 3 | 5.15 | down | 0.00286 |
| rc_N80129_i_at | N80129 | 2703 | extracellular matrix protein 2, female organ and | 66.48 | down | 0.00415 |
| rc_N80129_f_at | N80129 | 2703 | metallothionein 1L | 13.6 | down | 0.00196 |
| rc_N81025_at | N81025 | 2705 EST | metallothionein 1L | 8.61 | down | 0.00015 |
| rc_N81036_at | N81036 | 2706 EST | | 6.89 | down | 0.00276 |
| N89302_s_at | N89302 | 2708 | HLA-B associated transcript-3 | 23.44 | down | 0.00192 |
| rc_N89738_at | N89738 | 2710 EST | | 10.06 | down | 0.00052 |
| rc_N90584_at | N90584 | 2714 EST | | 3.08 | down | 0.02602 |
| N90820_at | N90820 | 2715 | DKFZP566B1346 protein | 4.86 | down | 0.03008 |
| N91087_at | N91087 | 2717 EST | | 6.91 | down | 0.00109 |
| rc_N91273_r_at | N91273 | 2718 EST | | 4.07 | down | 0.02965 |
| rc_N91882_at | N91882 | 2720 | alpha2,3-sialyltransferase | 14.52 | down | 0.00024 |
| rc_N93155_f_at | N93155 | 2729 | calmodulin 1 (phosphorylase kinase, delta) | 4.39 | down | 0.0002 |
| rc_N93155_i_at | N93155 | 2729 | calmodulin 1 (phosphorylase kinase, delta) | 3.46 | down | 0.00031 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_N93191_at | N93191 | 2730 | EST | 3.25 | down | 0.00232 |
| rc_N93246_f_at | N93246 | 2731 | EST | 3.03 | down | 0.00049 |
| rc_N93764_at | N93764 | 2737 | EST | 5.92 | down | 0.0109 |
| N94146_at | N94146 | 2739 | EST | 8.05 | down | 0 |
| rc_N94367_at | N94367 | 2740 | EST | 8.79 | down | 0.01003 |
| rc_N94930_at | N94930 | 2741 | multiple PDZ domain protein | 10.06 | down | 0.00226 |
| rc_N95495_at | N95495 | 2742 | EST | 5.61 | down | 0.00308 |
| rc_N95585_at | N95585 | 2743 | EST | 3.1 | down | 0.0083 |
| N99542_at | N99542 | 2747 | orosomucoid 1 | 8.41 | down | 0.00001 |
| rc_N99866_at | N99866 | 2748 | EST | 3.13 | down | 0.04148 |
| rc_R00296_at | R00296 | 2750 | EST | 3.98 | down | 0.04632 |
| rc_R00843_s_at | R00843 | 2751 | fragile histidine triad gene | 3.68 | down | 0.03578 |
| rc_R01023_s_at | R01023 | 2752 | glucokinase (hexokinase 4) regulatory protein | 50.71 | down | 0.00321 |
| rc_R01081_at | R01081 | 2753 | EST | 3.3 | down | 0.00839 |
| rc_R02365_f_at | R02365 | 2755 | glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) | 17.17 | down | 0.00124 |
| rc_R02371_at | R02371 | 2756 | EST | 3.75 | down | 0.00009 |
| rc_R02572_at | R02572 | 2757 | fibronectin 1 | 7.1 | down | 0.00059 |
| rc_R02752_at | R02752 | 2758 | EST | 3.05 | down | 0.00362 |
| rc_R05309_f_at | R05309 | 2759 | EST | 3.72 | down | 0.0008 |
| rc_R05490_at | R05490 | 2761 | SEC24 (S. cerevisiae) related gene family, | 3.03 | down | 0.00317 |
| rc_R05518_at | R05518 | 2762 | EST | 4.15 | down | 0.0125 |
| rc_R06002_s_at | R06002 | 2763 | EST | 10.15 | down | 0.00003 |
| rc_R06271_s_at | R06271 | 2766 | EST | 6.14 | down | 0.00063 |
| rc_R06726_s_at | R06726 | 2770 | protease inhibitor 1 (anti-elastase), alpha-1- | 12.26 | down | 0.03905 |
| rc_R06746_at | R06746 | 2771 | EST | 15.77 | down | 0.00009 |
| rc_R06764_s_at | R06764 | 2772 | apolipoprotein B (including Ag(x) antigen) | 4.91 | down | 0.00167 |
| rc_R06977_f_at | R06977 | 2775 | glucokinase (hexokinase 4) regulatory protein | 6.1 | down | 0.00049 |
| rc_R07637_at | R07637 | 2778 | EST | 3.04 | down | 0.00118 |
| rc_R08548_at | R08548 | 2779 | EST | 9.94 | down | 0.00326 |
| rc_R08564_at | R08564 | 2780 | plasminogen-like | 60.18 | down | 0.00091 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_R08615_s_at | R08615 | 2781 | homogentisate 1,2-dioxygenase (homogentisate | 21.85 | down | 0.00026 |
| rc_R08850_at | R08850 | 2782 | EST | 12.55 | down | 0.00009 |
| rc_R09053_at | R09053 | 2783 | EST | 5.9 | down | 0.0002 |
| rc_R10138_at | R10138 | 2784 | EST | 4 | down | 0.00032 |
| rc_R10287_at | R10287 | 2785 | EST | 11.2 | down | 0.0003 |
| rc_R10378_s_at | R10378 | 2786 | fibrinogen-like 1 | 8.13 | down | 0.00189 |
| rc_R10662_f_at | R10662 | 2787 | mutL (E. coli) homolog 1 (colon cancer, | 3.2 | down | 0.0005 |
| rc_R10684_at | R10684 | 2788 | EST | 5.51 | down | 0.00741 |
| rc_R12472_at | R12472 | 2789 | EST | 55.18 | down | 0.00011 |
| rc_R12579_at | R12579 | 2790 | EST | 3.5 | down | 0.00137 |
| rc_R15825_r_at | R15825 | 2792 | KIAA0946 protein; Huntingtin interacting protein | 5.33 | down | 0.00391 |
| rc_R16098_at | R16098 | 2793 | EST | 63.41 | down | 0.00038 |
| rc_R17762_at | R17762 | 2795 | EST | 3.37 | down | 0.01822 |
| rc_R21232_at | R21232 | 2798 | EST | 3.56 | down | 0.00246 |
| rc_R22196_at | R22196 | 2799 | EST | 3.75 | down | 0.02867 |
| rc_R22905_at | R22905 | 2801 | EST | 4.64 | down | 0.0043 |
| rc_R26904_f_at | R26904 | 2805 | EST | 3.51 | down | 0.00058 |
| R31641_at | R31641 | 2814 | EST | 9.96 | down | 0.00011 |
| rc_R31917_s_at | R31917 | 2815 | EST | 3.91 | down | 0.00071 |
| rc_R32036_s_at | R32036 | 2816 | interleukin 1 receptor-like 1 | 4.02 | down | 0.00051 |
| rc_R32440_at | R32440 | 2817 | EST | 7.41 | down | 0.00159 |
| rc_R32490_s_at | R32490 | 2818 | EST | 8.95 | down | 0.00215 |
| rc_R33146_at | R33146 | 2819 | EST | 7 | down | 0.00043 |
| rc_R34133_at | R34133 | 2821 | EST | 4.13 | down | 0.00008 |
| rc_R34362_at | R34362 | 2822 | KIAA0327 gene product | 5.4 | down | 0.04615 |
| rc_R36228_at | R36228 | 2824 | EST | 4.39 | down | 0.00033 |
| rc_R36989_s_at | R36989 | 2826 | hypothetical protein, estradiol-induced | 13.7 | down | 0.00056 |
| rc_R37128_s_at | R37128 | 2827 | complement component 4A | 39.51 | down | 0.00364 |
| rc_R38185_at | R38185 | 2829 | EST | 6.32 | down | 0.00063 |
| rc_R38709_s_at | R38709 | 2833 | superoxide dismutase 2, mitochondrial | 8.23 | down | 0.01578 |
| rc_R39234_r_at | R39234 | 2835 | EST | 3.24 | down | 0.0412 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Ally ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_R40395_s_at | R40395 | 2841 | lecithin-cholesterol acyltransferase | 37.33 | down | 0.00032 |
| rc_R40492_at | R40492 | 2842 | EST | 8.89 | down | 0.00229 |
| rc_R40556_s_at | R40556 | 2843 | EST | 3.57 | down | 0.00184 |
| rc_R40899_f_at | R40899 | 2844 | glycine receptor, beta | 9.11 | down | 0.0009 |
| rc_R40946_f_at | R40946 | 2845 | crystallin, zeta (quinone reductase) | 6.14 | down | 0.00156 |
| rc_R42241_at | R42241 | 2846 | EST | 3.97 | down | 0.00129 |
| rc_R43166_i_at | R43166 | 2847 | EST | 3.37 | down | 0.00919 |
| rc_R43174_s_at | R43174 | 2848 | paraoxonase 1 | 74.04 | down | 0.00038 |
| rc_R43365_at | R43365 | 2850 | EST | 5.37 | down | 0.00103 |
| rc_R43799_at | R43799 | 2851 | EST | 16.35 | down | 0.00208 |
| rc_R43910_at | R43910 | 2852 | EST | 5.71 | down | 0 |
| rc_R44025_at | R44025 | 2854 | EST | 4.4 | down | 0.01325 |
| rc_R44761_at | R44761 | 2858 | aryl hydrocarbon receptor nuclear translocator | 3.12 | down | 0.02663 |
| rc_R45656_i_at | R45656 | 2865 | EST | 10.21 | down | 0.00179 |
| rc_R48307_at | R48307 | 2870 | EST | 7.18 | down | 0.00007 |
| rc_R48540_s_at | R48540 | 2873 | EST | 6.05 | down | 0.00086 |
| rc_R48732_s_at | R48732 | 2876 | EST | 5.12 | down | 0.00837 |
| rc_R49035_at | R49035 | 2877 | EST | 8.02 | down | 0.00991 |
| rc_R49459_s_at | R49459 | 2882 | transferrin receptor 2 | 85.61 | down | 0.00048 |
| rc_R49602_at | R49602 | 2885 | EST | 36.5 | down | 0.00001 |
| R50008_s_at | R50008 | 2887 | 7-dehydrocholesterol reductase | 6.67 | down | 0.00409 |
| rc_R51256_at | R51256 | 2889 | EST | 3.04 | down | 0.00286 |
| rc_R51309_at | R51309 | 2890 | KIAA1077 protein | 3.54 | down | 0.04112 |
| rc_R51831_at | R51831 | 2891 | EST | 5.03 | down | 0.00761 |
| rc_R52800_at | R52800 | 2895 | EST | 3.96 | down | 0.00749 |
| rc_R52822_i_at | R52822 | 2896 | EST | 12.79 | down | 0.00001 |
| rc_R52949_at | R52949 | 2897 | EST | 3.46 | down | 0.00395 |
| rc_R54416_at | R54416 | 2901 | EST | 3.14 | down | 0.00236 |
| rc_R56094_at | R56094 | 2905 | EST | 4.87 | down | 0.00214 |
| rc_R56602_at | R56602 | 2907 | Ig superfamily protein | 3.06 | down | 0.02464 |
| rc_R59221_at | R59221 | 2912 | progesterone binding protein | 7.54 | down | 0.00159 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_R59325_at | R59325 | 2914 | EST | 4.48 | down | 0.00117 |
| rc_R59722_at | R59722 | 2916 | EST | 19.74 | down | 0.00016 |
| rc_R61740_f_at | R61740 | 2923 | EST | 4.02 | down | 0.00321 |
| rc_R62173_f_at | R62173 | 2924 | UDP-glucose dehydrogenase | 5.76 | down | 0.0006 |
| rc_R62519_f_at | R62519 | 2926 | EST | 10.83 | down | 0.00243 |
| R63545_at | R63545 | 2927 | EST | 5.4 | down | 0.00202 |
| rc_R64131_at | R64131 | 2930 | EST | 20.58 | down | 0.01028 |
| rc_R64144_s_at | R64144 | 2932 | cAMP responsive element binding protein-like 2 | 4.58 | down | 0.00495 |
| R64199_at | R64199 | 2933 | SEC22, vesicle trafficking protein (S. cerevisiae)- | 9.19 | down | 0.00387 |
| rc_R65593_s_at | R65593 | 2935 | kynurenine 3-monooxygenase (kynurenine 3- | 21.27 | down | 0.00007 |
| R67751_at | R67751 | 2939 | EST | 3.12 | down | 0.00319 |
| rc_R67970_s_at | R67970 | 2940 | gamma-glutamyl carboxylase | 9.45 | down | 0.00212 |
| rc_R69031_at | R69031 | 2941 | EST | 3.19 | down | 0.00798 |
| R69417_at | R69417 | 2942 | EST | 7.79 | down | 0.03795 |
| rc_R70790_at | R70790 | 2948 | EST | 4.07 | down | 0.02354 |
| rc_R71491_at | R71491 | 2954 | EST | 3.55 | down | 0.01903 |
| rc_R73485_at | R73485 | 2958 | EST | 7.77 | down | 0.0009 |
| rc_R73816_at | R73816 | 2961 | EST | 11.53 | down | 0.00259 |
| R77628_at | R77628 | 2966 | insulin induced gene 1 | 29.23 | down | 0.00122 |
| R80048_at | R80048 | 2972 | EST | 12.28 | down | 0.00128 |
| R80573_at | R80573 | 2973 | EST | 3.08 | down | 0.02126 |
| rc_R82074_f_at | R82074 | 2974 | syndecan 1 | 6.66 | down | 0.01336 |
| R82229_at | R82229 | 2975 | phosphatidylserine decarboxylase | 3.08 | down | 0.03455 |
| rc_R82837_at | R82837 | 2976 | KIAA0970 protein | 5 | down | 0.00181 |
| R87373_s_at | R87373 | 2978 | EST | 4.09 | down | 0.02253 |
| rc_R89811_s_at | R89811 | 2980 | HGF activator | 62.51 | down | 0.00148 |
| rc_R91503_s_at | R91503 | 2982 | ATP-binding cassette, sub-family C (CFTR/MRP), | 9.64 | down | 0.00584 |
| rc_R92458_f_at | R92458 | 2986 | hemoglobin, gamma G | 3.31 | down | 0.00763 |
| rc_R92475_s_at | R92475 | 2987 | flavin containing monooxygenase 3 | 26.13 | down | 0 |
| rc_R92737_at | R92737 | 2988 | EST | 4.53 | down | 0.04447 |
| rc_R92768_at | R92768 | 2989 | EST | 13.2 | down | 0.00001 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_R93714_at | R93714 | 2992 | fetuin B | 10.42 | down | 0.00043 |
| R93776_s_at | R93776 | 2993 | EST | 39.32 | down | 0.00176 |
| rc_R93908_at | R93908 | 2994 | EST | 5.8 | down | 0.02699 |
| R94662_at | R94662 | 2995 | heme-binding protein | 4.41 | down | 0.02301 |
| rc_R94674_s_at | R94674 | 2996 | EST | 10.76 | down | 0.00008 |
| R96417_at | R96417 | 2998 | EST | 3.9 | down | 0.00019 |
| rc_R96822_at | R96822 | 3000 | EST | 8.25 | down | 0.00008 |
| rc_R97302_at | R97302 | 3003 | EST | 3.73 | down | 0.01887 |
| rc_R97419_at | R97419 | 3004 | cytochrome P450, subfamily VIIIIB (sterol 12- | | | |
| rc_R97711_at | R97711 | 3005 | alpha-hydroxylase), polypeptide 1 | 65.07 | down | 0.0039 |
| rc_R97798_at | R97798 | 3007 | EST | 3.37 | down | 0.00838 |
| R98073_at | R98073 | 3009 | EST | 3.79 | down | 0.00015 |
| rc_R98074_at | R98074 | 3010 | EST | 46.87 | down | 0 |
| rc_R98413_at | R98413 | 3012 | EST | 9.21 | down | 0.00048 |
| rc_R98624_at | R98624 | 3013 | EST | 9.71 | down | 0.00007 |
| rc_R98774_at | R98774 | 3014 | EST | 21.32 | down | 0 |
| rc_R99591_at | R99591 | 3016 | CD5 antigen-like (scavenger receptor cysteine | 3.93 | down | 0.00001 |
| rc_R99909_at | R99909 | 3017 | EST | 9.52 | down | 0.00006 |
| S48983_at | S48983 | 3018 | serum amyloid A4, constitutive | 4.27 | down | 0.00045 |
| S52028_s_at | S52028 | 3019 | cystathionase (cystathionine gamma-lyase) | 23.04 | down | 0.00022 |
| S62539_s_at | S62539 | 3022 | insulin receptor substrate 1 | 3.21 | down | 0.00476 |
| S67325_at | S67325 | 3024 | propionyl Coenzyme A carboxylase, beta | 3.7 | down | 0.01307 |
| | | | aldo-keto reductase family 1, member C4 | 4.19 | down | 0.00151 |
| | | | (chlordecone reductase; 3-alpha hydroxysteroid | | | |
| S68287_at | S68287 | 3025 | dehydrogenase, type I; dihydrodiol | 24.11 | down | 0 |
| S68805_at | S68805 | 3026 | glycine amidinotransferase (L-arginine:glycine | 18.19 | down | 0.00083 |
| S69232_at | S69232 | 3027 | electron-transferring-flavoprotein dehydrogenase | 4.9 | down | 0.00017 |
| S70004_at | S70004 | 3029 | glycogen synthase 2 (liver) | 9.96 | down | 0.00001 |
| S72370_at | S72370 | 3030 | pyruvate carboxylase | 5.31 | down | 0.00075 |
| S72370_at | S72370 | 3030 | pyruvate carboxylase | 4.54 | down | 0.0001 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| S74728_at | S74728 | 3033 | antiqutin 1 | 5.01 | down | 0.00008 |
| S77356_at | S77356 | 3034 | EST | 5.83 | down | 0.00122 |
| S77410_at | S77410 | 3035 | angiotensin receptor 1 | 10.4 | down | 0 |
| S90469_at | S90469 | 3040 | P450 (cytochrome) oxidoreductase | 4.32 | down | 0.0182 |
| S95936_at | S95936 | 3041 | transferrin | 19.76 | down | 0.02009 |
| rc_T03441_f_at | T03441 | 3044 | cytochrome b-561 | 5.74 | down | 0.02781 |
| rc_T03651_s_at | T03651 | 3047 | tubulin, beta polypeptide | 6.47 | down | 0.00843 |
| T08879_at | T08879 | 3049 | cathepsin F | 5.29 | down | 0.0008 |
| rc_T10108_s_at | T10108 | 3050 | EST | 3.85 | down | 0.01155 |
| rc_T10264_s_at | T10264 | 3051 | EST | 3.84 | down | 0.00874 |
| rc_T10322_at | T10322 | 3053 | dihydropyrimidinase-like 2 | 4.23 | down | 0.01527 |
| rc_T10822_at | T10822 | 3055 | EST | 3.16 | down | 0.00635 |
| rc_T15482_f_at | T15482 | 3060 | EST | 5.04 | down | 0.00233 |
| rc_T15674_f_at | T15674 | 3061 | EST | 4.12 | down | 0.02111 |
| rc_T16175_s_at | T16175 | 3064 | protein tyrosine phosphatase, non-receptor type | 3.07 | down | 0.01007 |
| rc_T16269_at | T16269 | 3067 | EST | 3.36 | down | 0.00282 |
| rc_T16478_at | T16478 | 3070 | EST | 4 | down | 0.01041 |
| rc_T16484_s_at | T16484 | 3071 | EST | 7.69 | down | 0.00805 |
| rc_T17411_s_at | T17411 | 3078 | transthyretin (prealbumin, amyloidosis type I) | 13.49 | down | 0.00203 |
| rc_T23430_at | T23430 | 3080 | EST | 3.12 | down | 0.00949 |
| rc_T23680_at | T23680 | 3084 | calcium channel, voltage-dependent, gamma | 3.29 | down | 0.0003 |
| rc_T23882_s_at | T23882 | 3085 | kininogen | 42.85 | down | 0.00641 |
| rc_T23986_s_at | T23986 | 3086 | hydroxyacyl glutathione hydrolase; glyoxalase 2 | 7.26 | down | 0.0062 |
| rc_T24055_s_at | T24055 | 3087 | ribosomal protein L26 | 3.9 | down | 0.00046 |
| rc_T24106_at | T24106 | 3089 | EST | 12.13 | down | 0.01687 |
| rc_T25506_at | T25506 | 3090 | EST | 4.51 | down | 0.00529 |
| T30341_s_at | T30341 | 3101 | EST | 3.04 | down | 0.04567 |
| rc_T33011_at | T33011 | 3104 | EST | 3.57 | down | 0.02486 |
| T39897_s_at | T39897 | 3114 | androgen induced protein | 10 | down | 0.00466 |
| rc_T40936_at | T40936 | 3118 | EST | 46.92 | down | 0.00056 |
| rc_T40995_f_at | T40995 | 3119 | alcohol dehydrogenase 3 (class I), gamma | 13.25 | down | 0.01531 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_T41047_s_at | T41047 | 3120 | EST | 4.74 | down | 0.00015 |
| rc_T41232_at | T41232 | 3122 | EST | 3.57 | down | 0.00846 |
| rc_T46901_at | T46901 | 3123 | EST | 77.28 | down | 0.0006 |
| rc_T47778_s_at | T47778 | 3127 | fibrinogen, A alpha polypeptide | 30 | down | 0.01401 |
| rc_T48039_s_at | T48039 | 3129 | protein C (inactivator of coagulation factors Va | 84.39 | down | 0.00112 |
| rc_T48075_f_at | T48075 | 3130 | hemoglobin, alpha 1 | 32.56 | down | 0.00172 |
| rc_T48278_at | T48278 | 3132 | EST | 15.04 | down | 0.04751 |
| rc_T48980_s_at | T48980 | 3134 | calmodulin 1 (phosphorylase kinase, delta) | 4.2 | down | 0.0046 |
| rc_T49061_at | T49061 | 3135 | EST | 3.06 | down | 0.00768 |
| rc_T51150_at | T51150 | 3137 | EST | 10.52 | down | 0.00377 |
| rc_T51617_at | T51617 | 3138 | solute carrier family 22 (extraneuronal | 17.67 | down | 0.00018 |
| rc_T51930_at | T51930 | 3139 | monoamine transporter), member 3 | 9.99 | down | 0.00066 |
| rc_T52564_at | T52564 | 3141 | EST | 3.28 | down | 0.01506 |
| rc_T52813_s_at | T52813 | 3142 | putative lymphocyte G0/G1 switch gene | 16.71 | down | 0.03897 |
| rc_T54160_s_at | T54160 | 3145 | EST | 3.24 | down | 0.00168 |
| rc_T55547_at | T55547 | 3148 | EST | 3.28 | down | 0.00047 |
| rc_T56264_s_at | T56264 | 3149 | apolipoprotein C-II | 53.04 | down | 0.00938 |
| rc_T56279_s_at | T56279 | 3150 | H factor (complement)-like 3 | 28.39 | down | 0.00016 |
| rc_T56281_f_at | T56281 | 3151 | RNA helicase-related protein | 32.34 | down | 0.00002 |
| T57140_s_at | T57140 | 3152 | paraoxonase 3 | 28.8 | down | 0 |
| rc_T58032_s_at | T58032 | 3153 | 3-hydroxyanthranilate 3,4-dioxygenase | 8.86 | down | 0.00023 |
| rc_T58756_at | T58756 | 3156 | EST | 13.39 | down | 0.00013 |
| rc_T58775_at | T58775 | 3157 | small inducible cytokine subfamily A (Cys-Cys), | 21.18 | down | 0.00006 |
| rc_T59148_s_at | T59148 | 3158 | carbamoyl-phosphate synthetase 1, mitochondrial | 88.89 | down | 0 |
| rc_T60407_at | T60407 | 3161 | EST | 6.6 | down | 0.00167 |
| rc_T61256_s_at | T61256 | 3162 | ketohexokinase (fructokinase) | 13.59 | down | 0.00425 |
| rc_T61373_s_at | T61373 | 3163 | vitronectin (serum spreading factor, somatomedin | 44.9 | down | 0.03172 |
| rc_T61389_f_at | T61389 | 3164 | B, complement S-protein) | 18.95 | down | 0.04873 |
| rc_T61649_f_at | T61649 | 3165 | haptoglobin | 26.09 | down | 0.00734 |
| | | | superoxide dismutase 2, mitochondrial | | | |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_T61801_s_at | T61801 | 3167 | hemopexin | 25.7 | down | 0.01362 |
| rc_T63364_at | T63364 | 3170 | ficolin (collagen/fibrinogen domain-containing) 3 | 6.72 | down | 0.00383 |
| rc_T63490_at | T63490 | 3171 | EST | 16.54 | down | 0 |
| rc_T64575_s_at | T64575 | 3172 | EST | 10.46 | down | 0.00014 |
| rc_T64887_f_at | T64887 | 3173 | protein phosphatase 5, catalytic subunit | 5.66 | down | 0.00349 |
| rc_T65972_at | T65972 | 3177 | EST | 3.21 | down | 0.04847 |
| rc_T66189_s_at | T66189 | 3178 | glutaryl-Coenzyme A dehydrogenase succinate dehydrogenase complex, subunit D, | 8.61 | down | 0.00003 |
| T67231_at | T67231 | 3181 | integral membrane protein | 7.04 | down | 0.03554 |
| rc_T67705_s_at | T67705 | 3183 | asialoglycoprotein receptor 2 | 31.6 | down | 0.00705 |
| rc_T67931_at | T67931 | 3184 | fibrinogen, B beta polypeptide | 49.55 | down | 0 |
| T68083_at | T68083 | 3185 | short-chain dehydrogenase/reductase 1 | 4.03 | down | 0.01593 |
| rc_T68426_s_at | T68426 | 3186 | CD81 antigen (target of antiproliferative antibody | 3.11 | down | 0.01634 |
| T68510_at | T68510 | 3187 | EST | 3.87 | down | 0.00617 |
| rc_T68711_at | T68711 | 3188 | EST | 37.65 | down | 0.00036 |
| rc_T68855_at | T68855 | 3189 | EST | 34.04 | down | 0 |
| rc_T68873_f_at | T68873 | 3190 | metallothionein 1L | 28.72 | down | 0.02953 |
| rc_T68878_f_at | T68878 | 3191 | carboxylesterase 1 (monocyte/macrophage | 60.35 | down | 0.00409 |
| rc_T69009_s_at | T69009 | 3192 | quinoid dihydropteridine reductase | 6.54 | down | 0.00145 |
| rc_T69020_s_at | T69020 | 3193 | EST | 5.39 | down | 0.00383 |
| rc_T69029_f_at | T69029 | 3194 | haptoglobin | 33.18 | down | 0.02825 |
| rc_T69164_at | T69164 | 3195 | EST | 4.38 | down | 0.00548 |
| rc_T69284_s_at | T69284 | 3196 | mannose-binding lectin (protein C) 2, soluble | 36.53 | down | 0 |
| T69384_at | T69384 | 3198 | period (Drosophila) homolog 1 | 5.88 | down | 0.01219 |
| rc_T69728_at | T69728 | 3199 | heat shock 90kD protein 1, beta | 3.98 | down | 0.00786 |
| rc_T70087_at | T70087 | 3200 | EST | 4.7 | down | 0.00173 |
| rc_T71012_s_at | T71012 | 3201 | fibrinogen, B beta polypeptide | 43.61 | down | 0.00743 |
| rc_T71021_at | T71021 | 3202 | EST | 6.74 | down | 0.0017 |
| rc_T71373_at | T71373 | 3203 | EST | 83.08 | down | 0.00069 |
| rc_T71776_at | T71776 | 3204 | EST | 10.3 | down | 0.00897 |
| rc_T71978_at | T71978 | 3205 | EST | 4.39 | down | 0.0017 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_T72171_s_at | T72171 | 3206 | thyroxin-binding globulin | 10.41 | down | 0.00163 |
| rc_T72268_s_at | T72268 | 3207 | B-factor, properdin | 7.43 | down | 0.01197 |
| rc_T72502_at | T72502 | 3208 | EST | 8.87 | down | 0.00009 |
| rc_T72629_i_at | T72629 | 3209 | EST | 3.24 | down | 0.00556 |
| rc_T72906_at | T72906 | 3210 | EST | 7.56 | down | 0.00062 |
| rc_T73420_at | T73420 | 3211 | short-chain dehydrogenase/reductase 1 | 4.58 | down | 0.00656 |
| rc_T73433_s_at | T73433 | 3212 | angiotensinogen | 48.3 | down | 0.00049 |
| rc_T73442_at | T73442 | 3213 | EST | 94.41 | down | 0 |
| rc_T73739_s_at | T73739 | 3214 | alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate | 16.18 | down | 0.00277 |
| rc_T74542_s_at | T74542 | 3215 | UDP glycosyltransferase 2 family, polypeptide | 32.36 | down | 0.00004 |
| rc_T74608_at | T74608 | 3216 | hydroxyacid oxidase (glycolate oxidase) 1 | 14.03 | down | 0 |
| rc_T74884_r_at | T74884 | 3217 | EST | 3.76 | down | 0.02547 |
| rc_T77729_f_at | T77729 | 3218 | pyruvate carboxylase | 7.29 | down | 0.00022 |
| rc_T78433_s_at | T78433 | 3220 | glycogen synthase 2 (liver) | 8.62 | down | 0.00072 |
| rc_T78889_s_at | T78889 | 3221 | fibronectin 1 | 19.87 | down | 0.00912 |
| rc_T79758_at | T79758 | 3224 | EST | 3.94 | down | 0.00581 |
| rc_T79842_at | T79842 | 3225 | EST | 3.16 | down | 0.03159 |
| rc_T79863_at | T79863 | 3226 | EST | 5.62 | down | 0.00074 |
| rc_T81315_at | T81315 | 3227 | EST | 4.28 | down | 0.00187 |
| rc_T82254_at | T82254 | 3229 | EST | 3.82 | down | 0.00091 |
| rc_T82259_at | T82259 | 3230 | EST | 3.12 | down | 0.01122 |
| rc_T82323_at | T82323 | 3231 | immunoglobulin superfamily, member 4 | 10.14 | down | 0 |
| rc_T83356_s_at | T83356 | 3232 | apolipoprotein H (beta-2-glycoprotein I) | 64.34 | down | 0.00802 |
| T83397_at | T83397 | 3233 | phytanoyl-CoA hydroxylase (Refsum disease) | 63.6 | down | 0 |
| T85532_f_at | T85532 | 3236 | EST | 4.33 | down | 0.00591 |
| rc_T86464_at | T86464 | 3237 | EST | 3.17 | down | 0.00498 |
| rc_T86482_at | T86482 | 3238 | transferrin | 11.15 | down | 0.00006 |
| rc_T86978_s_at | T86978 | 3239 | glutamate dehydrogenase 1 | 9.44 | down | 0.00006 |
| rc_T87174_at | T87174 | 3240 | EST | 21.71 | down | 0.00681 |
| rc_T90037_at | T90037 | 3246 | EST | 3.99 | down | 0.0016 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_T90492_at | T90492 | 3248 | EST | 3.88 | down | 0.00454 |
| rc_T90520_at | T90520 | 3249 | EST | 8.67 | down | 0.00072 |
| rc_T90531_at | T90531 | 3250 | EST | 3.6 | down | 0.00301 |
| rc_T90841_f_at | T90841 | 3251 | EST | 5.74 | down | 0.01876 |
| rc_T91161_at | T91161 | 3253 | EST | 3.48 | down | 0.00002 |
| rc_T91348_at | T91348 | 3254 | EST | 3.57 | down | 0.00011 |
| rc_T92950_at | T92950 | 3256 | EST | 3.01 | down | 0.00497 |
| rc_T94862_at | T94862 | 3258 | EST | 3.07 | down | 0.01417 |
| rc_T95064_at | T95064 | 3260 | EST | 5.75 | down | 0.00604 |
| rc_T95515_s_at | T95515 | 3261 | KIAA0249 gene product | 6.77 | down | 0.0001 |
| T95813_f_at | T95813 | 3262 | KIAA1051 protein | 38.38 | down | 0.00008 |
| rc_T96969_at | T96969 | 3264 | EST | 3.42 | down | 0.00053 |
| rc_T97234_at | T97234 | 3265 | EST | 4.34 | down | 0.00263 |
| rc_T98199_i_at | T98199 | 3267 | EST | 4.86 | down | 0.00431 |
| rc_T98676_at | T98676 | 3269 | EST | 46.94 | down | 0.0001 |
| rc_T99636_s_at | T99636 | 3271 | complement component 3 | 29.6 | down | 0.00051 |
| U00115_at | U00115 | 3272 | B-cell CLL/lymphoma 6 (zinc finger protein 51) | 5.18 | down | 0.00045 |
| U01120_at | U01120 | 3274 | glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) | 13.41 | down | 0.00147 |
| U01824_at | U01824 | 3276 | solute carrier family 1 (glial high affinity glutamate transporter), member 2 | 3.2 | down | 0.00021 |
| U02020_at | U02020 | 3277 | pre-B-cell colony-enhancing factor | 3.37 | down | 0.01112 |
| U02388_at | U02388 | 3278 | cytochrome P450, subfamily IVF, polypeptide 2 | 9.38 | down | 0.00001 |
| U03056_at | U03056 | 3280 | hyaluronoglucosaminidase 1 | 6.64 | down | 0 |
| U03105_at | U03105 | 3281 | proline-rich protein with nuclear targeting signal | 4.69 | down | 0.00017 |
| U05861_at | U05861 | 3285 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) | 23.22 | down | 0.00002 |
| U06641_s_at | U06641 | 3287 | UDP glycosyltransferase 2 family, polypeptide | 24.32 | down | 0.00001 |
| U06863_at | U06863 | 3288 | folistatin-like 1 | 3.09 | down | 0.00091 |
| U08006_s_at | U08006 | 3290 | complement component 8, alpha polypeptide | 16 | down | 0.00111 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|---------------|---------|--------|--|-------------|-----------|---------|
| U08198_ma1_at | U08198 | 3292 | complement component 8, gamma polypeptide | 19.71 | down | 0 |
| U08854_s_at | U08854 | 3293 | UDP glycosyltransferase 2 family, polypeptide | 7.38 | down | 0.00005 |
| U11313_at | U11313 | 3297 | sterol carrier protein 2 | 5.44 | down | 0.00187 |
| U12778_at | U12778 | 3301 | acyl-Coenzyme A dehydrogenase, sulfotransferase family 2A, | 5.68 | down | 0.00116 |
| U13061_ma1_at | U13061 | 3302 | dehydroepiandrosterone (DHEA) -preferring, | 11.32 | down | 0.00048 |
| U16660_at | U16660 | 3313 | enoyl Coenzyme A hydratase 1, peroxisomal | 3.96 | down | 0.00002 |
| U19495_s_at | U19495 | 3319 | stromal cell-derived factor 1 | 4.59 | down | 0.00011 |
| U19523_at | U19523 | 3320 | GTP cyclohydrolase 1 (dopa-responsive | 5.25 | down | 0.00029 |
| U20530_at | U20530 | 3322 | secreted phosphoprotein 2, 24kD | 16.93 | down | 0 |
| U20938_at | U20938 | 3324 | dihydropyrimidine dehydrogenase | 3.92 | down | 0.00053 |
| U21931_at | U21931 | 3326 | fructose-bisphosphatase 1 | 3.4 | down | 0.00709 |
| U22029_f_at | U22029 | 3327 | cytochrome P450, subfamily IIA (phenobarbital- | 71.98 | down | 0 |
| U22961_s_at | U22961 | 3330 | inducible), polypeptide 7 | 22.22 | down | 0.01531 |
| U24266_at | U24266 | 3331 | albumin | 14.54 | down | 0 |
| U25182_at | U25182 | 3333 | aldehyde dehydrogenase 4 (glutamate gamma-semialdehyde dehydrogenase; pyrroline-5-thio | 3.13 | down | 0.02543 |
| U26173_s_at | U26173 | 3335 | thioredoxin peroxidase (antioxidant enzyme) | 6.4 | down | 0.00001 |
| U27460_at | U27460 | 3339 | nuclear factor, interleukin 3 regulated | 11.46 | down | 0.00088 |
| U27699_at | U27699 | 3340 | UDP-glucose pyrophosphorylase 2 | 3.65 | down | 0.00381 |
| U28833_at | U28833 | 3341 | solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 | 3.3 | down | 0.00306 |
| U29953_ma1_at | U29953 | 3342 | Down syndrome candidate region 1 | 15.33 | down | 0.00212 |
| U31449_at | U31449 | 3345 | pigment epithelium-derived factor | 11.53 | down | 0.00187 |
| U32576_ma1_at | U32576 | 3347 | transmembrane 4 superfamily member 4 | 18.59 | down | 0.00005 |
| U32576_ma1_at | U32576 | 3347 | apolipoprotein C-IV | 5.81 | down | 0.04343 |
| U32989_at | U32989 | 3348 | apolipoprotein C-IV | 10.07 | down | 0.02825 |
| U34252_at | U34252 | 3350 | tryptophan 2,3-dioxygenase | 4.31 | down | 0.00613 |
| U36922_at | U36922 | 3352 | aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 EST | 3.06 | down | 0.01388 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|--|-------------|-----------|---------|
| U37055_rna1_s_at | U37055 | 3353 | macrophage stimulating 1 (hepatocyte growth factor-like), macrophage stimulating, pseudogene | 18.28 | down | 0 |
| U44111_at | U44111 | 3363 | histamine N-methyltransferase | 3.5 | down | 0.00942 |
| U46499_at | U46499 | 3365 | microsomal glutathione S-transferase 1 | 4.27 | down | 0.00244 |
| U46689_at | U46689 | 3366 | aldehyde dehydrogenase 10 (fatty aldehyde | 3.5 | down | 0.01292 |
| U48296_at | U48296 | 3369 | protein tyrosine phosphatase type IVA, member 1 | 4.25 | down | 0.02037 |
| U48707_at | U48707 | 3371 | protein phosphatase 1, regulatory (inhibitor) | 14.22 | down | 0 |
| U48959_at | U48959 | 3372 | myosin, light polypeptide kinase | 3.61 | down | 0.00084 |
| U49082_at | U49082 | 3373 | transporter protein | 9.17 | down | 0.00088 |
| U49248_at | U49248 | 3374 | ATP-binding cassette, sub-family C (CFTR/MRP), | 7.06 | down | 0.00067 |
| U49352_at | U49352 | 3375 | 2,4-dienoyl CoA reductase 1, mitochondrial | 5.41 | down | 0.02371 |
| U49785_at | U49785 | 3376 | D-dopachrome tautomerase | 3.84 | down | 0.00044 |
| U50196_at | U50196 | 3377 | adenosine kinase | 3.82 | down | 0.01425 |
| U50527_s_at | U50527 | 3378 | EST | 3.93 | down | 0.00123 |
| U50929_at | U50929 | 3380 | betaine-homocysteine methyltransferase | 36.91 | down | 0 |
| U51010_s_at | U51010 | 3381 | nicotinamide N-methyltransferase | 27.79 | down | 0.00366 |
| U51333_s_at | U51333 | 3383 | hexokinase 3 (white cell) | 4.88 | down | 0.00055 |
| U51903_at | U51903 | 3387 | IQ motif containing GTPase activating protein 2 | 3.23 | down | 0.00242 |
| U53003_at | U53003 | 3388 | ES1 (zebrafish) protein, human homolog of | 4.84 | down | 0.00077 |
| U56814_at | U56814 | 3393 | deoxyribonuclease I-like 3 | 29.43 | down | 0.00003 |
| U56814_at | U56814 | 3393 | deoxyribonuclease I-like 3 | 11.36 | down | 0.00001 |
| U57721_at | U57721 | 3395 | kynureninase (L-kynurenine hydrolase) | 4.34 | down | 0.0197 |
| U60205_at | U60205 | 3401 | sterol-C4-methyl oxidase-like | 5.16 | down | 0.00061 |
| U62389_at | U62389 | 3402 | isocitrate dehydrogenase 1 (NADP+), soluble | 3.15 | down | 0.03949 |
| U66674_at | U66674 | 3408 | ATP-binding cassette, sub-family C (CFTR/MRP), | 6.13 | down | 0.00127 |
| U67963_at | U67963 | 3410 | lysophospholipase-like | 3.19 | down | 0.00029 |
| U68233_at | U68233 | 3412 | nuclear receptor subfamily 1, group H, member 4 | 6.76 | down | 0.00022 |
| U68494_at | U68494 | 3413 | EST | 4.82 | down | 0.00881 |
| U69141_at | U69141 | 3414 | glutaryl-Coenzyme A dehydrogenase | 3.06 | down | 0.00053 |
| U70732_rna1_at | U70732 | 3415 | glutamic-pyruvate transaminase (alanine | 27.63 | down | 0 |
| U70732_rna1_at | U70732 | 3415 | glutamic-pyruvate transaminase (alanine | 5.64 | down | 0.00146 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|---|-------------|-----------|---------|
| U73514_at | U73514 | 3419 | hydroxacyl-Coenzyme A dehydrogenase, type II | 3.79 | down | 0.01392 |
| U73682_at | U73682 | 3420 | meningioma expressed antigen 6 (coiled-coil | 3.08 | down | 0.01249 |
| U76376_at | U76376 | 3425 | harakiri, BCL2-interacting protein (contains only | 11.77 | down | 0.00002 |
| U77396_at | U77396 | 3426 | LPS-induced TNF-alpha factor | 4.47 | down | 0.00108 |
| U77594_at | U77594 | 3428 | retinoic acid receptor responder (tazarotene | 11.95 | down | 0.00527 |
| U78190_ma1_at | U78190 | 3431 | GTP cyclohydrolase I feedback regulatory protein | 3.94 | down | 0.034 |
| U79294_at | U79294 | 3435 | Phosphatidic acid phosphatase type 2b | 3.13 | down | 0.00129 |
| U79303_at | U79303 | 3436 | protein predicted by clone 23882 | 4.45 | down | 0 |
| U79716_at | U79716 | 3437 | reelin | 3.51 | down | 0.00053 |
| U82108_s_at | U82108 | 3441 | solute carrier family 9 (sodium/hydrogen | | | |
| U82468_at | U82468 | 3442 | exchanger), isoform 3 regulatory factor 2 | 3.19 | down | 0.01545 |
| U84569_at | U84569 | 3445 | tubby like protein 1 | 3.34 | down | 0.0097 |
| U86529_at | U86529 | 3451 | chromosome 21 open reading frame 2 | 3.46 | down | 0.01844 |
| U90544_at | U90544 | 3454 | glutathione S-transferase zeta 1 | 3.41 | down | 0.0118 |
| U90545_at | U90545 | 3455 | solute carrier family 17 (sodium phosphate), | 6.42 | down | 0.00023 |
| U95090_at | U95090 | 3464 | solute carrier family 17 (sodium phosphate), | 4.14 | down | 0.00005 |
| U95090_at | U95090 | 3464 | nephrosis 1, congenital, Finnish type (nephtrin) | 14.01 | down | 0.00018 |
| W03796_at | W03796 | 3468 | nephrosis 1, congenital, Finnish type (nephtrin) | 7.44 | down | 0.00004 |
| W07723_at | W07723 | 3471 | EST | 8.3 | down | 0.0032 |
| rc_W15528_at | W15528 | 3475 | EST | 3.51 | down | 0.00026 |
| W20094_at | W20094 | 3477 | EST | 3.56 | down | 0.00424 |
| W20276_f_at | W20276 | 3478 | DKFZP586A0522 protein | 38.09 | down | 0.00188 |
| rc_W20467_f_at | W20467 | 3480 | EST | 3.82 | down | 0.00033 |
| W26769_at | W26769 | 3483 | CGI-86 protein | 7.76 | down | 0.00008 |
| W26996_at | W26996 | 3484 | EST | 8.14 | down | 0.00204 |
| W27023_at | W27023 | 3485 | neuroendocrine-specific protein C like (foocen) | 6.42 | down | 0.00005 |
| W28798_at | W28798 | 3492 | phosphodiesterase 6A, cGMP-specific, rod, alpha | 6.79 | down | 0.00805 |
| W28824_at | W28824 | 3493 | EST | 7.01 | down | 0.00017 |
| W28944_at | W28944 | 3494 | EST | 15.8 | down | 0.00006 |
| rc_W31478_s_at | W31478 | 3496 | EST | 37.07 | down | 0.00205 |
| | | | | 3.36 | down | 0.01511 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_W33167_at | W33167 | 3499 | EST | 8.01 | down | 0.00026 |
| W35309_at | W35309 | 3500 | EST | 3.11 | down | 0.029 |
| W36290_s_at | W36290 | 3501 | Kreisler (mouse) maf-related leucine zipper | 3.94 | down | 0.02718 |
| rc_W37382_at | W37382 | 3502 | EST | 4.37 | down | 0.00677 |
| rc_W38407_at | W38407 | 3506 | EST | 4.17 | down | 0.00392 |
| rc_W42483_at | W42483 | 3510 | EST | 3.04 | down | 0.02518 |
| rc_W42789_at | W42789 | 3515 | EST | 9.38 | down | 0.00059 |
| rc_W42996_at | W42996 | 3517 | EST | 6.18 | down | 0.00587 |
| rc_W44745_at | W44745 | 3520 | EST | 9.02 | down | 0.00276 |
| rc_W45051_at | W45051 | 3521 | EST | 4.68 | down | 0.00433 |
| W45259_at | W45259 | 3522 | EST | 3.78 | down | 0.00069 |
| rc_W45560_at | W45560 | 3525 | EST | 5.06 | down | 0.00996 |
| rc_W46391_at | W46391 | 3527 | alpha integrin binding protein 63 | 4.03 | down | 0.01363 |
| rc_W46404_at | W46404 | 3528 | EST | 3.73 | down | 0.00116 |
| rc_W47175_at | W47175 | 3534 | 3-prime-phosphoadenosine 5-prime- | 5.54 | down | 0.00914 |
| rc_W51951_s_at | W51951 | 3542 | dCMP deaminase | 3.14 | down | 0.01691 |
| W52581 | W52581 | 3543 | CD36 antigen (collagen type I receptor, | | | |
| W52821_at | W52821 | 3544 | thrombospondin receptor)-like 2 (lysosomal | 3.08 | down | 0.00091 |
| W55903_at | W55903 | 3546 | leucine aminopeptidase | 4.02 | down | 0.03787 |
| rc_W57821_at | W57821 | 3548 | adipose differentiation-related protein; adipophilin | 9.12 | down | 0.00459 |
| W58540_at | W58540 | 3553 | EST | 5.03 | down | 0.00277 |
| rc_W58756_at | W58756 | 3554 | KIAA1131 protein | 4.28 | down | 0.0184 |
| rc_W60002_s_at | W60002 | 3555 | EST | 12.17 | down | 0.00087 |
| rc_W60186_at | W60186 | 3557 | plastin 3 (T isoform) | 4.88 | down | 0.01694 |
| rc_W61000_at | W61000 | 3560 | EST | 3.24 | down | 0.00228 |
| rc_W61319_at | W61319 | 3561 | EST | 3.15 | down | 0.03143 |
| W61377_at | W61377 | 3562 | EST | 3.02 | down | 0.00031 |
| rc_W61378_s_at | W61378 | 3563 | EST | 9.33 | down | 0.0012 |
| rc_W63728_at | W63728 | 3565 | EST | 8.31 | down | 0 |
| rc_W63785_at | W63785 | 3567 | EST | 5.03 | down | 0.00311 |
| | | | | 3.91 | down | 0.04089 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_W67147_at | W67147 | 3568 | deleted in liver cancer 1 | 9.74 | down | 0.00002 |
| rc_W67199_at | W67199 | 3569 | EST | 3.09 | down | 0.01528 |
| rc_W67564_s_at | W67564 | 3571 | nuclear receptor subfamily 0, group B, member 2 | 30.34 | down | 0 |
| rc_W68721_f_at | W68721 | 3572 | cleft lip and palate associated transmembrane | 6.34 | down | 0.01504 |
| rc_W69675_at | W69675 | 3575 | EST | 4.42 | down | 0.00019 |
| rc_W70115_s_at | W70115 | 3576 | histidine ammonia-lyase | 11.65 | down | 0.0003 |
| rc_W70313_at | W70313 | 3578 | EST | 3 | down | 0.00643 |
| rc_W72044_at | W72044 | 3580 | insulin induced gene 1 | 24.58 | down | 0.00001 |
| rc_W72079_at | W72079 | 3581 | EST | 6.36 | down | 0.00641 |
| rc_W72972_at | W72972 | 3587 | EST | 5.61 | down | 0.00939 |
| rc_W73194_at | W73194 | 3590 | dermatopontin | 3.45 | down | 0.02211 |
| rc_W73601_at | W73601 | 3592 | EST | 32.25 | down | 0 |
| rc_W73818_at | W73818 | 3593 | EST | 4.32 | down | 0.00385 |
| rc_W73889_s_at | W73889 | 3594 | tetranectin (plasminogen-binding protein) | 7.45 | down | 0.00091 |
| W74158_at | W74158 | 3596 | EST | 4.81 | down | 0.00233 |
| W79046_at | W79046 | 3602 | peroxisomal D3,D2-enoyl-CoA isomerase | 27.9 | down | 0.00023 |
| rc_W79422_s_at | W79422 | 3604 | fumarylacetoacetate | 14.94 | down | 0.00059 |
| rc_W80609_at | W80609 | 3606 | EST | 4.68 | down | 0.01729 |
| W81053_at | W81053 | 3610 | EST | 4.91 | down | 0.00164 |
| rc_W81079_at | W81079 | 3611 | EST | 3.31 | down | 0.0167 |
| | | | protein kinase, interferon-inducible double | | | |
| W81268_at | W81268 | 3612 | stranded RNA dependent | 4.2 | down | 0.00007 |
| rc_W85765_at | W85765 | 3618 | EST | 3.83 | down | 0.00379 |
| rc_W85847_at | W85847 | 3619 | EST | 7.28 | down | 0.00024 |
| rc_W85886_at | W85886 | 3621 | EST | 3.46 | down | 0.00814 |
| rc_W85888_at | W85888 | 3622 | EST | 3.99 | down | 0.00697 |
| rc_W86075_at | W86075 | 3624 | EST | 13.83 | down | 0.00057 |
| rc_W86375_s_at | W86375 | 3626 | EST | 19.29 | down | 0.0061 |
| rc_W86431_s_at | W86431 | 3627 | protein C inhibitor (plasminogen activator inhibitor | 14.94 | down | 0.00152 |
| rc_W86600_at | W86600 | 3628 | EST | 32.14 | down | 0 |
| rc_W86756_at | W86756 | 3630 | retinoid X receptor, alpha | 3.77 | down | 0.02472 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_W86850_f_at | W86850 | 3631 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 4.9 | down | 0.03105 |
| rc_W87454_at | W87454 | 3632 | homogentisate 1,2-dioxygenase (homogentisate | 7.93 | down | 0.00149 |
| rc_W87480_at | W87480 | 3633 | STAT induced STAT inhibitor-2 | 3.24 | down | 0.01063 |
| rc_W87532_at | W87532 | 3634 | putative glycine-N-acyltransferase | 12.34 | down | 0.00014 |
| rc_W87606_s_at | W87606 | 3635 | protein Z, vitamin K-dependent plasma | 9.23 | down | 0.00085 |
| rc_W87781_at | W87781 | 3636 | EST | 6.1 | down | 0.00045 |
| rc_W87824_at | W87824 | 3637 | EST | 3.67 | down | 0.01559 |
| rc_W88568_at | W88568 | 3638 | glycogenin 2 | 4.16 | down | 0.00111 |
| rc_W88946_at | W88946 | 3639 | putative glycine-N-acyltransferase | 58.26 | down | 0 |
| rc_W88985_at | W88985 | 3640 | KIAA0903 protein | 3.94 | down | 0.00295 |
| rc_W89178_at | W89178 | 3641 | transferrin receptor 2 | 10.85 | down | 0.00116 |
| rc_W90128_s_at | W90128 | 3643 | X-box binding protein 1 | 10.04 | down | 0.00018 |
| rc_W90455_s_at | W90455 | 3646 | alpha-2-macroglobulin | 10.35 | down | 0.00063 |
| rc_W90560_at | W90560 | 3647 | EST | 3.35 | down | 0.00388 |
| rc_W90583_r_at | W90583 | 3648 | EST | 4.35 | down | 0.00318 |
| rc_W90766_at | W90766 | 3649 | EST | 7.58 | down | 0.00057 |
| rc_W92148_s_at | W92148 | 3650 | kininogen | 51.09 | down | 0.00376 |
| rc_W92713_at | W92713 | 3654 | EST | 16.55 | down | 0.00097 |
| rc_W92771_s_at | W92771 | 3655 | glycine cleavage system protein H (aminomethyl | 4.36 | down | 0.0064 |
| rc_W94427_at | W94427 | 3659 | EST | 3.86 | down | 0.02649 |
| rc_W94942_i_at | W94942 | 3661 | dual specificity phosphatase 10 | 7.23 | down | 0.00137 |
| rc_W95041_at | W95041 | 3662 | EST | 12.79 | down | 0.00001 |
| W95795_at | W95795 | 3665 | EST | 7.8 | down | 0.00359 |
| X00129_at | X00129 | 3667 | retinol-binding protein 4, interstitial | 18.57 | down | 0.02378 |
| X00351 | X00351 | 3668 | actin, beta | 4.76 | down | 0.0003 |
| X01038 | X01038 | 3669 | apolipoprotein A-I, apolipoprotein C-III | 19.97 | down | 0.0275 |
| X01388_at | X01388 | 3670 | apolipoprotein C-III | 10.9 | down | 0.01246 |
| X02160_at | X02160 | 3671 | insulin receptor | 5.29 | down | 0.0001 |
| X02160_at | X02160 | 3671 | insulin receptor | 3.27 | down | 0.0007 |
| X02176_s_at | X02176 | 3672 | complement component 9 | 9.61 | down | 0.00004 |

AFFX-HSAC07/X00351_M_st

X01038_ma1_s_at

X01388_at

X02160_at

X02160_at

X02176_s_at

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| X02750_at | X02750 | 3673 | protein C (inactivator of coagulation factors Va vitronectin (serum spreading factor, somatomedin B, complement S-protein) | 7.04 | down | 0.00079 |
| X03168_at | X03168 | 3674 | | 25.88 | down | 0.00911 |
| X03350_at | X03350 | 3676 | alcohol dehydrogenase 2 (class I), beta | 19.32 | down | 0.00001 |
| X04085_rna1_at | X04085 | 3678 | catalase | 11.27 | down | 0.0002 |
| X04325_at | X04325 | 3679 | gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked) | 10.17 | down | 0.00061 |
| X04729_s_at | X04729 | 3682 | plasminogen activator inhibitor, type I | 3.15 | down | 0.01337 |
| X04828_at | X04828 | 3683 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 | 5.22 | down | 0.01278 |
| X05409_at | X05409 | 3684 | aldehyde dehydrogenase 2, mitochondrial | 3.99 | down | 0.01029 |
| X06562_at | X06562 | 3686 | growth hormone receptor | 10.87 | down | 0.00001 |
| X07173_at | X07173 | 3690 | inter-alpha (globulin) inhibitor, H2 polypeptide cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a | 30.3 | down | 0.00016 |
| X07618_s_at | X07618 | 3691 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a | 35.79 | down | 0.00065 |
| X07618_s_at | X07618 | 3691 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a | 13.58 | down | 0 |
| X07619_s_at | X07619 | 3692 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a | 4.96 | down | 0.00004 |
| X07732_at | X07732 | 3693 | hepsin (transmembrane protease, serine 1) | 28.21 | down | 0 |
| X07767_at | X07767 | 3694 | protein kinase, cAMP-dependent, catalytic, alpha | 5.94 | down | 0.00028 |
| X12662_rna1_at | X12662 | 3697 | arginase, liver | 20.59 | down | 0 |
| X13227_at | X13227 | 3698 | D-amino-acid oxidase | 4.81 | down | 0.0002 |
| X13334_at | X13334 | 3699 | CD14 antigen | 12.77 | down | 0.00887 |
| X13930_f_at | X13930 | 3700 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 38.52 | down | 0 |
| X14690_s_at | X14690 | 3703 | pre-alpha (globulin) inhibitor, H3 polypeptide | 16.07 | down | 0.00438 |
| X14787_at | X14787 | 3704 | thrombospondin 1 | 3.69 | down | 0.01115 |
| X14813_at | X14813 | 3705 | acetyl-Coenzyme A acyltransferase 1 | | | |
| X15422_at | X15422 | 3708 | (peroxisomal 3-oxoacyl-Coenzyme A thiolase) mannose-binding lectin (protein C) 2, soluble | 11.61 | down | 0.0002 |
| | | | | 8.29 | down | 0.00015 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|--|-------------|-----------|---------|
| X16260_s_at | X16260 | 3710 | inter-alpha (globulin) inhibitor, H1 polypeptide | 44.65 | down | 0.00933 |
| X16260_s_at | X16260 | 3710 | inter-alpha (globulin) inhibitor, H1 polypeptide | 26.39 | down | 0.0004 |
| X16349_s_at | X16349 | 3712 | sex hormone-binding globulin | 9.34 | down | 0.00007 |
| X17025_at | X17025 | 3715 | isopentenyl-diphosphate delta isomerase | 3.13 | down | 0.0043 |
| | | | paired basic amino acid cleaving enzyme (furin, | | | |
| X17094_at | X17094 | 3717 | membrane associated receptor protein) | 8.5 | down | 0 |
| X52150_rna1_s_at | X52150 | 3722 | arylsulfatase A | 3.51 | down | 0.00113 |
| X52520_at | X52520 | 3723 | tyrosine aminotransferase | 13.51 | down | 0.00002 |
| X52541_at | X52541 | 3724 | early growth response 1 | 3.77 | down | 0.00894 |
| | | | alanine-glyoxylate aminotransferase (oxalosis I; | | | |
| X53414_at | X53414 | 3728 | hyperoxaluria I; glycolicaciduria; serine-pyruvate | 13.87 | down | 0.00003 |
| X53595_s_at | X53595 | 3729 | apolipoprotein H (beta-2-glycoprotein I) | 27.28 | down | 0.0066 |
| X54380_at | X54380 | 3730 | pregnancy-zone protein | 8.44 | down | 0.00059 |
| X55283_rna1_s_at | X55283 | 3734 | asialoglycoprotein receptor 2 | 84.99 | down | 0.00084 |
| X56411_rna1_at | X56411 | 3737 | alcohol dehydrogenase 4 (class II), pi polypeptide | 25.14 | down | 0.00144 |
| X56692_at | X56692 | 3739 | C-reactive protein, pentraxin-related | 15.15 | down | 0.01884 |
| X57025_at | X57025 | 3742 | insulin-like growth factor 1 (somatomedin C) | 4.72 | down | 0.00087 |
| X58022_at | X58022 | 3747 | corticotropin releasing hormone-binding protein | 4.09 | down | 0.00076 |
| X58528_s_at | X58528 | 3748 | ATP-binding cassette, sub-family D (ALD), | 4.91 | down | 0.00728 |
| X59766_at | X59766 | 3749 | alpha-2-glycoprotein 1, zinc | 12.96 | down | 0.00043 |
| | | | cytochrome P450, subfamily XXVIIA (steroid 27- | | | |
| X59812_at | X59812 | 3750 | hydroxylase, cerebrotendinous xanthomatosis), | 4.65 | down | 0.036 |
| X59834_at | X59834 | 3751 | glutamate-ammonia ligase (glutamine synthase) | 4.29 | down | 0.00255 |
| X60673_s_at | X60673 | 3752 | adenylate kinase 3 | 8.3 | down | 0.00016 |
| X61123_at | X61123 | 3753 | B-cell translocation gene 1, anti-proliferative | 3.2 | down | 0.00796 |
| X62822_at | X62822 | 3758 | sialyltransferase 1 (beta-galactoside alpha-2,6- | 4.89 | down | 0.00274 |
| X63359_at | X63359 | 3759 | UDP glycosyltransferase 2 family, polypeptide | 13.66 | down | 0.00051 |
| X64877_at | X64877 | 3766 | H factor (complement)-like 3 | 14.6 | down | 0 |
| X64877_s_at | X64877 | 3766 | H factor (complement)-like 3 | 12.33 | down | 0 |
| X65727_cds2_s_at | X65727 | 3768 | glutathione S-transferase A2 glutathione S- | 73.64 | down | 0 |
| X65962_s_at | X65962 | 3769 | cytochrome P450, subfamily IIC (mephenytoin 4- | 5.47 | down | 0.00014 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|-------------------|---------|--------|---|-------------|-----------|---------|
| X67235_s_at | X67235 | 3773 | hematopoietically expressed homeobox | 3.17 | down | 0.0045 |
| X67491_f_at | X67491 | 3776 | glutamate dehydrogenase 1 | 7.45 | down | 0.00019 |
| X68277_at | X68277 | 3777 | dual specificity phosphatase 1 | 6.68 | down | 0.0036 |
| X68679_s_at | X68679 | 3779 | complement factor H related 3, complement factor | 38.22 | down | 0.00036 |
| X68733_ma1_at | X68733 | 3781 | alpha-1-antichymotrypsin | 7.87 | down | 0.03266 |
| X72012_at | X72012 | 3789 | endoglin (Osler-Rendu-Weber syndrome 1) | 4.2 | down | 0.005 |
| X72177_ma1_at | X72177 | 3790 | complement component 6 | 12.94 | down | 0.00011 |
| X75252_at | X75252 | 3793 | prostatic binding protein | 3.78 | down | 0.00231 |
| X76105_at | X76105 | 3794 | death-associated protein | 3.02 | down | 0.00944 |
| X76648_at | X76648 | 3796 | glutaredoxin (thioltransferase) | 4 | down | 0.00211 |
| X76717_at | X76717 | 3797 | metallothionein 1L | 8.09 | down | 0.00025 |
| X77548_at | X77548 | 3798 | nuclear receptor coactivator 4 | 3.76 | down | 0.00758 |
| X78706_at | X78706 | 3801 | carnitine acetyltransferase | 4.65 | down | 0.00442 |
| X78992_at | X78992 | 3802 | butyrate response factor 2 (EGF-response factor | 4.69 | down | 0.01995 |
| | | | prion protein (p27-30) (Creutzfeld-Jakob disease, | | | |
| X83416_s_at | X83416 | 3811 | Gerstmann-Strausler-Scheinker syndrome, fatal | 3.28 | down | 0.00221 |
| | | | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase | | | |
| X83618_at | X83618 | 3813 | 2 (mitochondrial) | 6.27 | down | 0.02099 |
| X85116_ma1_s_at | X85116 | 3814 | erythrocyte membrane protein band 7.2 | 6.37 | down | 0.00356 |
| X86401_s_at | X86401 | 3815 | glycine amidinotransferase (L-arginine:glycine | 22.7 | down | 0 |
| X87344_cds10_r_at | X87344 | 3817 | EST | 3.04 | down | 0.02779 |
| X90579_s_at | X90579 | 3819 | EST | 29.82 | down | 0.00273 |
| X90999_at | X90999 | 3820 | hydroxyacyl glutathione hydrolase; glyoxalase 2 | 5.27 | down | 0.00047 |
| X91148_at | X91148 | 3821 | microsomal triglyceride transfer protein (large | 5.91 | down | 0.00045 |
| X92720_at | X92720 | 3826 | phosphoenolpyruvate carboxykinase 2 | 7.6 | down | 0.00001 |
| X92744_at | X92744 | 3827 | defensin, beta 1 | 4.96 | down | 0.01804 |
| X94563_xpt2_r_at | X94563 | 3831 | EST | 3.52 | down | 0.00928 |
| X95190_at | X95190 | 3832 | acyl-Coenzyme A oxidase 2, branched chain | 12.81 | down | 0 |
| X95384_at | X95384 | 3833 | translational inhibitor protein p14.5 | 17.69 | down | 0.00048 |
| X95715_at | X95715 | 3835 | ATP-binding cassette, sub-family C (CFTR/MRP), | 6.78 | down | 0.00045 |
| X95876_at | X95876 | 3836 | G protein-coupled receptor 9 | 3.12 | down | 0.001 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|---------------|---------|--------|--|-------------|-----------|---------|
| X96752_at | X96752 | 3837 | L-3-hydroxyacyl-Coenzyme A dehydrogenase, | 4.94 | down | 0.00359 |
| X97324_at | X97324 | 3839 | adipose differentiation-related protein; adipophilin | 5.97 | down | 0.04638 |
| X98337_s_at | X98337 | 3840 | complement factor H related 3, complement factor | 13.5 | down | 0.00001 |
| Y00097_s_at | Y00097 | 3844 | annexin A6 | 3.4 | down | 0.00233 |
| Y00317_at | Y00317 | 3845 | UDP glycosyltransferase 2 family, polypeptide B4 | 18.34 | down | 0.00001 |
| Y00317_at | Y00317 | 3845 | UDP glycosyltransferase 2 family, polypeptide B4 | 8.97 | down | 0.00025 |
| Y00318_at | Y00318 | 3846 | I factor (complement) | 10 | down | 0.00019 |
| Y00339_s_at | Y00339 | 3847 | carbonic anhydrase II | 6.89 | down | 0 |
| Y00451_s_at | Y00451 | 3848 | aminolevulinatase, delta-, synthase 1 | 10.52 | down | 0.00107 |
| Y08374_ma1_at | Y08374 | 3853 | chitinase 3-like 1 (cartilage glycoprotein-39) | 3.5 | down | 0.04208 |
| Y08409_at | Y08409 | 3854 | thyroid hormone responsive SPOT14 (rat) | 5.84 | down | 0.00455 |
| Y09616_at | Y09616 | 3857 | carboxylesterase 2 (intestine, liver) | 18.78 | down | 0.00026 |
| Y10032_at | Y10032 | 3858 | serum/glucocorticoid regulated kinase | 4.24 | down | 0.00148 |
| Y10659_at | Y10659 | 3859 | interleukin 13 receptor, alpha 1 | 4.22 | down | 0.00061 |
| Y10659_at | Y10659 | 3859 | interleukin 13 receptor, alpha 1 | 3.17 | down | 0.00095 |
| Y12711_at | Y12711 | 3861 | progesterone binding protein | 14.83 | down | 0.00285 |
| Z11559_at | Z11559 | 3862 | iron-responsive element binding protein 1 | 4.3 | down | 0.00066 |
| Z11737_at | Z11737 | 3863 | flavin containing monooxygenase 4 | 3.84 | down | 0.00043 |
| Z11737_at | Z11737 | 3863 | flavin containing monooxygenase 4 | 3.67 | down | 0.00632 |
| Z11793_at | Z11793 | 3864 | selenoprotein P, plasma, 1 | 9.94 | down | 0.00021 |
| | | | branched chain keto acid dehydrogenase E1, | | | |
| Z14093_at | Z14093 | 3865 | alpha polypeptide (maple syrup urine disease) | 3.24 | down | 0.00301 |
| Z20777_at | Z20777 | 3866 | EST | 29.59 | down | 0.00044 |
| Z24459_ma1_at | Z24459 | 3869 | mature T-cell proliferation 1 | 5.29 | down | 0.00001 |
| Z24725_at | Z24725 | 3870 | mitogen inducible 2 | 7.9 | down | 0 |
| Z26491_s_at | Z26491 | 3873 | catechol-O-methyltransferase | 3.08 | down | 0.00877 |
| | | | aldo-keto reductase family 1, member D1 (delta 4- | | | |
| Z28339_at | Z28339 | 3875 | 3-ketosteroid-5-beta-reductase) | 24.66 | down | 0 |
| Z29481_at | Z29481 | 3877 | 3-hydroxyanthranilate 3,4-dioxygenase | 6.39 | down | 0.00029 |
| Z29481_at | Z29481 | 3877 | 3-hydroxyanthranilate 3,4-dioxygenase | 3.64 | down | 0.00096 |
| Z30425_at | Z30425 | 3878 | nuclear receptor subfamily 1, group 1, member 3 | 26.64 | down | 0 |

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|-----------------|---------|--------|---|-------------|-----------|---------|
| Z30425_at | Z30425 | 3878 | nuclear receptor subfamily 1, group I, member 3 | 7.88 | down | 0.00006 |
| Z31357_at | Z31357 | 3880 | cysteine dioxygenase, type I | 11.2 | down | 0.0001 |
| Z31690_s_at | Z31690 | 3881 | lipase A, lysosomal acid, cholesterol esterase | 3.83 | down | 0.00103 |
| rc_Z38161_at | Z38161 | 3884 | EST | 4.38 | down | 0.0011 |
| rc_Z38192_s_at | Z38192 | 3885 | EST | 3.35 | down | 0.00184 |
| rc_Z38435_at | Z38435 | 3890 | ribosomal protein L21 | 3.12 | down | 0.03617 |
| rc_Z38777_f_at | Z38777 | 3895 | nuclear receptor binding factor-2 | 3.28 | down | 0.022 |
| rc_Z39059_at | Z39059 | 3899 | EST | 5.19 | down | 0.0014 |
| rc_Z39406_at | Z39406 | 3905 | nuclear receptor co-repressor 1 | 4.18 | down | 0.00439 |
| rc_Z39431_at | Z39431 | 3907 | KIAA1086 protein | 3.68 | down | 0.0013 |
| rc_Z39476_at | Z39476 | 3908 | EST | 5.9 | down | 0.00687 |
| rc_Z39622_s_at | Z39622 | 3910 | EST | 4.4 | down | 0.00001 |
| rc_Z39818_at | Z39818 | 3912 | EST | 3.26 | down | 0.00089 |
| rc_Z39833_at | Z39833 | 3913 | GTP-binding protein | 16.89 | down | 0.00034 |
| rc_Z39976_at | Z39976 | 3915 | EST | 5.76 | down | 0.00012 |
| rc_Z39978_at | Z39978 | 3916 | EST | 3.56 | down | 0.04051 |
| rc_Z40192_at | Z40192 | 3918 | EST | 3.89 | down | 0.00223 |
| rc_Z40259_s_at | Z40259 | 3919 | EST | 8.18 | down | 0.00002 |
| rc_Z40305_at | Z40305 | 3920 | EST | 6.45 | down | 0.00001 |
| rc_Z40715_at | Z40715 | 3923 | delta-6 fatty acid desaturase | 18.68 | down | 0.0007 |
| rc_Z40902_at | Z40902 | 3926 | SEC14 (S. cerevisiae)-like 2 | 12.87 | down | 0.00001 |
| rc_Z41042_at | Z41042 | 3928 | EST | 3.63 | down | 0.00943 |
| Z47553_at | Z47553 | 3939 | flavin containing monooxygenase 5 | 6.17 | down | 0.00011 |
| Z48199_at | Z48199 | 3942 | syndecan 1 | 4.43 | down | 0.00408 |
| Z48475_at | Z48475 | 3943 | glucokinase (hexokinase 4) regulatory protein | 13.84 | down | 0 |
| Z49269_at | Z49269 | 3945 | small inducible cytokine subfamily A (Cys-Cys), | 18.46 | down | 0.00001 |
| Z49878_at | Z49878 | 3946 | guanidinoacetate N-methyltransferase | 13.96 | down | 0.00021 |
| Z69923_at | Z69923 | 3948 | HGF activator | 11.37 | down | 0.00053 |
| Z80345_ma1_s_at | Z80345 | 3951 | acyl-Coenzyme A dehydrogenase, C-2 to C-3 | 5.93 | down | 0.0024 |
| Z84718_cds1_at | Z84718 | 3952 | EST | 3.26 | down | 0.02252 |
| Z84721_cds2_at | Z84721 | 3953 | hemoglobin, zeta | 8.77 | down | 0.01446 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA005358_at | AA005358 | 14 | EST | 5.51 | down | 0.00059 |
| rc_AA007395_s_at | AA007395 | 17 | alcohol dehydrogenase 4 (class II), pi polypeptide | 37.78 | down | 0.00939 |
| rc_AA007629_at | AA007629 | 19 | EST | 5.56 | down | 0.00005 |
| rc_AA010205_at | AA010205 | 23 | EST | 5.71 | down | 0.00014 |
| rc_AA010605_s_at | AA010605 | 26 | 4-hydroxyphenylpyruvate dioxygenase | 25.52 | down | 0.00855 |
| rc_AA010619_at | AA010619 | 27 | EST | 5.28 | down | 0.002 |
| rc_AA018922_s_at | AA018922 | 40 | core promoter element binding protein | 3.39 | down | 0.01801 |
| rc_AA035245_s_at | AA035245 | 79 | aldehyde oxidase 1 | 7.97 | down | 0.02387 |
| rc_AA035457_at | AA035457 | 80 | EST | 3.41 | down | 0.00968 |
| rc_AA039335_s_at | AA039335 | 89 | coagulation factor XII (Hageman factor) | 5.33 | down | 0.03807 |
| rc_AA039616_at | AA039616 | 90 | EST | 3.84 | down | 0.00997 |
| rc_AA046457_at | AA046457 | 111 | EST | 3.05 | down | 0.02078 |
| rc_AA046747_at | AA046747 | 114 | EST | 4.77 | down | 0.00023 |
| rc_AA056482_at | AA056482 | 141 | EST | 3.06 | down | 0.01313 |
| rc_AA057678_at | AA057678 | 143 | EST | 6.63 | down | 0.00089 |
| rc_AA069696_at | AA069696 | 150 | EST | 3.07 | down | 0.01569 |
| rc_AA070191_at | AA070191 | 154 | EST | 3.24 | down | 0.00216 |
| rc_AA074885_at | AA074885 | 161 | macrophage receptor with collagenous structure | 10.88 | down | 0.00087 |
| rc_AA076326_at | AA076326 | 170 | SEC14 (S. cerevisiae)-like 2 | 3.85 | down | 0.0349 |
| rc_AA076383_at | AA076383 | 171 | EST | 4.65 | down | 0.00593 |
| rc_aa084668_at | AA084668 | 180 | ubiquitin-like 3 | 3.31 | down | 0.02055 |
| rc_AA085987_s_at | AA085987 | 183 | UDP glycosyltransferase 1 | 4.74 | down | 0.03035 |
| AA090257_at | AA090257 | 190 | superoxide dismutase 2, mitochondrial | 3.03 | down | 0.02774 |
| AA090439_at | AA090439 | 192 | ribosomal protein S6 | 5.11 | down | 0.01108 |
| rc_AA099225_at | AA099225 | 206 | EST | 6.59 | down | 0.00064 |
| rc_AA100026_at | AA100026 | 211 | EST | 4.18 | down | 0.00567 |
| rc_AA112101_f_at | AA112101 | 222 | EST | 4.36 | down | 0.03175 |
| rc_AA122345_f_at | AA122345 | 238 | glutamate dehydrogenase 1 | 3.75 | down | 0.01058 |
| rc_AA129390_at | AA129390 | 262 | EST | 4.03 | down | 0.00128 |
| rc_AA142849_at | AA142849 | 306 | EST | 3.45 | down | 0.03495 |
| rc_aa147646_s_at | AA147646 | 317 | DKFZP586A0522 protein | 3.19 | down | 0.00508 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA150776_at | AA150776 | 330 | EST | 6.17 | down | 0.00004 |
| rc_AA151676_at | AA151676 | 337 | peptidyl arginine deiminase, type II | 3.85 | down | 0.00875 |
| | | | aldo-keto reductase family 7, member A2 (aflatoxin) | | | |
| rc_AA157799_at | AA157799 | 348 | aldehyde reductase) | 3.08 | down | 0.00207 |
| rc_AA164586_s_at | AA164586 | 359 | estrogen receptor 1 | 3.56 | down | 0.01231 |
| rc_AA167565_at | AA167565 | 362 | EST | 3.81 | down | 0.04057 |
| rc_AA172372_at | AA172372 | 370 | EST | 5.12 | down | 0.00032 |
| rc_AA182030_at | AA182030 | 387 | EST | 3.51 | down | 0.0403 |
| AA188921_at | AA188921 | 393 | similar to Caenorhabditis elegans protein C42C1.9 | 3.38 | down | 0.00862 |
| rc_AA194997_s_at | AA194997 | 412 | EST | 4.8 | down | 0.00153 |
| rc_AA196287_at | AA196287 | 420 | EST | 4.86 | down | 0.01656 |
| rc_AA210850_at | AA210850 | 431 | EST | 3.12 | down | 0.00288 |
| rc_AA223902_at | AA223902 | 450 | EST | 4.22 | down | 0.01315 |
| rc_AA232114_s_at | AA232114 | 463 | epoxide hydrolase 2, cytoplasmic | 6.18 | down | 0.00231 |
| rc_AA233152_at | AA233152 | 467 | EST | 5.8 | down | 0.00272 |
| rc_AA233837_at | AA233837 | 474 | EST | 3.46 | down | 0.01365 |
| rc_AA235310_at | AA235310 | 496 | EST | 7.08 | down | 0.04056 |
| rc_AA236401_at | AA236401 | 510 | EST | 5.31 | down | 0.01787 |
| rc_AA236455_r_at | AA236455 | 512 | EST | 6.73 | down | 0.02418 |
| rc_AA236455_s_at | AA236455 | 512 | EST | 5.1 | down | 0.00307 |
| rc_AA253216_at | AA253216 | 561 | EST | 4.14 | down | 0.0014 |
| rc_AA253369_s_at | AA253369 | 563 | EST | 5.64 | down | 0.00478 |
| rc_AA256367_s_at | AA256367 | 579 | paraoxonase 3 | 8.37 | down | 0.02326 |
| rc_AA258350_at | AA258350 | 592 | EST | 4.1 | down | 0.02962 |
| rc_AA279676_s_at | AA279676 | 630 | deoxyribonuclease I-like 3 | 10.52 | down | 0.00181 |
| rc_AA282061_at | AA282061 | 652 | KIAA0962 protein | 3.46 | down | 0.00698 |
| rc_AA282886_at | AA282886 | 663 | EST | 3.29 | down | 0.00025 |
| rc_AA284795_at | AA284795 | 678 | phosphatidylethanolamine N-methyltransferase | 5.7 | down | 0.00004 |
| rc_AA285053_at | AA285053 | 681 | EST | 5 | down | 0.00718 |
| rc_AA287122_at | AA287122 | 686 | EST | 5.21 | down | 0.00523 |
| rc_AA287566_at | AA287566 | 690 | KIAA0187 gene product | 6.99 | down | 0.00023 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA291749_s_at | AA291749 | 703 | estrogen receptor 1 | 5.06 | down | 0.00044 |
| rc_AA297532_f_at | AA297532 | 725 | EST | 5.01 | down | 0.00745 |
| rc_AA343142_at | AA343142 | 751 | EST | 5.79 | down | 0.02747 |
| rc_AA348922_s_at | AA348922 | 758 | fatty acid-Coenzyme A ligase, long-chain 1, fatty acid- | 11.4 | down | 0.00848 |
| AA376875_at | AA376875 | 770 | Coenzyme A ligase, long-chain 2 | 3.45 | down | 0.00105 |
| rc_AA377087_at | AA377087 | 771 | monoamine oxidase A | 4.61 | down | 0.01616 |
| AA397841_at | AA397841 | 780 | EST | 3.29 | down | 0.00825 |
| rc_AA398892_at | AA398892 | 800 | similar to yeast BET3 (S. cerevisiae) | 4.33 | down | 0.01326 |
| AA400177_at | AA400177 | 808 | EST | 3.21 | down | 0.03901 |
| rc_AA401376_at | AA401376 | 829 | EST | 3.39 | down | 0.01403 |
| rc_AA401562_s_at | AA401562 | 830 | EST | 7.97 | down | 0.00527 |
| rc_AA402224_at | AA402224 | 836 | growth arrest and DNA-damage-inducible, gamma | 3.66 | down | 0.0033 |
| rc_AA404487_at | AA404487 | 851 | EST | 3.01 | down | 0.0059 |
| rc_AA417046_at | AA417046 | 915 | fatty acid-Coenzyme A ligase, very long-chain 1 | 8.49 | down | 0.02476 |
| rc_AA426640_at | AA426640 | 969 | small inducible cytokine subfamily B (Cys-X-Cys), | 4.8 | down | 0.00539 |
| rc_AA428325_at | AA428325 | 988 | member 14 (BRAK) | 4.09 | down | 0.02486 |
| rc_AA433946_at | AA433946 | 1033 | EST | 10.24 | down | 0.00663 |
| rc_AA435746_f_at | AA435746 | 1043 | GTPase activating protein-like | 4.21 | down | 0.03192 |
| rc_AA435985_at | AA435985 | 1049 | EST | 3.86 | down | 0.01713 |
| AA442334_at | AA442334 | 1069 | EST | 3.02 | down | 0.01936 |
| rc_AA446864_at | AA446864 | 1095 | EST | 11.57 | down | 0.0001 |
| rc_AA448002_at | AA448002 | 1113 | putative type II membrane protein | 14.14 | down | 0 |
| rc_AA448300_at | AA448300 | 1116 | FXRD domain-containing ion transport regulator 1 | 9.27 | down | 0.00108 |
| rc_AA450114_at | AA450114 | 1131 | (phospholemman) | 3.29 | down | 0.01171 |
| rc_AA450127_at | AA450127 | 1132 | EST | 3.37 | down | 0.00647 |
| rc_AA453988_at | AA453988 | 1160 | growth arrest and DNA-damage-inducible, beta | 7.78 | down | 0.02695 |
| rc_AA454733_s_at | AA454733 | 1169 | methionine adenosyltransferase I, alpha | 5.73 | down | 0.00748 |
| rc_AA455367_at | AA455367 | 1176 | EST | 3.47 | down | 0.00138 |
| | | | DKFZP586F1018 protein | | | |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA455988_at | AA455988 | 1184 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase | 12.51 | down | 0 |
| rc_AA458652_at | AA458652 | 1202 | EST | 5.03 | down | 0.00065 |
| rc_AA460012_at | AA460012 | 1224 | solute carrier family 22 (extraneuronal monoamine transporter), member 3 | 3.73 | down | 0.0313 |
| rc_AA460449_at | AA460449 | 1228 | EST | 3.53 | down | 0.01247 |
| rc_AA460661_at | AA460661 | 1229 | EST | 5.46 | down | 0.00151 |
| rc_AA461444_at | AA461444 | 1239 | EST | 3.19 | down | 0.02844 |
| rc_AA465233_s_at | AA465233 | 1269 | succinate-CoA ligase, GDP-forming, beta subunit | 3.19 | down | 0.00036 |
| rc_AA477119_at | AA477119 | 1289 | EST | 4.62 | down | 0.00072 |
| rc_AA477919_at | AA477919 | 1293 | EST | 3.9 | down | 0.00265 |
| rc_AA478298_s_at | AA478298 | 1297 | adipose specific 2 | 5.29 | down | 0.00943 |
| rc_AA480991_s_at | AA480991 | 1323 | EST | 4.83 | down | 0.03498 |
| rc_AA486511_at | AA486511 | 1349 | EST | 3.9 | down | 0.01409 |
| rc_AA490620_at | AA490620 | 1378 | EST | 6.25 | down | 0.03613 |
| rc_AA599472_at | AA599472 | 1451 | succinate-CoA ligase, GDP-forming, beta subunit | 3.31 | down | 0.02619 |
| rc_AA599814_at | AA599814 | 1456 | EST | 4.09 | down | 0.00235 |
| rc_AA599937_s_at | AA599937 | 1458 | insulin-like growth factor-binding protein 4 | 6.31 | down | 0.0477 |
| rc_AA608802_at | AA608802 | 1470 | EST | 3.44 | down | 0.01709 |
| rc_AA608837_at | AA608837 | 1472 | EST | 5.15 | down | 0.00005 |
| rc_AA609519_at | AA609519 | 1482 | EST | 5.23 | down | 0.00068 |
| rc_AA609537_s_at | AA609537 | 1483 | hepatic leukemia factor | 4.88 | down | 0.00118 |
| rc_AA621131_at | AA621131 | 1513 | EST | 4.57 | down | 0.03867 |
| rc_AA621209_at | AA621209 | 1516 | similar to Caenorhabditis elegans protein C42C1.9 | 4.01 | down | 0.00563 |
| C02386_s_at | C02386 | 1561 | hypothetical protein | 3.66 | down | 0.00673 |
| C02460_at | C02460 | 1562 | EST | 3.92 | down | 0.03073 |
| rc_C20653_at | C20653 | 1578 | EST | 4.32 | down | 0.00718 |
| rc_C20810_at | C20810 | 1579 | EST | 3.57 | down | 0.02116 |
| rc_C21130_at | C21130 | 1583 | EST | 3.24 | down | 0.03355 |
| D00003_at | D00003 | 1586 | cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3 | 9.46 | down | 0.00001 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| D00003_s_at | D00003 | 1586 | cytochrome P450, subfamily IIIA (naphthepine oxidase), polypeptide 3 | 6.8 | down | 0.01328 |
| D00408_s_at | D00408 | 1589 | cytochrome P450, subfamily IIIA (naphthepine oxidase), polypeptide 3, cytochrome P450, subfamily IIIA (naphthepine oxidase), polypeptide 5, cytochrome P450, subfamily IIIA, polypeptide 7 | 3.58 | down | 0.02048 |
| D10040_at | D10040 | 1593 | fatty acid-Coenzyme A ligase, long-chain 2 | 4.15 | down | 0.02947 |
| rc_D11756_f_at | D11756 | 1596 | EST | 4.08 | down | 0.02972 |
| D12620_s_at | D12620 | 1601 | cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) | 6.03 | down | 0.03947 |
| D12620_s_at | D12620 | 1601 | cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) | 4.7 | down | 0.04091 |
| D13243_s_at | D13243 | 1602 | pyruvate kinase, liver and RBC | 5.58 | down | 0.04029 |
| D13705_s_at | D13705 | 1610 | cytochrome P450, subfamily IVA, polypeptide 11 | 3.3 | down | 0.0051 |
| D14012_s_at | D14012 | 1612 | HGF activator | 7.27 | down | 0.00145 |
| D31628_s_at | D31628 | 1646 | 4-hydroxyphenylpyruvate dioxygenase | 13.18 | down | 0.02064 |
| rc_D45529_at | D45529 | 1662 | EST | 3.01 | down | 0.03105 |
| D49357_at | D49357 | 1665 | methionine adenosyltransferase I, alpha | 4.85 | down | 0.04435 |
| rc_D62518_at | D62518 | 1708 | EST | 5.96 | down | 0.00027 |
| D63160_at | D63160 | 1709 | ficollin (collagen/fibrinogen domain-containing lectin) 2 (hucollin) | 3.72 | down | 0.00312 |
| D78011_at | D78011 | 1717 | dihydropyrimidinase | 5.54 | down | 0.0312 |
| D78725_at | D78725 | 1720 | KIAA0914 gene product | 3.19 | down | 0.01083 |
| D79276_at | D79276 | 1722 | succinate-CoA ligase, GDP-forming, beta subunit | 4.34 | down | 0.00836 |
| D90042_at | D90042 | 1767 | N-acetyltransferase 2 (arylamine N-acetyltransferase) | 3.79 | down | 0.00697 |
| rc_F02028_at | F02028 | 1774 | EST | 3.15 | down | 0.00902 |
| rc_F02245_at | F02245 | 1776 | monoamine oxidase A | 3.51 | down | 0.01692 |
| rc_F03969_at | F03969 | 1785 | matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) | 3.36 | down | 0.01685 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|--------------------|---------------|--------|--|-------------|-----------|---------|
| rc_H02855_at | H02855 | 1832 | EST | 4.29 | down | 0.0138 |
| rc_H05704_s_at | H05704 | 1848 | EST | 3.07 | down | 0.00363 |
| rc_H06935_s_at | H06935 | 1855 | electron-transferring-flavoprotein dehydrogenase | 4.04 | down | 0.01498 |
| rc_H08102_at | H08102 | 1858 | breast cell glutaminase | 12.85 | down | 0.0424 |
| rc_H09317_at | H09317 | 1864 | EST | 3.2 | down | 0.00914 |
| | | | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase | | | |
| rc_H10779_s_at | H10779 | 1872 | formyltetrahydrofolate synthetase | 3.09 | down | 0.0496 |
| rc_H20543_at | H20543 | 1897 | DKFZP586B1621 protein | 13.06 | down | 0.00218 |
| rc_H27330_at | H27330 | 1909 | EST | 3.37 | down | 0.01318 |
| rc_H29568_at | H29568 | 1914 | EST | 5 | down | 0.00426 |
| rc_H55759_at | H55759 | 1949 | EST | 4.36 | down | 0.0398 |
| rc_H57060_s_at | H57060 | 1954 | EST | 7.57 | down | 0.00875 |
| rc_H57816_at | H57816 | 1957 | EST | 3.09 | down | 0.01327 |
| rc_H58673_at | H58673 | 1959 | EST | 15.49 | down | 0.00002 |
| rc_h58692_s_at | H58692 | 1960 | formyltetrahydrofolate dehydrogenase | 20.18 | down | 0.00485 |
| rc_H59136_at | H59136 | 1962 | EST | 6.63 | down | 0.00033 |
| rc_H62212_at | H62212 | 1969 | telomeric repeat binding factor 2 | 3.23 | down | 0.00513 |
| H66367_at | H66367 | 1977 | EST | 3.84 | down | 0.00133 |
| rc_H66840_at | H66840 | 1978 | EST | 3.34 | down | 0.01884 |
| rc_H77597_f_at | H77597 | 2000 | metallothionein 1H | 9.01 | down | 0.00022 |
| | | | ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) | | | |
| rc_H80901_s_at | H80901 | 2005 | antigen | 18.59 | down | 0 |
| rc_H81070_f_at | H81070 | 2006 | RNA helicase-related protein | 39.64 | down | 0.00002 |
| rc_H87765_at | H87765 | 2017 | KIAA0626 gene product | 3.94 | down | 0.00123 |
| H93246_s_at | H93246 | 2035 | EST | 4.14 | down | 0.00058 |
| rc_H93381_at | H93381 | 2036 | EST | 8.62 | down | 0.01271 |
| rc_H99727_at | H99727 | 2080 | adipose differentiation-related protein; adipophilin | 3.91 | down | 0.00325 |
| HG1428-HT1428_s_at | HG1428-HT1428 | | hemoglobin, beta | 8.98 | down | 0.02071 |
| HG2379-HT3996_s_at | HG2379-HT3996 | | serine hydroxymethyltransferase 1 (soluble) | 3.81 | down | 0.01837 |
| HG2730-HT2827_s_at | HG2730-HT2827 | | fibrinogen, A alpha polypeptide | 3.84 | down | 0.00795 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|--------------------|---------------|--------|--|-------------|-----------|---------|
| HG2730-HT2828_s_at | HG2730-HT2828 | | fibrinogen, A alpha polypeptide | 3.62 | down | 0.01013 |
| HG2841-HT2968_s_at | HG2841-HT2968 | | albumin | 4.62 | down | 0.00552 |
| HG4533-HT4938_s_at | HG4533-HT4938 | | protease inhibitor 4 (kallistatin) | 3.35 | down | 0.01605 |
| J02843_at | J02843 | 2088 | cytochrome P450, subfamily IIE (ethanol-inducible) | 6.18 | down | 0.01308 |
| J03810_at | J03810 | 2099 | solute carrier family 2 (facilitated glucose transporter), member 2 | 3.6 | down | 0.02376 |
| J03910_ma1_at | J03910 | 2101 | EST | 18.13 | down | 0.00119 |
| J04093_s_at | J04093 | 2106 | UDP glycosyltransferase 1 | 3.28 | down | 0.02286 |
| J04449_at | J04449 | 2110 | cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3 | 5.07 | down | 0.01733 |
| J05158_at | J05158 | 2117 | carboxypeptidase N, polypeptide 2, 83kD | 3.37 | down | 0.01156 |
| J05428_at | J05428 | 2120 | UDP glycosyltransferase 2 family, polypeptide B7 | 4.86 | down | 0.03414 |
| K02402_at | K02402 | 2125 | coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) | 6.64 | down | 0.04082 |
| K02766_at | K02766 | 2126 | complement component 9 | 5.03 | down | 0.0433 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 14.19 | down | 0.0307 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 8.02 | down | 0.03483 |
| L00352_at | L00352 | 2131 | low density lipoprotein receptor (familial hypercholesterolemia) | 3.3 | down | 0.03487 |
| L00389_f_at | L00389 | 2132 | cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2 | 3.87 | down | 0.00844 |
| L04751_at | L04751 | 2138 | cytochrome P450, subfamily IVA, polypeptide 11 | 8.13 | down | 0.02065 |
| L05144_at | L05144 | 2139 | phosphoenolpyruvate carboxykinase 1 (soluble) | 4 | down | 0.021 |
| L09229_s_at | L09229 | 2150 | fatty-acid-Coenzyme A ligase, long-chain 1, fatty-acid-Coenzyme A ligase, long-chain 2 | 4.5 | down | 0.01347 |
| L11931_at | L11931 | 2159 | serine hydroxymethyltransferase 1 (soluble) | 3.74 | down | 0.0056 |
| L12760_s_at | L12760 | 2162 | phosphoenolpyruvate carboxykinase 1 (soluble) | 6.06 | down | 0.01005 |
| L16883_s_at | L16883 | 2166 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 | 5.85 | down | 0.04368 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------|---------|--------|--|-------------|-----------|---------|
| L21893_at | L21893 | 2176 | solute carrier family 10 (sodium/bile acid cotransporter family), member 1 | 5.23 | down | 0.03367 |
| L27050_at | L27050 | 2186 | apolipoprotein F | 4.18 | down | 0.04901 |
| L32140_at | L32140 | 2192 | afamin | 5.39 | down | 0.02767 |
| M10942_at | M10942 | 2233 | metallothionein 1E (functional) | 4.05 | down | 0.01412 |
| M10943_at | M10943 | 2234 | metallothionein 1F (functional) | 6.23 | down | 0.00007 |
| M13143_at | M13143 | 2249 | kalikrein B plasma, (Fletcher factor) 1 | 3.04 | down | 0.008 |
| M14777_s_at | M14777 | 2263 | glutathione S-transferase A2, glutathione S-transferase A3 | 13.23 | down | 0.03224 |
| M16594_at | M16594 | 2272 | glutathione S-transferase A2 | 5.42 | down | 0.03813 |
| M16750_s_at | M16750 | 2273 | pim-1 oncogene | 3.07 | down | 0.02391 |
| M16974_s_at | M16974 | 2277 | complement component 8, alpha polypeptide | 10.85 | down | 0.02313 |
| M25079_s_at | M25079 | 2305 | hemoglobin, beta | 4.31 | down | 0.01567 |
| M26393_s_at | M26393 | 2309 | acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain | 4.3 | down | 0.02294 |
| M29873_s_at | M29873 | 2318 | cytochrome P450, subfamily IIB (phenobarbital-inducible) | 17.92 | down | 0.01469 |
| M29874_s_at | M29874 | 2319 | cytochrome P450, subfamily IIB (phenobarbital-inducible) | 8.13 | down | 0.01064 |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, plasma | 3.82 | down | 0.00131 |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, plasma | 3.31 | down | 0.00109 |
| M31667_f_at | M31667 | 2331 | cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2 | 4.47 | down | 0.01116 |
| M33317_f_at | M33317 | 2338 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 | 11.47 | down | 0.02611 |
| M34276_at | M34276 | 2341 | plasminogen | 3.08 | down | 0.02754 |
| M57731_s_at | M57731 | 2359 | GRO2 oncogene | 3.16 | down | 0.02204 |
| M61854_s_at | M61854 | 2370 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase) | 3.45 | down | 0.02949 |
| M63967_at | M63967 | 2378 | aldehyde dehydrogenase 5 | 3.88 | down | 0.00274 |
| M68840_at | M68840 | 2388 | monoamine oxidase A | 3.1 | down | 0.01953 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|---|-------------|-----------|---------|
| M68895_rna1_at | M68895 | 2390 | alcohol dehydrogenase 6 (class V) | 3.21 | down | 0.02095 |
| M72885_rna1_s_at | M72885 | 2393 | putative lymphocyte G0/G1 switch gene | 3.34 | down | 0.02943 |
| M76665_at | M76665 | 2398 | hydroxysteroid (11-beta) dehydrogenase 1 | 6.06 | down | 0.01317 |
| M81349_at | M81349 | 2405 | serum amyloid A4, constitutive | 10.97 | down | 0.01946 |
| M83652_s_at | M83652 | 2408 | properdin P factor, complement | 6 | down | 0.00002 |
| M83772_at | M83772 | 2409 | flavin containing monooxygenase 3 | 5.14 | down | 0.02023 |
| M86826_at | M86826 | 2413 | insulin-like growth factor binding protein, acid labile subunit | 3.75 | down | 0.01157 |
| M93405_at | M93405 | 2424 | methylmalonate-semialdehyde dehydrogenase | 3.09 | down | 0.03285 |
| M94065_s_at | M94065 | 2425 | dihydroorotate dehydrogenase | 7.87 | down | 0.0011 |
| M94065_at | M94065 | 2425 | dihydroorotate dehydrogenase | 3.61 | down | 0.00229 |
| M95585_s_at | M95585 | 2430 | hepatic leukemia factor | 3.36 | down | 0.00492 |
| M99439_at | M99439 | 2438 | transducin-like enhancer of split 4, homolog of Drosophila E(sp1) | 4.82 | down | 0.00121 |
| rc_N22404_at | N22404 | 2450 | EST | 3.44 | down | 0.02267 |
| rc_N22938_s_at | N22938 | 2453 | serum amyloid A4, constitutive | 4.91 | down | 0.01918 |
| rc_N29353_at | N29353 | 2477 | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | 3.44 | down | 0.01212 |
| rc_N29764_at | N29764 | 2482 | EST | 4.48 | down | 0.013 |
| rc_N31741_at | N31741 | 2489 | serine hydroxymethyltransferase 1 (soluble) | 5.66 | down | 0.00212 |
| rc_N34804_at | N34804 | 2497 | DKFZP434J214 protein | 3.97 | down | 0.0175 |
| rc_N39163_at | N39163 | 2509 | metallothionein 1L | 4.3 | down | 0.03917 |
| rc_N39201_at | N39201 | 2510 | protease inhibitor 4 (kallistatin) | 4.79 | down | 0.02015 |
| rc_N49902_at | N49902 | 2540 | EST | 3.02 | down | 0.00951 |
| rc_N51117_at | N51117 | 2544 | EST | 8.17 | down | 0.00105 |
| rc_N51773_at | N51773 | 2549 | EST | 6.92 | down | 0.01839 |
| rc_N52271_at | N52271 | 2552 | LIM protein (similar to rat protein kinase C-binding enigma) | 3.67 | down | 0.01102 |
| rc_N52322_at | N52322 | 2553 | EST | 4.58 | down | 0.02077 |
| rc_N54053_at | N54053 | 2561 | secreted phosphoprotein 2, 24kD | 12.87 | down | 0.01821 |
| rc_N54417_s_at | N54417 | 2567 | fibrinogen, A alpha polypeptide | 6.47 | down | 0.00733 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_N54429_at | N54429 | 2568 | EST | 6.85 | down | 0.03334 |
| rc_N54950_s_at | N54950 | 2573 | ketohexokinase (fructokinase) | 6.47 | down | 0.0223 |
| N57464_at | N57464 | 2576 | CCAAT/enhancer binding protein (C/EBP), delta | 4.87 | down | 0.00111 |
| rc_N57934_s_at | N57934 | 2577 | formiminotransferase cyclodeaminase | 3.28 | down | 0.01555 |
| rc_N58009_at | N58009 | 2578 | formiminotransferase cyclodeaminase | 8.52 | down | 0.01808 |
| rc_N59550_at | N59550 | 2588 | EST | 4.78 | down | 0.02924 |
| rc_N63391_at | N63391 | 2600 | EST | 3.87 | down | 0.02935 |
| rc_N63845_at | N63845 | 2605 | phytanoyl-CoA hydroxylase (Refsum disease) | 6.82 | down | 0.00369 |
| rc_N64036_s_at | N64036 | 2607 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A | | | |
| rc_N65959_at | N65959 | 2612 | dehydrogenase | 6.12 | down | 0.00476 |
| rc_N66066_at | N66066 | 2613 | EST | 3.38 | down | 0.00785 |
| rc_N67105_at | N67105 | 2624 | EST | 4.33 | down | 0.0184 |
| rc_N68596_s_at | N68596 | 2636 | betaine-homocysteine methyltransferase | 4.69 | down | 0.00194 |
| rc_N70358_s_at | N70358 | 2657 | growth hormone receptor | 10.46 | down | 0.01971 |
| rc_N70966_s_at | N70966 | 2663 | solute carrier family 10 (sodium/bile acid cotransporter family), member 1 | 8.47 | down | 0.00816 |
| rc_N73543_at | N73543 | 2675 | EST | | | |
| rc_N74025_at | N74025 | 2685 | deiodinase, iodothyronine, type I | 10.8 | down | 0.02894 |
| N77326_at | N77326 | 2696 | EST | 4.64 | down | 0.03981 |
| rc_N80129_i_at | N80129 | 2703 | metallothionein 1L | 8.18 | down | 0.01363 |
| rc_N80129_f_at | N80129 | 2703 | metallothionein 1L | 4.08 | down | 0.00768 |
| rc_N90584_at | N90584 | 2714 | EST | 26.87 | down | 0.00999 |
| N91087_at | N91087 | 2717 | EST | 11.48 | down | 0.00167 |
| N99542_at | N99542 | 2747 | orosomucoid 1 | 3.36 | down | 0.01561 |
| rc_R01023_s_at | R01023 | 2752 | glucokinase (hexokinase 4) regulatory protein | 3.66 | down | 0.00725 |
| rc_R08564_at | R08564 | 2780 | plasminogen-like | 3.53 | down | 0.00607 |
| rc_R09053_at | R09053 | 2783 | EST | 4.56 | down | 0.04036 |
| rc_R12472_at | R12472 | 2789 | EST | 8.77 | down | 0.01284 |
| rc_R22905_at | R22905 | 2801 | EST | 3.45 | down | 0.03074 |
| rc_R40395_s_at | R40395 | 2841 | lecithin-cholesterol acyltransferase | 12.09 | down | 0.02379 |
| | | | | 4.31 | down | 0.01744 |
| | | | | 12.85 | down | 0.01334 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_R40492_at | R40492 | 2842 | EST | 6.4 | down | 0.00527 |
| rc_R40899_f_at | R40899 | 2844 | glycine receptor, beta | 4.84 | down | 0.02369 |
| rc_R43799_at | R43799 | 2851 | EST | 3.93 | down | 0.005 |
| rc_R49602_at | R49602 | 2885 | EST | 16.17 | down | 0.00279 |
| rc_R59722_at | R59722 | 2916 | EST | 6.24 | down | 0.02361 |
| rc_R65593_s_at | R65593 | 2935 | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | 6.6 | down | 0.01982 |
| rc_R66002_at | R66002 | 2936 | EST | 4.33 | down | 0.00789 |
| R69417_at | R69417 | 2942 | EST | 6.43 | down | 0.00778 |
| rc_R73816_at | R73816 | 2961 | EST | 7.05 | down | 0.01287 |
| R77628_at | R77628 | 2966 | insulin induced gene 1 | 5.51 | down | 0.0404 |
| R79750_at | R79750 | 2971 | EST | 4.89 | down | 0.00695 |
| R80048_at | R80048 | 2972 | EST | 3.61 | down | 0.01209 |
| rc_R89811_s_at | R89811 | 2980 | HGF activator | 13.29 | down | 0.00148 |
| rc_R92475_s_at | R92475 | 2987 | flavin containing monooxygenase 3 | 6.46 | down | 0.02269 |
| rc_R93714_at | R93714 | 2992 | fetuin B | 4.65 | down | 0.03704 |
| R93776_s_at | R93776 | 2993 | EST | 5.55 | down | 0.00084 |
| rc_R94674_s_at | R94674 | 2996 | EST | 4.58 | down | 0.0047 |
| rc_R97419_at | R97419 | 3004 | cytochrome P450, subfamily VIII B (sterol 12-alpha-hydroxylase), polypeptide 1 | 19.3 | down | 0.00807 |
| R98073_at | R98073 | 3009 | EST | 8.37 | down | 0.01436 |
| rc_R99591_at | R99591 | 3016 | CD5 antigen-like (scavenger receptor cysteine rich family) aldo-keo reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4) | 7.41 | down | 0.00043 |
| S68287_at | S68287 | 3025 | glycogen synthase 2 (liver) | 5.04 | down | 0.02895 |
| S70004_at | S70004 | 3029 | EST | 5.13 | down | 0.00183 |
| S77356_at | S77356 | 3034 | EST | 3.55 | down | 0.03874 |
| rc_T10264_s_at | T10264 | 3051 | EST | 3.26 | down | 0.01718 |
| rc_T16484_s_at | T16484 | 3071 | EST | 4.78 | down | 0.00009 |
| rc_T40936_at | T40936 | 3118 | EST | 4.62 | down | 0.02844 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_T40995_f_at | T40995 | 3119 | alcohol dehydrogenase 3 (class I), gamma polypeptide | 3.42 | down | 0.00957 |
| rc_T41047_s_at | T41047 | 3120 | EST | 3.08 | down | 0.00553 |
| rc_T41232_at | T41232 | 3122 | EST | 3.14 | down | 0.02012 |
| rc_T47778_s_at | T47778 | 3127 | fibrinogen, A alpha polypeptide | 3.33 | down | 0.00637 |
| rc_T48075_f_at | T48075 | 3130 | hemoglobin, alpha 1 | 35.75 | down | 0.00471 |
| rc_T48278_at | T48278 | 3132 | EST | 24.1 | down | 0.00595 |
| rc_T51150_at | T51150 | 3137 | EST | 8.65 | down | 0.00553 |
| rc_T51617_at | T51617 | 3138 | solute carrier family 22 (extraneuronal monoamine transporter), member 3 | 6.16 | down | 0.04198 |
| rc_T52813_s_at | T52813 | 3142 | putative lymphocyte G0/G1 switch gene | 5.4 | down | 0.02021 |
| rc_T56281_f_at | T56281 | 3151 | RNA helicase-related protein | 14.64 | down | 0.00027 |
| T57140_s_at | T57140 | 3152 | paraoxonase 3 | 8.47 | down | 0.01048 |
| rc_T58756_at | T58756 | 3156 | EST | 16.61 | down | 0 |
| rc_T61256_s_at | T61256 | 3162 | ketoheokinase (fructokinase) | 3.56 | down | 0.04957 |
| rc_T61649_f_at | T61649 | 3165 | superoxide dismutase 2, mitochondrial | 4.08 | down | 0.0389 |
| rc_T63364_at | T63364 | 3170 | ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) | 6.27 | down | 0.00455 |
| rc_T64575_s_at | T64575 | 3172 | EST | 3.16 | down | 0.01855 |
| rc_T67931_at | T67931 | 3184 | fibrinogen, B beta polypeptide | 17.25 | down | 0.00128 |
| T68510_at | T68510 | 3187 | EST | 3.19 | down | 0.01504 |
| rc_T68711_at | T68711 | 3188 | EST | 35.98 | down | 0.0003 |
| rc_T68873_f_at | T68873 | 3190 | metallothionein 1L | 13.68 | down | 0.00593 |
| rc_T68878_f_at | T68878 | 3191 | carboxylesterase 1 (monocyte/macrophage serine esterase 1) | 4.18 | down | 0.02474 |
| rc_T69305_at | T69305 | 3197 | EST | 15.87 | down | 0.02258 |
| rc_T72502_at | T72502 | 3208 | EST | 4.74 | down | 0.00404 |
| rc_T72906_at | T72906 | 3210 | EST | 4.91 | down | 0.00512 |
| rc_T74542_s_at | T74542 | 3215 | UDP glycosyltransferase 2 family, polypeptide B10 | 7.19 | down | 0.011 |
| rc_T74608_at | T74608 | 3216 | hydroxyacid oxidase (glycolate oxidase) 1 | 6.1 | down | 0.00249 |
| rc_T78433_s_at | T78433 | 3220 | glycogen synthase 2 (liver) | 5.74 | down | 0.00949 |
| T83397_at | T83397 | 3233 | phytanoyl-CoA hydroxylase (Refsum disease) | 8.03 | down | 0.02173 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_T87174_at | T87174 | 3240 | EST | 3.46 | down | 0.00026 |
| T95813_f_at | T95813 | 3262 | KIAA1051 protein | 20.36 | down | 0.01361 |
| rc_T98199_l_at | T98199 | 3267 | EST | 4.05 | down | 0.00753 |
| rc_T98676_at | T98676 | 3269 | EST | 11.15 | down | 0.0323 |
| U02388_at | U02388 | 3278 | cytochrome P450, subfamily IVF, polypeptide 2 | 4.4 | down | 0.00761 |
| U06641_s_at | U06641 | 3287 | UDP glycosyltransferase 2 family, polypeptide B15 | 6.37 | down | 0.01594 |
| U08006_s_at | U08006 | 3290 | complement component 8, alpha polypeptide | 3.96 | down | 0.04272 |
| U08021_at | U08021 | 3291 | nicotinamide N-methyltransferase | 3.63 | down | 0.03726 |
| U20530_at | U20530 | 3322 | secreted phosphoprotein 2, 24kD | 5.31 | down | 0.01119 |
| U21931_at | U21931 | 3326 | fructose-bisphosphatase 1 | 3.17 | down | 0.0143 |
| U22029_f_at | U22029 | 3327 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 | 11.85 | down | 0.03538 |
| U27699_at | U27699 | 3340 | solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 | 3.65 | down | 0.00381 |
| U50196_at | U50196 | 3377 | adenosine kinase | 3.03 | down | 0.00975 |
| U50929_at | U50929 | 3380 | betaine-homocysteine methyltransferase | 8.04 | down | 0.0188 |
| U51010_s_at | U51010 | 3381 | nicotinamide N-methyltransferase | 4.69 | down | 0.03099 |
| U56814_at | U56814 | 3393 | deoxyribonuclease I-like 3 | 17.69 | down | 0.00007 |
| U56814_at | U56814 | 3393 | deoxyribonuclease I-like 3 | 5.75 | down | 0.00152 |
| U65932_at | U65932 | 3405 | extracellular matrix protein 1 | 3.18 | down | 0.00575 |
| U95090_at | U95090 | 3464 | nephrosis 1, congenital, Finnish type (nephtrin) | 4.63 | down | 0.01595 |
| W07723_at | W07723 | 3471 | EST | 3.51 | down | 0.00026 |
| W26996_at | W26996 | 3484 | EST | 4.46 | down | 0.00734 |
| W28414_at | W28414 | 3490 | EST | 4.06 | down | 0.00083 |
| W28798_at | W28798 | 3492 | phosphodiesterase 6A, cGMP-specific, rod, alpha | 3.33 | down | 0.00222 |
| W28944_at | W28944 | 3494 | EST | 6.9 | down | 0.01014 |
| rc_W44745_at | W44745 | 3520 | EST | 3.87 | down | 0.01051 |
| rc_W45560_at | W45560 | 3525 | EST | 3.48 | down | 0.0179 |
| W55903_at | W55903 | 3546 | adipose differentiation-related protein; adipophilin | 5.64 | down | 0.00014 |
| rc_W63728_at | W63728 | 3565 | EST | 3.86 | down | 0.00288 |
| rc_W67147_at | W67147 | 3568 | deleted in liver cancer 1 | 4.37 | down | 0.00069 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_W72044_at | W72044 | 3580 | insulin induced gene 1 | 3.1 | down | 0.03445 |
| rc_W72382_at | W72382 | 3584 | oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase | 9.89 | down | 0.03091 |
| rc_W73601_at | W73601 | 3592 | EST | 3.45 | down | 0.01382 |
| rc_W73818_at | W73818 | 3593 | EST | 3.47 | down | 0.00927 |
| rc_W81552_at | W81552 | 3615 | EST | 12.97 | down | 0.00244 |
| rc_W86075_at | W86075 | 3624 | EST | 6.04 | down | 0.01486 |
| rc_W86600_at | W86600 | 3628 | EST | 3.67 | down | 0.04208 |
| rc_W87532_at | W87532 | 3634 | putative glycine-N-acyltransferase | 5.5 | down | 0.00739 |
| rc_W87781_at | W87781 | 3636 | EST | 4.02 | down | 0.00284 |
| rc_W88946_at | W88946 | 3639 | putative glycine-N-acyltransferase | 25.28 | down | 0.00221 |
| rc_W95041_at | W95041 | 3662 | EST | 4.22 | down | 0.01005 |
| X02176_s_at | X02176 | 3672 | complement component 9 | 3.84 | down | 0.01793 |
| X06562_at | X06562 | 3686 | growth hormone receptor | 4.8 | down | 0.00507 |
| X06985_at | X06985 | 3689 | heme oxygenase (decycling) 1 | 3.34 | down | 0.00045 |
| X13227_at | X13227 | 3698 | D-amino-acid oxidase | 3.22 | down | 0.01753 |
| X13930_f_at | X13930 | 3700 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 8.1 | down | 0.0219 |
| X14813_at | X14813 | 3705 | acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase) | 3.53 | down | 0.00059 |
| X16260_s_at | X16260 | 3710 | inter-alpha (globulin) inhibitor, H1 polypeptide | 3.76 | down | 0.00291 |
| X16349_s_at | X16349 | 3712 | sex hormone-binding globulin | 6.61 | down | 0.00008 |
| X54380_at | X54380 | 3730 | pregnancy-zone protein | 7.71 | down | 0.00069 |
| X56411_rna1_at | X56411 | 3737 | alcohol dehydrogenase 4 (class II), pi polypeptide | 9.87 | down | 0.01416 |
| X58022_at | X58022 | 3747 | corticotropin releasing hormone-binding protein | 4.09 | down | 0.00076 |
| X63359_at | X63359 | 3759 | UDP glycosyltransferase 2 family, polypeptide B10 | 4.26 | down | 0.01725 |
| X64177_f_at | X64177 | 3763 | metallothionein 1H | 3.26 | down | 0.03928 |
| X67491_f_at | X67491 | 3776 | glutamate dehydrogenase 1 | 4.06 | down | 0.00273 |
| X72177_rna1_at | X72177 | 3790 | complement component 6 | 4.25 | down | 0.01598 |
| X76717_at | X76717 | 3797 | metallothionein 1L | 5.64 | down | 0.00215 |
| X90579_s_at | X90579 | 3819 | EST | 4.26 | down | 0.04759 |

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P Value |
|------------------|---------|--------|--|-------------|-----------|---------|
| X95190_at | X95190 | 3832 | acyl-Coenzyme A oxidase 2, branched chain | 6.22 | down | 0.00162 |
| X97324_at | X97324 | 3839 | adipose differentiation-related protein; adipophilin | 3.72 | down | 0.00202 |
| Y00317_at | Y00317 | 3845 | UDP glycosyltransferase 2 family, polypeptide B4 | 4.63 | down | 0.02986 |
| Z20777_at | Z20777 | 3866 | EST | 15.73 | down | 0.00147 |
| Z28339_at | Z28339 | 3875 | aldo-kefo reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) | 8.03 | down | 0.00853 |
| Z31690_s_at | Z31690 | 3881 | lipase A, lysosomal acid, cholesterol esterase (Wolman disease) | 3.29 | down | 0.00161 |
| rc_Z40259_s_at | Z40259 | 3919 | EST | 4.47 | down | 0.00093 |
| rc_Z40305_at | Z40305 | 3920 | EST | 4.09 | down | 0.00096 |
| rc_Z40902_at | Z40902 | 3926 | SEC14 (S. cerevisiae)-like 2 | 4.97 | down | 0.04627 |
| rc_Z41042_at | Z41042 | 3928 | EST | 3.37 | down | 0.00703 |
| Z48475_at | Z48475 | 3943 | glucokinase (hexokinase 4) regulatory protein | 4.6 | down | 0.01693 |
| Z49269_at | Z49269 | 3945 | small inducible cytokine subfamily A (Cys-Cys), member 14 | 7.24 | down | 0.01047 |
| Z69923_at | Z69923 | 3948 | HGF activator | 3.95 | down | 0.00012 |
| Z80345_rna1_s_at | Z80345 | 3951 | acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain | 3.21 | down | 0.04734 |
| Z84721_cds2_at | Z84721 | 3953 | hemoglobin, zeta | 7.39 | down | 0.01921 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA001504_f_at | AA001504 | 2 | EST | 4.44 | up | 0.03077 |
| rc_AA005262_at | AA005262 | 13 | EST | 3.09 | up | 0.0064 |
| rc_AA007507_at | AA007507 | 18 | KIAA1080 protein; Golgi-associated, gamma-adaptin ear | 5.23 | up | 0.00159 |
| rc_AA010065_s_at | AA010065 | 22 | containing, ARF-binding protein 2 | 3.71 | up | 0.00432 |
| rc_AA011209_s_at | AA011209 | 30 | CDC28 protein kinase 2 | 6.45 | up | 0.00088 |
| rc_AA011679_at | AA011679 | 32 | melanoma-associated antigen recognised by T | 3.08 | up | 0.03649 |
| rc_AA018346_at | AA018346 | 38 | EST | 3.69 | up | 0.04582 |
| rc_AA021549_at | AA021549 | 42 | EST | 3.17 | up | 0.00158 |
| rc_AA022623_at | AA022623 | 44 | EST | 3.27 | up | 0.01556 |
| rc_AA024658_at | AA024658 | 47 | ribosomal protein S19 | 7.55 | up | 0.00592 |
| rc_AA024776_at | AA024776 | 48 | EST | 3.44 | up | 0.00334 |
| rc_AA025166_s_at | AA025166 | 50 | fusion, derived from t(12;16) malignant liposarcoma | 3.17 | up | 0.00009 |
| rc_AA026356_at | AA026356 | 57 | EST | 5.04 | up | 0.02483 |
| rc_AA027833_i_at | AA027833 | 59 | EST | 5.02 | up | 0.01123 |
| rc_AA029288_at | AA029288 | 65 | EST | 3.36 | up | 0.04908 |
| rc_AA031814_at | AA031814 | 70 | KIAA0958 protein | 3.07 | up | 0.00681 |
| rc_AA037058_s_at | AA037058 | 84 | laminin, gamma 1 (formerly LAMB2) | 4.11 | up | 0.02264 |
| rc_AA037433_at | AA037433 | 86 | EST | 4.9 | up | 0.0194 |
| rc_AA037766_at | AA037766 | 87 | EST | 3.63 | up | 0.0328 |
| rc_AA040465_at | AA040465 | 95 | EST | 3.63 | up | 0.01806 |
| AA043111_s_at | AA043111 | 97 | EST | 6.36 | up | 0.0005 |
| rc_AA043959_at | AA043959 | 101 | tropomyosin 4 | 4.37 | up | 0.01641 |
| rc_AA045365_at | AA045365 | 106 | EST | 3.17 | up | 0.0149 |
| rc_AA046103_at | AA046103 | 109 | EST | 3.75 | up | 0.02893 |
| rc_AA046410_s_at | AA046410 | 110 | EST | 3.18 | up | 0.00797 |
| rc_AA046745_at | AA046745 | 113 | Wolf-Hirschhorn syndrome candidate 1 | 3.33 | up | 0.00648 |
| rc_AA047379_s_at | AA047379 | 119 | karyopherin (importin) beta 1 | 3.15 | up | 0.01572 |
| rc_AA047704_at | AA047704 | 120 | EST | 3.2 | up | 0.0029 |
| rc_AA052941_at | AA052941 | 121 | EST | 3.36 | up | 0.00088 |
| rc_AA053662_f_at | AA053662 | 129 | EST | 3.3 | up | 0.00558 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA053680_at | AA053680 | 130 | high-mobility group protein 2-like 1 | 4.07 | up | 0.03144 |
| rc_AA055892_at | AA055892 | 134 | EST | 3.02 | up | 0.04984 |
| rc_AA055896_at | AA055896 | 135 | collagen, type V, alpha 1 | 10.87 | up | 0.00907 |
| rc_AA070206_at | AA070206 | 155 | EST | 3.15 | up | 0.03914 |
| rc_AA070485_at | AA070485 | 156 | interleukin 13 receptor, alpha 1 | 3.19 | up | 0.03465 |
| rc_AA070827_at | AA070827 | 157 | EST | 4.37 | up | 0.02617 |
| AA071387_at | AA071387 | 158 | jumping translocation breakpoint | 3.31 | up | 0.0001 |
| rc_AA074162_s_at | AA074162 | 159 | superkiller viralicidic activity 2 (S. cerevisiae homolog)- | 3.23 | up | 0.00642 |
| rc_AA076138_at | AA076138 | 167 | H2A histone family, member Y | 3.75 | up | 0.01442 |
| rc_AA086071_at | AA086071 | 184 | chromosome-associated polypeptide C | 3.77 | up | 0.01993 |
| | | | kangai 1 (suppression of tumorigenicity 6, prostate; | | | |
| | | | CD82 antigen (R2 leukocyte antigen, antigen detected | | | |
| | | | by monoclonal and antibody IA4)) | | | |
| rc_AA086232_f_at | AA086232 | 186 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 | 4.52 | up | 0.00452 |
| rc_AA086412_at | AA086412 | 187 | EST | 3.13 | up | 0.00327 |
| AA089997_at | AA089997 | 189 | EST | 4.9 | up | 0.0241 |
| AA091752_at | AA091752 | 193 | purine-rich element binding protein B | 3.25 | up | 0.01419 |
| AA092129_f_at | AA092129 | 194 | EST | 5.67 | up | 0.00011 |
| AA092290_f_at | AA092290 | 195 | EST | 3.25 | up | 0.01616 |
| AA094752_at | AA094752 | 203 | hypothetical 43.2 Kd protein | 3.44 | up | 0.04445 |
| rc_AA099404_s_at | AA099404 | 208 | EST | 20.22 | up | 0 |
| rc_AA101272_at | AA101272 | 215 | EST | 3.83 | up | 0.0386 |
| rc_AA102489_at | AA102489 | 219 | EST | 5.28 | up | 0.02122 |
| rc_AA102837_f_at | AA102837 | 221 | EST | 4.13 | up | 0.0067 |
| rc_AA112679_at | AA112679 | 224 | EST | 4.19 | up | 0.00572 |
| rc_AA115562_at | AA115562 | 229 | EST | 3.35 | up | 0.00283 |
| rc_AA115735_s_at | AA115735 | 230 | EST | 4.8 | up | 0.02671 |
| rc_AA116036_at | AA116036 | 233 | chromosome 20 open reading frame 1 | 3.41 | up | 0.00089 |
| rc_AA122386_at | AA122386 | 239 | collagen, type V, alpha 2 | 3.44 | up | 0.02566 |
| rc_AA125808_at | AA125808 | 240 | EST | 3.04 | up | 0.02112 |
| rc_AA127444_at | AA127444 | 252 | EST | 3.87 | up | 0.01751 |
| rc_AA127741_at | AA127741 | 256 | EST | 4.49 | up | 0.0463 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA128407_at | AA128407 | 259 | EST | 3.33 | up | 0.02298 |
| rc_AA129757_at | AA129757 | 264 | EST | 3.75 | up | 0.0166 |
| rc_AA131220_at | AA131220 | 267 | EST | 3.18 | up | 0.00974 |
| rc_AA132032_s_at | AA132032 | 271 | trinucleotide repeat containing 1 | 3.84 | up | 0.01136 |
| rc_AA132514_at | AA132514 | 272 | EST | 3.2 | up | 0.00876 |
| rc_AA133527_at | AA133527 | 281 | EST | 5.23 | up | 0.00037 |
| rc_AA133666_s_at | AA133666 | 283 | cysteine-rich protein 2 | 5.35 | up | 0.00433 |
| rc_AA134052_s_at | AA134052 | 285 | Rab geranyltransferase, alpha subunit | 5.47 | up | 0.00982 |
| rc_AA135153_at | AA135153 | 291 | EST | 5.58 | up | 0.00327 |
| rc_AA135871_at | AA135871 | 294 | EST | 3.56 | up | 0.01718 |
| rc_AA136269_at | AA136269 | 298 | EST | 7.5 | up | 0.00014 |
| rc_AA136474_at | AA136474 | 301 | Meis (mouse) homolog 2 | 3.15 | up | 0.02837 |
| rc_AA136547_at | AA136547 | 302 | EST | 4.19 | up | 0.00098 |
| rc_AA136864_at | AA136864 | 304 | zinc finger protein homologous to Zfp-36 in mouse | 3.31 | up | 0.00346 |
| rc_AA142857_at | AA142857 | 307 | EST | 9.48 | up | 0.00376 |
| rc_AA142858_at | AA142858 | 308 | EST | 4.07 | up | 0.0022 |
| rc_AA146849_s_at | AA146849 | 313 | target of myb1 (chicken) homolog | 4.72 | up | 0.00326 |
| rc_AA148885_at | AA148885 | 320 | minichromosome maintenance deficient (S. cerevisiae) 4 | 6.59 | up | 0.00112 |
| rc_AA148977_at | AA148977 | 322 | EST | 9.3 | up | 0.00002 |
| rc_AA149889_at | AA149889 | 326 | neighbor of A-kinase anchoring protein 95 | 8.55 | up | 0.00224 |
| rc_AA151435_at | AA151435 | 336 | EST | 4.52 | up | 0.01134 |
| rc_AA156187_at | AA156187 | 339 | ATP synthase, H+ transporting, mitochondrial F0 | 9.38 | up | 0.02007 |
| rc_AA156460_at | AA156460 | 343 | complex, subunit b, isoform 1 | 4.39 | up | 0.01223 |
| rc_AA159025_at | AA159025 | 353 | EST | 6.58 | up | 0.01946 |
| rc_AA160775_s_at | AA160775 | 355 | BCL2-antagonist of cell death | 3.8 | up | 0.01145 |
| rc_AA165526_at | AA165526 | 360 | 3-prime-phosphoadenosine 5-prime-phosphosulfate | 3.68 | up | 0.00021 |
| rc_AA167708_at | AA167708 | 363 | synthase 1 | 3.19 | up | 0.01871 |
| rc_AA171760_at | AA171760 | 367 | EST | 4.39 | up | 0.04582 |
| rc_AA173430_at | AA173430 | 371 | EST | 3.74 | up | 0.01159 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| AA173505_at | AA173505 | 372 | EST | 3 | up | 0.01736 |
| AA173597_at | AA173597 | 373 | EST | 3.37 | up | 0.03622 |
| rc_AA173755_at | AA173755 | 374 | EST | 6.73 | up | 0.00666 |
| rc_AA179787_at | AA179787 | 380 | polyglutamine binding protein 1 | 4.71 | up | 0.00725 |
| rc_AA179845_at | AA179845 | 381 | EST | 3.55 | up | 0.02484 |
| rc_AA181580_s_at | AA181580 | 383 | karyopherin (importin) beta 1 | 3.01 | up | 0.0125 |
| rc_AA181705_f_at | AA181705 | 385 | EST | 5.9 | up | 0.00023 |
| rc_AA182001_r_at | AA182001 | 386 | EST | 3.78 | up | 0.04446 |
| AA187579_at | AA187579 | 390 | MCT-1 protein | 3.4 | up | 0.02455 |
| rc_AA188378_i_at | AA188378 | 392 | EST | 4.88 | up | 0.01653 |
| rc_AA194730_at | AA194730 | 410 | EST | 4.57 | up | 0.00801 |
| rc_AA194998_at | AA194998 | 413 | purinergic receptor (family A group 5) | 3.06 | up | 0.04752 |
| rc_AA195067_i_at | AA195067 | 414 | GTPase activating protein-like | 3.24 | up | 0.00606 |
| rc_AA204927_at | AA204927 | 425 | tropomyosin 1 (alpha) | 6.11 | up | 0.0014 |
| rc_AA207103_at | AA207103 | 429 | EST | 3.36 | up | 0.00131 |
| rc_AA211483_at | AA211483 | 435 | EST | 4.11 | up | 0.0365 |
| AA215299_s_at | AA215299 | 439 | U6 snRNA-associated Sm-like protein LSM7 | 4.81 | up | 0.00119 |
| rc_AA215379_at | AA215379 | 440 | EST | 4.44 | up | 0.01675 |
| rc_AA218663_at | AA218663 | 444 | acid-inducible phosphoprotein | 4.34 | up | 0.00161 |
| rc_AA226932_at | AA226932 | 453 | DKFZP564F0923 protein | 5.25 | up | 0.00612 |
| rc_AA227145_at | AA227145 | 454 | EST | 3.4 | up | 0.03422 |
| rc_AA227541_at | AA227541 | 457 | NS1-binding protein | 3.6 | up | 0.02801 |
| AA232837_at | AA232837 | 465 | EST | 8.85 | up | 0.0048 |
| rc_AA233897_at | AA233897 | 476 | EST | 3.8 | up | 0.02145 |
| rc_AA234096_at | AA234096 | 479 | EST | 5.75 | up | 0.01169 |
| rc_AA235289_at | AA235289 | 495 | RAP2A, member of RAS oncogene family | 4.31 | up | 0.00135 |
| AA235448_s_at | AA235448 | 497 | EST | 5.62 | up | 0.00077 |
| rc_AA235853_at | AA235853 | 503 | CGI-96 protein | 3.16 | up | 0.00744 |
| rc_AA235868_at | AA235868 | 504 | nuclear transcription factor Y, beta | 3.49 | up | 0.01897 |
| | | | 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1 | | | |
| rc_AA236150_at | AA236150 | 507 | | 3.46 | up | 0.0008 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| AA236412_at | AA236412 | 511 | EST | 3.1 | up | 0.04463 |
| rc_AA236532_s_at | AA236532 | 513 | EST | 3.04 | up | 0.03747 |
| rc_AA236672_at | AA236672 | 515 | EST | 4.37 | up | 0.00385 |
| rc_AA236904_at | AA236904 | 518 | EST | 3.07 | up | 0.01503 |
| rc_AA242757_at | AA242757 | 522 | EST | 3.27 | up | 0.00286 |
| rc_AA243133_at | AA243133 | 525 | serine/threonine kinase 15 | 7.03 | up | 0.00005 |
| rc_AA243173_at | AA243173 | 526 | EST | 3.49 | up | 0.0401 |
| AA249819_s_at | AA249819 | 535 | EST | 5.22 | up | 0.00049 |
| rc_AA251230_at | AA251230 | 540 | EST | 3.25 | up | 0.01417 |
| rc_AA251299_s_at | AA251299 | 541 | KIAA0014 gene product | 4.74 | up | 0.0252 |
| rc_AA251428_at | AA251428 | 542 | DKFZP586I2223 protein | 3.15 | up | 0.01223 |
| rc_AA251766_at | AA251766 | 543 | EST | 3.06 | up | 0.0098 |
| rc_AA251769_at | AA251769 | 544 | EST | 4.45 | up | 0.01431 |
| rc_AA251792_at | AA251792 | 546 | fatty-acid-Coenzyme A ligase, long-chain 4 | 7.44 | up | 0.00285 |
| rc_AA251909_at | AA251909 | 549 | EST | 3.59 | up | 0.01129 |
| rc_AA252060_at | AA252060 | 550 | EST | 4.88 | up | 0.00169 |
| rc_AA252355_at | AA252355 | 553 | EST | 3.02 | up | 0.00715 |
| rc_AA252524_at | AA252524 | 555 | EST | 3.17 | up | 0.00686 |
| rc_AA252627_s_at | AA252627 | 556 | chaperonin containing TCP1, subunit 6A (zeta 1),homeo box B5 | 4.28 | up | 0.00363 |
| rc_AA253011_f_at | AA253011 | 558 | KIAA0713 protein | 3.15 | up | 0.00035 |
| rc_AA255486_at | AA255486 | 568 | EST | 3.72 | up | 0.00154 |
| rc_AA256131_at | AA256131 | 574 | glycophosphatidylinositol anchor attachment 1 | 3.16 | up | 0.00011 |
| rc_AA256268_at | AA256268 | 576 | EST | 3.13 | up | 0.03874 |
| rc_AA256524_at | AA256524 | 580 | AD022 protein | 3.06 | up | 0.00626 |
| rc_AA256606_at | AA256606 | 581 | EST | 3.92 | up | 0.03087 |
| rc_AA256688_s_at | AA256688 | 584 | EST | 4.23 | up | 0.03094 |
| rc_AA258131_at | AA258131 | 587 | putative GTP-binding protein similar to RAY/RAB1C | 6.23 | up | 0.00931 |
| rc_AA258182_at | AA258182 | 589 | EST | 3.55 | up | 0.01198 |
| rc_AA258387_at | AA258387 | 594 | EST | 3.15 | up | 0.02028 |
| rc_AA258421_at | AA258421 | 595 | hypothetical protein | 6.5 | up | 0.00559 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA258614_s_at | AA258614 | 599 | EST | 3.94 | up | 0.0048 |
| rc_AA262477_at | AA262477 | 608 | ribonuclease HI, large subunit | 4.57 | up | 0.00724 |
| rc_AA262957_at | AA262957 | 612 | EST | 3.76 | up | 0.00157 |
| AA263032_s_at | AA263032 | 614 | ATP synthase, H+ transporting, mitochondrial F0 | | | |
| rc_AA278768_f_at | AA278768 | 617 | complex, subunit b, isoform 1 | 6.73 | up | 0.04478 |
| rc_AA278817_at | AA278817 | 618 | EST | 3.77 | up | 0.03239 |
| rc_AA279418_at | AA279418 | 626 | EST | 3.5 | up | 0.01159 |
| rc_AA280734_i_at | AA280734 | 639 | EST | 3.23 | up | 0.02054 |
| rc_AA280840_at | AA280840 | 641 | KIAA0618 gene product | 6.83 | up | 0.001 |
| rc_AA281599_at | AA281599 | 647 | casein kinase 1, gamma 2 | 4.51 | up | 0.0186 |
| rc_AA282247_at | AA282247 | 657 | EST | 4.87 | up | 0.00248 |
| rc_AA282343_at | AA282343 | 658 | EST | 5.88 | up | 0.01112 |
| rc_AA282571_at | AA282571 | 662 | purine-rich element binding protein B | 5.78 | up | 0.00128 |
| rc_AA283182_at | AA283182 | 668 | FSHD region gene 1 | 3.16 | up | 0.01355 |
| rc_AA283832_at | AA283832 | 672 | EST | 6.78 | up | 0.01784 |
| rc_AA284565_f_at | AA284565 | 675 | EST | 4.77 | up | 0.00156 |
| rc_AA284720_at | AA284720 | 676 | EST | 3.27 | up | 0.0362 |
| rc_AA284945_at | AA284945 | 680 | EST | 3.03 | up | 0.00252 |
| rc_AA285132_at | AA285132 | 682 | EST | 6.25 | up | 0.0002 |
| rc_AA286911_at | AA286911 | 684 | apoptotic protease activating factor | 3.1 | up | 0.00844 |
| rc_AA291137_at | AA291137 | 694 | EST | 3.36 | up | 0.00037 |
| rc_AA291139_at | AA291139 | 695 | EST | 3.67 | up | 0.03243 |
| rc_AA291168_at | AA291168 | 696 | EST | 6.22 | up | 0.03491 |
| rc_AA291644_at | AA291644 | 701 | EST | 4.93 | up | 0.01633 |
| rc_AA291659_at | AA291659 | 702 | EST | 3.28 | up | 0.00033 |
| AA291786_s_at | AA291786 | 704 | FE65-LIKE 2 | 4.15 | up | 0.00019 |
| rc_AA292765_at | AA292765 | 712 | ZW10 interactor | 4.15 | up | 0.00362 |
| rc_AA292788_s_at | AA292788 | 714 | EST | 7.24 | up | 0.00498 |
| rc_AA293420_s_at | AA293420 | 717 | EST | 3.65 | up | 0.01765 |
| rc_AA293589_s_at | AA293589 | 719 | zinc finger protein | 4.05 | up | 0.01189 |
| | | | | 3.02 | up | 0.01809 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| AA293868_s_at | AA293868 | 721 | EST | 3.04 | up | 0.0054 |
| AA296994_s_at | AA296994 | 724 | seven transmembrane domain protein | 3.16 | up | 0.0076 |
| AA313213_at | AA313213 | 732 | flotillin 1 | 3.59 | up | 0.00878 |
| AA320369_s_at | AA320369 | 735 | chromosome 19 open reading frame 3 | 3.88 | up | 0.00452 |
| rc_AA321833_at | AA321833 | 736 | EST | 3.16 | up | 0.00523 |
| rc_AA335191_f_at | AA335191 | 741 | creatine kinase, brain | 6.47 | up | 0.01462 |
| rc_AA338760_at | AA338760 | 744 | EST | 3.96 | up | 0.01307 |
| rc_AA365708_s_at | AA365708 | 764 | microfibrillar-associated protein 1 | 3.01 | up | 0.02372 |
| AA365742_s_at | AA365742 | 765 | tetraspan NET-6 protein | 4.12 | up | 0.00255 |
| rc_AA370163_at | AA370163 | 766 | EST | 3.41 | up | 0.00134 |
| AA384184_s_at | AA384184 | 774 | DKFZP586B0519 protein | 3.42 | up | 0.01222 |
| AA393139_at | AA393139 | 775 | geminin | 7.44 | up | 0.00888 |
| rc_AA394258_s_at | AA394258 | 779 | RD RNA-binding protein | 7.27 | up | 0.00054 |
| rc_AA398141_at | AA398141 | 788 | EST | 3.3 | up | 0.00211 |
| rc_AA398205_at | AA398205 | 789 | EST | 4.22 | up | 0.00059 |
| rc_AA398563_at | AA398563 | 797 | EST | 3.14 | up | 0.01895 |
| rc_AA398908_at | AA398908 | 801 | EST | 20.72 | up | 0.00114 |
| rc_AA398926_f_at | AA398926 | 802 | EST | 8.25 | up | 0.00066 |
| rc_AA399251_at | AA399251 | 804 | EST | 4.3 | up | 0.01578 |
| rc_AA399264_at | AA399264 | 805 | EST | 3.51 | up | 0.00327 |
| rc_AA400184_at | AA400184 | 809 | KIAA0907 protein | 4.11 | up | 0.01123 |
| AA400643_s_at | AA400643 | 817 | GAS2-related on chromosome 22 | 4.04 | up | 0.03751 |
| rc_AA400896_at | AA400896 | 822 | EST | 3.54 | up | 0.00889 |
| rc_AA401965_at | AA401965 | 833 | tumor suppressor deleted in oral cancer-related 1 | 7.58 | up | 0.00089 |
| rc_AA402272_at | AA402272 | 837 | EST | 3.73 | up | 0.02336 |
| rc_AA402968_at | AA402968 | 844 | EST | 3.68 | up | 0.00123 |
| | | | O-linked N-acetylglucosamine (GlcNAc) transferase | | | |
| | | | (UDP-N-acetylglucosamine:polypeptide-N- | | | |
| | | | acetylglucosaminyl transferase) | | | |
| rc_AA404560_at | AA404560 | 853 | EST | 3.73 | up | 0.0143 |
| rc_AA405098_at | AA405098 | 855 | EST | 6.09 | up | 0.01224 |
| rc_AA405505_at | AA405505 | 860 | RNA helicase family | 4.05 | up | 0.00747 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|-------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA405544_f_at | AA405544 | 861 | EST | 3.09 | up | 0.04146 |
| rc_AA405791_at | AA405791 | 864 | EST | 11.79 | up | 0.00587 |
| rc_AA406216_at | AA406216 | 871 | EST | 3.4 | up | 0.00529 |
| rc_AA406384_at | AA406384 | 875 | KIAA0670 protein/acinus | 3.23 | up | 0.00486 |
| rc_AA410469_at | AA410469 | 883 | EST | 5.45 | up | 0.00068 |
| rc_AA410962_s_at | AA410962 | 887 | peroxisome proliferative activated receptor, delta | 4.91 | up | 0.0044 |
| rc_AA412301_at | AA412301 | 899 | EST | 3.42 | up | 0.0129 |
| rc_AA412720_at | AA412720 | 905 | EST | 3.06 | up | 0.02153 |
| rc_AA416970_at | AA416970 | 912 | Mad4 homolog | 5.3 | up | 0.00418 |
| rc_AA416973_at | AA416973 | 913 | EST | 4.29 | up | 0.00155 |
| rc_AA417030_at | AA417030 | 914 | EST | 7.35 | up | 0.00555 |
| rc_AA417884_at | AA417884 | 919 | cyclin-dependent kinase inhibitor 2C (p18, inhibits | 3.42 | up | 0.02997 |
| AA421213_at | AA421213 | 931 | Lsm3 protein | 3.34 | up | 0.00198 |
| rc_AA421562_at | AA421562 | 934 | anterior gradient 2 (Xenopus laevis) homolog | 5.02 | up | 0.02818 |
| rc_AA421951_at | AA421951 | 936 | EST | 6.69 | up | 0.00013 |
| rc_AA423827_f_at | AA423827 | 941 | chromosome 22 open reading frame 3 | 4.39 | up | 0.00345 |
| rc_AA423841_f_at | AA423841 | 942 | EST | 3.71 | up | 0.01481 |
| rc_AA424029_at | AA424029 | 943 | EST | 4.54 | up | 0.02721 |
| rc_AA424487_at | AA424487 | 945 | EST | 4.68 | up | 0.0013 |
| rc_AA424881_at | AA424881 | 949 | EST | 3.39 | up | 0.03546 |
| rc_AA425544_s_at | AA425544 | 955 | eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) | 3.05 | up | 0.0346 |
| rc_AA425852_s_at, | AA425852 | 958 | EST | 3.98 | up | 0.02796 |
| rc_AA425852_i_at | AA425852 | 958 | EST | 3.82 | up | 0.0395 |
| rc_AA426291_at | AA426291 | 961 | EST | 3.03 | up | 0.00365 |
| rc_AA426374_f_at | AA426374 | 964 | tubulin, alpha 2 | 3.25 | up | 0.04346 |
| rc_AA426447_at | AA426447 | 965 | EST | 3.01 | up | 0.02414 |
| rc_AA426521_at | AA426521 | 967 | Sjogren's syndrome nuclear autoantigen 1 | 3.33 | up | 0.01163 |
| rc_AA427734_at | AA427734 | 977 | cholinergic receptor, nicotinic, epsilon polypeptide | 3.08 | up | 0.04796 |
| AA428172_f_at | AA428172 | 986 | Notch (Drosophila) homolog 3 | 9.63 | up | 0.00195 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA428204_at | AA428204 | 987 | cofactor required for Sp1 transcriptional activation, | 3.08 | up | 0.00313 |
| rc_AA429470_at | AA429470 | 996 | subunit 6 (77kD) | 3.2 | up | 0.0153 |
| rc_AA429472_at | AA429472 | 997 | EST | 8.78 | up | 0.00063 |
| AA429539_f_at | AA429539 | 999 | DKFZP434P106 protein | 4.3 | up | 0.01035 |
| rc_AA429572_at | AA429572 | 1000 | EST | 3.31 | up | 0.02144 |
| AA429825_at | AA429825 | 1003 | ribosomal protein S6 | 3.11 | up | 0.01857 |
| rc_AA430032_at | AA430032 | 1009 | DKFZP566B023 protein | 10.67 | up | 0.00052 |
| rc_AA430048_at | AA430048 | 1012 | pituitary tumor-transforming 1 | 4.32 | up | 0.00279 |
| rc_AA430154_at | AA430154 | 1014 | KIAA0160 protein | 3.09 | up | 0.04401 |
| rc_AA430474_at | AA430474 | 1015 | EST | 4.69 | up | 0.00007 |
| rc_AA430675_at | AA430675 | 1019 | Fanconi anemia, complementation group G | 3.16 | up | 0.01007 |
| rc_AA431571_at | AA431571 | 1024 | EST | 4.62 | up | 0.0174 |
| rc_AA431719_at | AA431719 | 1025 | EST | 3.19 | up | 0.00294 |
| rc_AA433947_at | AA433947 | 1034 | EST | 3.09 | up | 0.00253 |
| rc_AA434418_at | AA434418 | 1036 | KIAA1115 protein | 6.75 | up | 0.0032 |
| rc_AA435662_f_at | AA435662 | 1039 | EST | 3.27 | up | 0.0433 |
| rc_AA435665_at | AA435665 | 1040 | EST | 3.94 | up | 0.00274 |
| rc_AA435681_s_at | AA435681 | 1041 | EST | 3.07 | up | 0.01166 |
| rc_AA435748_at | AA435748 | 1044 | EST | 5.01 | up | 0.01812 |
| rc_aa435769_s_at | AA435769 | 1046 | EST | 3.06 | up | 0.00615 |
| AA442054_s_at | AA442054 | 1067 | phospholipase C, gamma 1 (formerly subtype 148) | 4.94 | up | 0.04102 |
| rc_AA442155_at | AA442155 | 1068 | transforming acidic coiled-coil containing protein 3 | 3.35 | up | 0.00344 |
| AA442400_at | AA442400 | 1071 | hepatitis B virus x-interacting protein (9.6kD) | 3.02 | up | 0.04037 |
| rc_AA442763_at | AA442763 | 1072 | cyclin B2 | 3.49 | up | 0.04176 |
| rc_AA443271_at | AA443271 | 1073 | KIAA0546 protein | 3.44 | up | 0.00324 |
| rc_AA443316_s_at | AA443316 | 1075 | v-Ha-ras Harvey rat sarcoma viral oncogene homolog | 3.4 | up | 0.00133 |
| rc_AA443602_at | AA443602 | 1078 | EST | 5.71 | up | 0.00736 |
| rc_AA443802_at | AA443802 | 1081 | EST | 4.07 | up | 0.01546 |
| rc_AA446242_at | AA446242 | 1087 | EST | 6.3 | up | 0.00169 |
| rc_AA446570_at | AA446570 | 1089 | EST | 3.12 | up | 0.02228 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA446581_at | AA446581 | 1090 | DKFZP564P0462 protein | 4.04 | up | 0.00479 |
| rc_AA446970_at | AA446970 | 1098 | EST | 3.09 | up | 0.01627 |
| rc_AA447574_at | AA447574 | 1102 | EST | 4.12 | up | 0.00779 |
| rc_AA448252_at | AA448252 | 1114 | EST | 3 | up | 0.00256 |
| rc_aa449073_s_at | AA449073 | 1117 | EST | 5.61 | up | 0.01214 |
| rc_aa449431_s_at | AA449431 | 1124 | translation initiation factor IF2 | 3.76 | up | 0.00571 |
| rc_AA449828_at | AA449828 | 1130 | EST | 3.35 | up | 0.01609 |
| rc_AA450247_at | AA450247 | 1133 | EST | 3.13 | up | 0.00531 |
| rc_AA451680_at | AA451680 | 1136 | hepatocellular carcinoma associated protein; breast | | | |
| rc_AA451877_at | AA451877 | 1138 | cancer associated gene 1 | 3.85 | up | 0.0018 |
| AA451992_at | AA451992 | 1140 | EST | 4.6 | up | 0.04045 |
| rc_AA452167_at | AA452167 | 1142 | HSPC039 protein | 3.33 | up | 0.01696 |
| AA452724_at | AA452724 | 1149 | EST | 3.29 | up | 0.03337 |
| rc_AA453628_at | AA453628 | 1154 | programmed cell death 5 | 7.7 | up | 0.00085 |
| rc_AA453656_at | AA453656 | 1155 | EST | 3.17 | up | 0.00849 |
| rc_AA453783_s_at | AA453783 | 1158 | EST | 3.02 | up | 0.00958 |
| rc_AA454597_s_at | AA454597 | 1166 | EST | 4.07 | up | 0.00786 |
| rc_AA454830_at | AA454830 | 1170 | DKFZP586M2123 protein | 4.23 | up | 0.00917 |
| AA454908_s_at | AA454908 | 1171 | KIAA0144 gene product | 6.48 | up | 0.00555 |
| rc_AA455239_at | AA455239 | 1174 | chromosome-associated polypeptide C | 6.39 | up | 0.01835 |
| rc_AA456415_at | AA456415 | 1192 | KIAA0537 gene product | 5.78 | up | 0.00003 |
| rc_AA456583_s_at | AA456583 | 1193 | PL6 protein | 3.32 | up | 0.00155 |
| rc_AA456646_at | AA456646 | 1196 | EST | 3.37 | up | 0.00139 |
| rc_AA456852_at | AA456852 | 1199 | suppressor of white apricot homolog 2 | 3.34 | up | 0.0309 |
| rc_AA458878_s_at | AA458878 | 1204 | EST | 3.66 | up | 0.00614 |
| rc_AA458890_at | AA458890 | 1206 | EST | 5.49 | up | 0.00977 |
| rc_AA459254_at | AA459254 | 1211 | EST | 3.27 | up | 0.00079 |
| AA459542_s_at | AA459542 | 1218 | regulatory factor X-associated ankyrin-containing protein | 6.22 | up | 0.00001 |
| rc_AA460665_at | AA460665 | 1230 | EST | 3.4 | up | 0.00841 |
| rc_aa460909_s_at | AA460909 | 1232 | EST | 4.01 | up | 0.01866 |
| | | | | 5.02 | up | 0.01354 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA461063_at | AA461063 | 1235 | EST | 4.3 | up | 0.00074 |
| AA461282_s_at | AA461282 | 1237 | dihydropyrimidinase-like 2 | 3.42 | up | 0.02014 |
| rc_AA461476_at | AA461476 | 1243 | EST | 3.72 | up | 0.00744 |
| rc_AA463254_s_at | AA463254 | 1247 | histone deacetylase 3 | 4.01 | up | 0.01856 |
| rc_AA463934_at | AA463934 | 1253 | splicing factor 3b, subunit 4, 49kD | 3.15 | up | 0.00952 |
| AA464043_s_at | AA464043 | 1255 | EST | 3.99 | up | 0.00056 |
| rc_AA464251_at | AA464251 | 1257 | EST | 3.45 | up | 0.02229 |
| rc_AA464414_i_at | AA464414 | 1258 | EST | 4.08 | up | 0.02299 |
| rc_AA464423_at | AA464423 | 1259 | EST | 3.06 | up | 0.01416 |
| rc_aa464722_s_at | AA464722 | 1263 | DKFZP566C243 protein | 3.51 | up | 0.00101 |
| rc_AA464963_at | AA464963 | 1265 | EST | 4.77 | up | 0.00086 |
| AA465000_s_at | AA465000 | 1266 | EST | 3.86 | up | 0.00431 |
| rc_AA465093_at | AA465093 | 1267 | TIA1 cytotoxic granule-associated RNA-binding protein | 3.3 | up | 0.01314 |
| rc_AA465218_at | AA465218 | 1268 | DKFZP586M1523 protein | 3.17 | up | 0.00357 |
| rc_AA465342_at | AA465342 | 1271 | EST | 3.21 | up | 0.01378 |
| rc_AA470156_at | AA470156 | 1276 | EST | 4.99 | up | 0.0206 |
| AA471384_at | AA471384 | 1278 | divalent cation tolerant protein CUTA | 3.44 | up | 0.01161 |
| rc_AA476473_at | AA476473 | 1285 | EST | 3 | up | 0.01324 |
| rc_AA476754_s_at | AA476754 | 1287 | EST | 3.18 | up | 0.01696 |
| rc_AA476944_at | AA476944 | 1288 | EST | 3.29 | up | 0.00189 |
| rc_AA477316_at | AA477316 | 1290 | calumenin | 3.05 | up | 0.00608 |
| rc_AA477549_s_at | AA477549 | 1291 | T-cell, immune regulator 1 | 4.84 | up | 0.04096 |
| rc_AA478017_at | AA478017 | 1295 | zyxin | 4.25 | up | 0.01223 |
| rc_AA478300_at | AA478300 | 1298 | CD39-like 2 | 3.75 | up | 0.00152 |
| rc_AA478415_at | AA478415 | 1299 | EST | 3.14 | up | 0.0483 |
| rc_AA478422_at | AA478422 | 1301 | unc-51 (C. elegans)-like kinase 1 | 3.83 | up | 0.00116 |
| rc_AA478615_s_at | AA478615 | 1305 | H1 histone family, member X disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) | 3.09 | up | 0.0499 |
| rc_AA478971_s_at | AA478971 | 1306 | phosphoprotein) | 3.25 | up | 0.02698 |
| rc_AA479096_at | AA479096 | 1308 | EST | 3.32 | up | 0.00118 |
| rc_AA479139_s_at | AA479139 | 1310 | acid phosphatase 1, soluble | 3.42 | up | 0.01853 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA479881_at | AA479881 | 1317 | EST | 3.34 | up | 0.03289 |
| rc_AA481060_at | AA481060 | 1326 | EST | 3.08 | up | 0.00029 |
| rc_AA481420_at | AA481420 | 1327 | EST | 3.08 | up | 0.0206 |
| rc_AA482104_s_at | AA482104 | 1332 | non-metastatic cells 3, protein expressed in | 4.78 | up | 0.00135 |
| rc_AA482224_f_at | AA482224 | 1334 | putative type II membrane protein | 4.47 | up | 0.0001 |
| AA482319_f_at | AA482319 | 1335 | putative type II membrane protein | 4.9 | up | 0.00028 |
| AA482319_i_at | AA482319 | 1335 | putative type II membrane protein | 3.13 | up | 0.00071 |
| rc_AA485060_at | AA485060 | 1339 | EST | 3.83 | up | 0.03172 |
| rc_AA485084_s_at | AA485084 | 1340 | EST | 3.31 | up | 0.01232 |
| rc_AA485431_s_at | AA485431 | 1345 | EST | 3.81 | up | 0.00441 |
| rc_AA485697_at | AA485697 | 1346 | EST | 3.53 | up | 0.03566 |
| rc_AA487218_at | AA487218 | 1355 | EST | 4.43 | up | 0.03198 |
| rc_AA487856_at | AA487856 | 1359 | KIAA0676 protein | 3.59 | up | 0.01408 |
| rc_AA488074_at | AA488074 | 1360 | cell division cycle 42 (GTP-binding protein, 25kD) | 3.74 | up | 0.01887 |
| rc_AA488432_at | AA488432 | 1361 | phosphoserine phosphatase | 4.2 | up | 0.00128 |
| rc_AA488872_s_at | AA488872 | 1363 | EST | 3.35 | up | 0.03191 |
| rc_AA488892_at | AA488892 | 1364 | EST | 4.14 | up | 0.04766 |
| rc_AA489091_at | AA489091 | 1368 | EST | 3.58 | up | 0.0002 |
| rc_AA489707_at | AA489707 | 1371 | EST | 3.5 | up | 0.03208 |
| rc_AA489712_at | AA489712 | 1372 | EST | 4.69 | up | 0.00587 |
| rc_AA490212_at | AA490212 | 1375 | H2A histone family, member Y | 3.52 | up | 0.02202 |
| AA491188_at | AA491188 | | solute carrier family 2 (facilitated glucose transporter), member 3 | 5.04 | up | 0.02291 |
| rc_AA491295_at | AA491295 | 1387 | | 3.71 | up | 0.0103 |
| AA495857_at | AA495857 | 1390 | calcium/calmodulin-dependent protein kinase kinase 2, | 3.21 | up | 0.02243 |
| rc_AA496715_f_at | AA496715 | 1394 | EST | 3.44 | up | 0.00069 |
| rc_AA496981_at | AA496981 | 1400 | spectrin SH3 domain binding protein 1 | | | |
| rc_AA497018_at | AA497018 | | v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 | 5.82 | up | 0.00521 |
| AA504413_at | AA504413 | 1404 | | 4.81 | up | 0.00352 |
| rc_AA504512_s_at | AA504512 | 1406 | adenylate cyclase 1 (brain) | 3.31 | up | 0.00036 |
| | | 1413 | EST | 5.72 | up | 0.00384 |
| | | 1415 | KIAA0943 protein | | | |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|---|-------------|-----------|---------|
| rc_AA505133_at | AA505133 | 1417 | solute carrier family 2 (facilitated glucose transporter), member 3 | 12.21 | up | 0.00169 |
| rc_AA505141_at | AA505141 | 1418 | | 3.08 | up | 0.02327 |
| rc_AA521149_at | AA521149 | 1420 | | 3.33 | up | 0.00211 |
| rc_AA598405_at | AA598405 | 1424 | | 3.87 | up | 0.00649 |
| rc_AA598447_at | AA598447 | 1428 | | 3.5 | up | 0.01201 |
| rc_AA598589_at | AA598589 | 1431 | exportin, tRNA (nuclear export receptor for tRNAs) | 3.24 | up | 0.00432 |
| rc_AA598648_s_at | AA598648 | 1432 | SWI/SNF related, matrix associated, actin dependent | | | |
| rc_AA598712_at | AA598712 | 1436 | regulator of chromatin, subfamily a, member 4 | 3.46 | up | 0.00293 |
| rc_AA598749_at | AA598749 | 1438 | EST | 3.45 | up | 0.00005 |
| | | | EST | 3.01 | up | 0.03714 |
| rc_AA598829_s_at | AA598829 | 1439 | heterogeneous nuclear ribonucleoprotein U (scaffold | | | |
| rc_AA598831_f_at | AA598831 | 1440 | attachment factor A) | 3.04 | up | 0.00967 |
| rc_AA599469_at | AA599469 | 1450 | EST | 3.41 | up | 0.00452 |
| rc_AA599808_at | AA599808 | 1455 | EST | 3.07 | up | 0.04154 |
| rc_AA599850_at | AA599850 | 1457 | EST | 3.09 | up | 0.00726 |
| rc_AA600153_at | AA600153 | 1460 | DEK oncogene (DNA binding) | 3.55 | up | 0.03215 |
| rc_AA608668_at | AA608668 | 1465 | erythrocyte membrane protein band 4.1-like 2 | 3.71 | up | 0.02967 |
| rc_AA608897_at | AA608897 | 1473 | EST | 3.33 | up | 0.02014 |
| rc_AA609008_at | AA609008 | 1475 | EST | 5.05 | up | 0.01782 |
| rc_AA609080_at | AA609080 | 1478 | EST | 4.04 | up | 0.00002 |
| rc_AA610073_at | AA610073 | 1497 | EST | 3.71 | up | 0.0306 |
| rc_AA610089_at | AA610089 | 1498 | U4/U6-associated RNA splicing factor | 3.25 | up | 0.00859 |
| rc_AA610116_l_at | AA610116 | 1499 | tetraspan NET-6 protein | 4.07 | up | 0.00361 |
| rc_AA620461_at | AA620461 | 1501 | EST | 16.35 | up | 0.00249 |
| rc_AA620553_s_at | AA620553 | 1504 | flap structure-specific endonuclease 1 | 3.45 | up | 0.01146 |
| rc_AA620761_at | AA620761 | 1507 | EST | 7.56 | up | 0.00101 |
| rc_AA620779_at | AA620779 | 1508 | golgin-67 | 3.3 | up | 0.00285 |
| rc_AA620881_at | AA620881 | 1510 | trinucleotide repeat containing 3 | 3.35 | up | 0.00297 |
| rc_AA621146_at | AA621146 | 1514 | MUF1 protein | 9.49 | up | 0.00062 |
| | | | | 3.15 | up | 0.02116 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|----------|--------|--|-------------|-----------|---------|
| rc_AA621242_s_at | AA621242 | 1518 | hypothetical protein, peptidylprolyl isomerase B | 4.59 | up | 0.00081 |
| rc_AA621367_at | AA621367 | 1523 | EST | 3.1 | up | 0.00066 |
| rc_AA621409_at | AA621409 | 1524 | putative type II membrane protein | 3.5 | up | 0.00462 |
| rc_AA621530_at | AA621530 | 1526 | EST | 3.26 | up | 0.00298 |
| rc_AA621535_at | AA621535 | 1527 | FE65-LIKE 2 | 3.37 | up | 0.0167 |
| rc_AA621752_at | AA621752 | 1529 | 26S proteasome-associated pad1 homolog | 3.13 | up | 0.01571 |
| AB002373_at | AB002373 | 1538 | KIAA0375 gene product | 4.41 | up | 0.00795 |
| AF003521_at | AF003521 | 1545 | jagged 2 | 3.58 | up | 0.00299 |
| AF004022_at | AF004022 | 1546 | serine/threonine kinase 12 | 3.29 | up | 0.00841 |
| C00358_at | C00358 | 1552 | nucleolar protein 3 (apoptosis repressor with CARD | 3.45 | up | 0.00985 |
| C01721_at | C01721 | 1558 | phospholipase C, beta 3, neighbor pseudogene | 5.89 | up | 0.0383 |
| C01766_s_at | C01766 | 1559 | EST | 8.18 | up | 0.00505 |
| rc_C14051_f_at | C14051 | 1565 | phosphoprotein enriched in astrocytes 15 | 4.79 | up | 0.00548 |
| rc_C14098_f_at | C14098 | 1566 | EST | 4.62 | up | 0.01654 |
| rc_C14756_f_at | C14756 | 1570 | MLN51 protein | 3.75 | up | 0.0226 |
| rc_C14835_f_at | C14835 | 1571 | EST | 3.35 | up | 0.0316 |
| D00596_at | D00596 | 1590 | thymidylate synthetase | 5.58 | up | 0.0098 |
| D13370_at | D13370 | 1603 | APEX nuclease (multifunctional DNA repair enzyme) | 3.07 | up | 0.00857 |
| | | | general transcription factor IIC, polypeptide 2 (beta | | | |
| D13636_at | D13636 | 1606 | subunit, 110kD) | 3.12 | up | 0.00022 |
| D13640_at | D13640 | 1608 | KIAA0015 gene product | 3.55 | up | 0.00347 |
| D14657_at | D14657 | 1615 | KIAA0101 gene product | 3.84 | up | 0.02048 |
| rc_D20899_at | D20899 | 1626 | EST | 3.13 | up | 0.02128 |
| | | | minichromosome maintenance deficient (S. cerevisiae) 2 | | | |
| D21063_at | D21063 | 1628 | (mitotin) | 3.25 | up | 0.03558 |
| D26129_at | D26129 | 1635 | ribonuclease, RNase A family, 1 (pancreatic) | 6.9 | up | 0.00008 |
| D28589_at | D28589 | 1637 | EST | 3.38 | up | 0.01144 |
| D30946_at | D30946 | 1638 | kinesin family member 3B | 3.43 | up | 0.01458 |
| D31094_at | D31094 | 1639 | G8 protein | 9.37 | up | 0.0048 |
| D31294_at | D31294 | 1643 | EST | 3.3 | up | 0.004 |
| D31417_at | D31417 | 1645 | secreted protein of unknown function | 3.69 | up | 0.0004 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| D38073_at | D38073 | 1651 | minichromosome maintenance deficient (S. cerevisiae) 3 | 4.1 | up | 0.01195 |
| D38305_at | D38305 | 1652 | transducer of ERBB2, 1 | 3.22 | up | 0.0215 |
| D42040_s_at | D42040 | 1657 | female sterile homeotic-related gene 1 (mouse homolog) | 4.02 | up | 0.00389 |
| rc_D51072_s_at | D51072 | 1674 | biliverdin reductase A | 3.34 | up | 0.0254 |
| rc_D51276_f_at | D51276 | 1678 | leukemia-associated phosphoprotein p18 (stathmin) | 9.42 | up | 0.00015 |
| D55716_at | D55716 | 1686 | minichromosome maintenance deficient (S. cerevisiae) 7 | 5.48 | up | 0.00003 |
| rc_D57317_at | D57317 | 1688 | activated RNA polymerase II transcription cofactor 4 | 3.17 | up | 0.00464 |
| rc_D59355_s_at | D59355 | 1696 | cytoskeleton-associated protein 1 | 6.05 | up | 0.0015 |
| rc_D59553_f_at | D59553 | 1697 | golgin-67 | 5.95 | up | 0.00169 |
| rc_D59570_f_at | D59570 | 1699 | EST | 4.34 | up | 0.00487 |
| rc_D60811_s_at | D60811 | 1704 | EST | 4.34 | up | 0.00217 |
| D63478_at | D63478 | 1711 | KIAA0144 gene product | 3.89 | up | 0.00253 |
| D63486_at | D63486 | 1712 | KIAA0152 gene product | 3.56 | up | 0.00063 |
| rc_D80420_at | D80420 | 1732 | ubiquinol-cytochrome c reductase hinge protein | 3.86 | up | 0.00412 |
| rc_D80710_f_at | D80710 | 1734 | integral type I protein | 3.17 | up | 0.04549 |
| rc_D80917_f_at | D80917 | 1736 | KIAA0670 protein/acinus | 3.09 | up | 0.00168 |
| rc_D80946_f_at | D80946 | 1737 | SFRS protein kinase 1 | 3.07 | up | 0.00986 |
| D81608_at | D81608 | 1740 | polymerase (RNA) II (DNA directed) polypeptide K | 3.52 | up | 0.00437 |
| D82226_s_at | D82226 | 1742 | proteasome (prosome, macropain) 26S subunit, | 4.35 | up | 0.00184 |
| D82277_s_at | D82277 | 1743 | LDL induced EC protein | 3.33 | up | 0.00355 |
| D82558_at | D82558 | 1746 | novel centrosomal protein RanBPM | 4.67 | up | 0.00458 |
| | | | trinucleotide repeat containing 11 (THR-associated | | | |
| D83783_at | D83783 | 1748 | protein, 230 kDa subunit) | 4.16 | up | 0.00055 |
| D84557_at | D84557 | 1749 | minichromosome maintenance deficient (mis5, S. | 3.97 | up | 0.0017 |
| D86957_at | D86957 | 1754 | KIAA0202 protein | 3.08 | up | 0.02949 |
| D86977_at | D86977 | 1757 | KIAA0224 gene product | 3.03 | up | 0.00053 |
| rc_F01538_s_at | F01538 | 1771 | RAP1, GTPase activating protein 1 | 4.88 | up | 0.00292 |
| rc_F01568_at | F01568 | 1772 | EST | 4.13 | up | 0.00084 |
| rc_F01831_at | F01831 | 1773 | EST | 5.95 | up | 0.00532 |
| rc_F02254_s_at | F02254 | 1777 | Fas-activated serine/threonine kinase | 5.1 | up | 0.00329 |
| rc_F02807_at | F02807 | 1781 | KIAA0838 protein | 5.67 | up | 0.02064 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_F02863_at | F02863 | 1782 | EST | 3.05 | up | 0.03504 |
| rc_F04320_s_at | F04320 | 1786 | replication factor C (activator 1) 4 (37kD) | 6.29 | up | 0.00042 |
| rc_F04444_at | F04444 | 1788 | EST | 4.13 | up | 0.00944 |
| rc_F04479_at | F04479 | 1789 | KIAA1067 protein | 3.23 | up | 0.04522 |
| rc_F08876_at | F08876 | 1797 | EST | 9.06 | up | 0 |
| rc_F09788_at | F09788 | 1808 | procollagen-proline, 2-oxoglutarate 4-dioxygenase | 3.67 | up | 0.01682 |
| rc_F10199_f_at | F10199 | 1813 | (proline 4-hydroxylase), alpha polypeptide II | 3.93 | up | 0.03209 |
| rc_F10290_at | F10290 | 1815 | EST | 3.39 | up | 0.02392 |
| rc_F10453_at | F10453 | 1819 | EST | 3.64 | up | 0.01878 |
| rc_F10741_at | F10741 | 1822 | KIAA0622 protein | 3.01 | up | 0.03079 |
| rc_F13809_f_at | F13809 | 1828 | tropomyosin 1 (alpha) | 4.4 | up | 0.01221 |
| rc_H00540_at | H00540 | 1829 | EST | 3.74 | up | 0.00234 |
| rc_H05084_at | H05084 | 1844 | EST | 5.85 | up | 0.0059 |
| rc_H07873_at | H07873 | 1856 | EST | 3.53 | up | 0.0391 |
| rc_H08863_at | H08863 | 1859 | hypothetical protein | 7.18 | up | 0.02102 |
| rc_H09241_s_at | H09241 | 1861 | EST | 3.05 | up | 0.01487 |
| rc_H09271_f_at | H09271 | 1862 | EST | 4.78 | up | 0.00072 |
| rc_H10933_at | H10933 | 1873 | EST | 6.18 | up | 0.00003 |
| rc_H11320_s_at | H11320 | 1875 | SUMO-1 activating enzyme subunit 2 | 3.06 | up | 0.00167 |
| rc_H16251_s_at | H16251 | 1886 | EST | 3.3 | up | 0.03286 |
| rc_H27188_f_at | H27188 | 1908 | collagen-binding protein 2 (collagen 2) | 5.84 | up | 0.01826 |
| rc_H27897_s_at | H27897 | 1911 | hypothetical protein | 3.01 | up | 0.00174 |
| rc_H28333_f_at | H28333 | 1912 | melanoma adhesion molecule | 4.94 | up | 0.00166 |
| rc_H41529_at | H41529 | 1926 | EST | 5.06 | up | 0.03309 |
| H46486_s_at | H46486 | 1932 | nesca protein | 4.57 | up | 0.00749 |
| rc_H47357_f_at | H47357 | 1934 | EST | 3.65 | up | 0.03799 |
| rc_H48459_s_at | H48459 | 1937 | KIAA0186 gene product | 3.1 | up | 0.02325 |
| rc_H52937_at | H52937 | 1944 | roundabout (axon guidance receptor, Drosophila) | 4.02 | up | 0.00163 |
| rc_H56345_r_at | H56345 | 1950 | EST | 3.73 | up | 0.00853 |
| rc_H57709_s_at | H57709 | 1956 | ribosomal protein L31 | 4.41 | up | 0.00091 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_H59617_at | H59617 | 1964 | EST | 5.81 | up | 0.0115 |
| rc_H62474_f_at | H62474 | 1970 | EST | 3.39 | up | 0.04173 |
| rc_H64493_f_at | H64493 | 1973 | immunoglobulin heavy constant gamma 3 (G3m marker) | 4.74 | up | 0.00751 |
| rc_H65030_s_at | H65030 | 1974 | phospholipase A2, group VII (platelet-activating factor) | | | |
| rc_H65042_at | H65042 | 1975 | acetylhydrolase, plasma) | 3.26 | up | 0.02278 |
| H67964_at | H67964 | 1981 | EST | 3.44 | up | 0.0006 |
| rc_H68794_at | H68794 | 1984 | EST | 3.06 | up | 0.02707 |
| rc_H70739_f_at | H70739 | 1991 | EST | 3.67 | up | 0.00327 |
| rc_H73484_s_at | H73484 | 1995 | ferritin, heavy polypeptide 1 | 4.34 | up | 0.00106 |
| rc_H78211_at | H78211 | 2001 | EST | 3.18 | up | 0.00432 |
| rc_H86072_f_at | H86072 | 2015 | EST | 7.5 | up | 0.02674 |
| rc_H88674_s_at | H88674 | 2021 | collagen, type I, alpha 2 | 4.49 | up | 0.01301 |
| rc_H89987_s_at | H89987 | 2027 | ATP-binding cassette, sub-family C (CFTR/MRP), | 4.15 | up | 0.02664 |
| rc_H91632_at | H91632 | 2031 | EST | 3.13 | up | 0.01194 |
| rc_H94471_at | H94471 | 2042 | occludin | 3.5 | up | 0.03688 |
| rc_H96850_at | H96850 | 2055 | dolichyl-diphosphooligosaccharide-protein | 6.26 | up | 0.00379 |
| rc_H97012_at | H97012 | 2058 | EST | 3.03 | up | 0.00679 |
| rc_H97013_at | H97013 | 2059 | ephrin-A4 | 3.51 | up | 0.03505 |
| rc_H97677_s_at | H97677 | 2062 | EST | 6.8 | up | 0.00023 |
| rc_H99261_s_at | H99261 | 2074 | EST | 4.34 | up | 0.00753 |
| rc_H99364_at | H99364 | 2075 | chloride channel 7 | 3.33 | up | 0.00319 |
| rc_H99473_s_at | H99473 | 2077 | regulator of nonsense transcripts 1 | 3.03 | up | 0.01727 |
| rc_H99489_s_at | H99489 | 2078 | quiescin Q6 | 6.51 | up | 0.00025 |
| rc_H99587_s_at | H99587 | 2079 | EST | 3.4 | up | 0.02682 |
| rc_H99774_at | H99774 | 2081 | EST | 4.44 | up | 0.00532 |
| rc_H99877_at | H99877 | 2083 | exportin, tRNA (nuclear export receptor for tRNAs) | 3.51 | up | 0.00009 |
| rc_H99879_at | H99879 | 2084 | EST | 3.75 | up | 0.00302 |
| | | | | 10.81 | up | 0.001 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|---|-------------|-----------|---------|
| J00231_f_at | J00231 | 2087 | immunoglobulin heavy constant gamma 3 (G3m marker) | 6.23 | up | 0.00177 |
| J03040_at | J03040 | 2091 | secreted protein, acidic, cysteine-rich (osteonectin) | 3.77 | up | 0.00594 |
| J03464_s_at | J03464 | 2094 | collagen, type I, alpha 2 | 10.37 | up | 0.00979 |
| J04029_s_at | J04029 | 2102 | keratin 10 (epidermolytic hyperkeratosis; keratosis | | | |
| J05614_at | J05614 | 2122 | palmaris et plantaris) | 3.02 | up | 0.00032 |
| L03411_s_at | L03411 | 2134 | EST | 3.73 | up | 0.03419 |
| L04270_at | L04270 | 2135 | RD RNA-binding protein | 4.06 | up | 0.00467 |
| L06797_s_at | L06797 | 2143 | lymphotoxin beta receptor (TNFR superfamily, member | 3.5 | up | 0.01547 |
| L11669_at | L11669 | 2157 | chemokine (C-X-C motif), receptor 4 (fusin) | 3.23 | up | 0.04782 |
| | | | tetracycline transporter-like protein | 3.4 | up | 0.02062 |
| | | | high-mobility group (nonhistone chromosomal) protein | | | |
| L17131_ma1_at | L17131 | 2168 | isoforms I and Y | 4.45 | up | 0.03141 |
| L25444_at | L25444 | 2181 | TATA box binding protein (TBP)-associated factor, RNA | | | |
| | | | polymerase II, E, 70/85kD | 3.78 | up | 0.00011 |
| L25876_at | L25876 | 2182 | cyclin-dependent kinase inhibitor 3 (CDK2-associated | 4.43 | up | 0.00082 |
| L28821_at | L28821 | 2188 | dual specificity phosphatase) | 4.63 | up | 0.00876 |
| L29218_s_at | L29218 | 2190 | mannosidase, alpha, class 2A, member 2 | 6.51 | up | 0.00019 |
| L29218_at | L29218 | 2190 | CDC-like kinase 2 | 3.82 | up | 0.00035 |
| L33930_s_at | L33930 | 2198 | CDC-like kinase 2 | 4.35 | up | 0.03968 |
| | | | CD24 antigen (small cell lung carcinoma cluster 4 | | | |
| | | | transcription elongation factor B (SIII), polypeptide 1 | | | |
| L34587_at | L34587 | 2200 | (15kD, elongin C) | 3.12 | up | 0.00946 |
| L47125_s_at | L47125 | 2218 | glypican 3 | 10.69 | up | 0.04129 |
| L76191_at | L76191 | 2222 | interleukin-1 receptor-associated kinase 1 | 3.85 | up | 0.00152 |
| | | | excision repair cross-complementing rodent repair | | | |
| L76568_xpt3_f_at | L76568 | 2225 | deficiency, complementation group 4 | 3.4 | up | 0.0172 |
| M12125_at | M12125 | 2241 | tropomyosin 2 (beta) | 7.13 | up | 0.0004 |
| M14483_ma1_s_at | M14483 | 2261 | prothymosin, alpha (gene sequence 28) | 3.36 | up | 0.00033 |
| M19267_s_at | M19267 | 2286 | tropomyosin 1 (alpha) | 4.3 | up | 0.00893 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|--|-------------|-----------|---------|
| M21259_at | M21259 | 2293 | small nuclear ribonucleoprotein polypeptide E | 3.68 | up | 0.00415 |
| M26576_cds2_at | M26576 | 2310 | EST | 3.48 | up | 0.00062 |
| AFFX-M27830_5_at | M27830 | 2314 | EST | 4.6 | up | 0.04719 |
| AFFX-M27830_M_at | M27830 | 2314 | EST | 3.54 | up | 0.00777 |
| AFFX-M27830_5_at | M27830 | 2314 | EST | 3.3 | up | 0.02453 |
| M31303_rna1_at | M31303 | 2327 | leukemia-associated phosphoprotein p18 (stathmin) | 5.86 | up | 0.00071 |
| M32977_s_at | M32977 | 2336 | vascular endothelial growth factor | 3.93 | up | 0.04917 |
| | | | v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 | | | |
| M34309_at | M34309 | 2342 | homolog 3 | 3.49 | up | 0.00191 |
| M35252_at | M35252 | 2343 | transmembrane 4 superfamily member 3 | 4.65 | up | 0.04128 |
| M37583_at | M37583 | 2349 | H2A histone family, member Z | 4.25 | up | 0.00135 |
| M55210_at | M55210 | 2353 | laminin, gamma 1 (formerly LAMB2) | 3.47 | up | 0.02551 |
| M55998_s_at | M55998 | 2356 | collagen, type I, alpha 1 | 3.54 | up | 0.01449 |
| M57710_at | M57710 | 2357 | lectin, galactoside-binding, soluble, 3 (galectin 3) | 6.76 | up | 0.00103 |
| M57730_at | M57730 | 2358 | ephrin-A1 | 3.39 | up | 0.00199 |
| M60784_s_at | M60784 | 2366 | small nuclear ribonucleoprotein polypeptide A | 4.74 | up | 0.00001 |
| M61916_at | M61916 | 2372 | laminin, beta 1 | 3.18 | up | 0.01171 |
| M63573_at | M63573 | 2377 | peptidylprolyl isomerase B (cyclophilin B) | 3.59 | up | 0.00916 |
| M68864_at | M68864 | 2389 | ORF | 3.95 | up | 0.00144 |
| M86667_at | M86667 | 2411 | nucleosome assembly protein 1-like 1 | 3.08 | up | 0.00473 |
| | | | stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) | | | |
| M86752_at | M86752 | 2412 | organizing protein | 5.15 | up | 0.02881 |
| M87339_at | M87339 | 2415 | replication factor C (activator 1) 4 (37kD) | 4.59 | up | 0.00116 |
| M91083_at | M91083 | 2419 | chromosome 11 open reading frame 13 | 3.19 | up | 0.00243 |
| | | | membrane component, chromosomal 4, surface marker | | | |
| M93036_at | M93036 | 2422 | (35kD glycoprotein) | 3.07 | up | 0.04199 |
| M94250_at | M94250 | 2426 | midkine (neurite growth-promoting factor 2) | 9.86 | up | 0.02104 |
| M94345_at | M94345 | 2427 | capping protein (actin filament), gelsolin-like | 3.59 | up | 0.04508 |
| M97856_at | M97856 | 2436 | nuclear autoantigenic sperm protein (histone-binding) | 3.21 | up | 0.00444 |
| rc_N21407_at | N21407 | 2443 | EST | 3.47 | up | 0.01037 |
| rc_N21648_s_at | N21648 | 2447 | MpV17 transgene, murine homolog, glomerulosclerosis | 3.73 | up | 0.00071 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_N26904_at | N26904 | 2469 | EST | 15.38 | up | 0.00077 |
| rc_N29484_at | N29484 | 2478 | EST | 3.08 | up | 0.04834 |
| rc_N29742_at | N29742 | 2481 | EST | 3.74 | up | 0.00104 |
| rc_N31597_s_at | N31597 | 2487 | DKFZP564G2022 protein | 3.17 | up | 0.03017 |
| rc_N33920_at | N33920 | 2493 | diubiquitin | 50.29 | up | 0 |
| rc_N34825_s_at | N34825 | 2498 | DKFZP434P106 protein | 3.27 | up | 0.01334 |
| rc_N35913_at | N35913 | 2503 | EST | 3.48 | up | 0.0016 |
| N36432_at | N36432 | 2507 | erythrocyte membrane protein band 4.1-like 2 | 7.95 | up | 0.00067 |
| rc_N39237_at | N39237 | 2511 | EST | 3.45 | up | 0.02481 |
| N42272_s_at | N42272 | 2515 | EST | 3.03 | up | 0.0017 |
| | | | eukaryotic translation initiation factor 3, subunit 3 | | | |
| rc_N47956_at | N47956 | 2524 | (gamma, 40kD) | 3.76 | up | 0.00968 |
| rc_N48790_at | N48790 | 2532 | EST | 3.32 | up | 0.00654 |
| rc_N51590_s_at | N51590 | 2546 | EST | 3.01 | up | 0.04345 |
| rc_N51771_at | N51771 | 2548 | KIAA0652 gene product | 3.5 | up | 0.00028 |
| | | | ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) | | | |
| rc_N51855_at | N51855 | 2550 | polymerase)-like 3 | 3.39 | up | 0.00115 |
| rc_N52168_at | N52168 | 2551 | EST | 3.66 | up | 0.00127 |
| rc_N53067_at | N53067 | 2557 | DKFZP547E1010 protein | 3.1 | up | 0.00101 |
| rc_N54067_at | N54067 | 2562 | mitogen-activated protein kinase kinase kinase 4 | 4.82 | up | 0.00229 |
| rc_N54841_at | N54841 | 2572 | EST | 5.87 | up | 0.02752 |
| rc_N56935_s_at | N56935 | 2575 | EST | 4.04 | up | 0.00797 |
| rc_N59536_at | N59536 | 2586 | EST | 11.68 | up | 0.00484 |
| rc_N62126_at | N62126 | 2589 | EST | 6.42 | up | 0.00109 |
| rc_N64374_at | N64374 | 2608 | KIAA0537 gene product | 3.25 | up | 0.01652 |
| rc_N67815_f_at | N67815 | 2627 | EST | 3.84 | up | 0.00439 |
| rc_N68018_at | N68018 | 2631 | TBP-associated factor 172 | 3.84 | up | 0.00277 |
| rc_N68241_at | N68241 | 2634 | EST | 4.32 | up | 0.00532 |
| rc_N69084_i_at | N69084 | 2643 | EST | 3.11 | up | 0.0094 |
| rc_N69252_f_at | N69252 | 2647 | ferritin, light polypeptide | 3.69 | up | 0.04116 |
| rc_N69263_at | N69263 | 2648 | EST | 5.26 | up | 0.0276 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_N69390_at | N69390 | 2650 | EST | 3.99 | up | 0.00016 |
| rc_N69879_s_at | N69879 | 2651 | drebrin 1 | 3.15 | up | 0.01659 |
| rc_N70481_at | N70481 | 2658 | EST | 4.13 | up | 0.0099 |
| rc_N70678_s_at | N70678 | 2660 | TAR (HIV) RNA-binding protein 1 | 3.78 | up | 0.02858 |
| | | | solute carrier family 11 (proton-coupled divalent metal | | | |
| | | | ion transporters), member 2 | | | |
| rc_N72116_s_at | N72116 | 2668 | | 5.57 | up | 0.00709 |
| rc_N73705_at | N73705 | 2677 | EST | 3.75 | up | 0.01762 |
| rc_N73762_f_at | N73762 | 2678 | EST | 3.67 | up | 0.00796 |
| rc_N73808_f_at | N73808 | 2679 | EST | 6.44 | up | 0.00352 |
| rc_N73865_at | N73865 | 2681 | EST | 4.43 | up | 0.00177 |
| rc_N75541_at | N75541 | 2692 | EST | 4.43 | up | 0.01059 |
| rc_N80703_at | N80703 | 2704 | EST | 5.65 | up | 0.0001 |
| rc_N90238_i_at | N90238 | 2712 | EST | 3.13 | up | 0.02492 |
| rc_N91773_at | N91773 | 2719 | lysyl oxidase | 4.31 | up | 0.00302 |
| rc_N92948_s_at | N92948 | 2726 | nuclear phosphoprotein similar to S. cerevisiae PWP1 | 4.09 | up | 0.0019 |
| rc_N93299_f_at | N93299 | 2732 | nuclear receptor co-repressor 1 | 6.99 | up | 0.0371 |
| rc_N93316_at | N93316 | 2733 | EST | 3.16 | up | 0.01262 |
| rc_N93798_at | N93798 | 2738 | protein tyrosine phosphatase type IVA, member 3 | 4.91 | up | 0.00245 |
| rc_N98464_s_at | N98464 | 2744 | EST | 3.68 | up | 0.03007 |
| rc_N98758_f_at | N98758 | 2745 | EST | 3.54 | up | 0.02609 |
| rc_N99944_s_at | N99944 | 2749 | EST | 3.46 | up | 0.00104 |
| rc_R05316_s_at | R05316 | 2760 | EST | 4.2 | up | 0.00011 |
| rc_R06251_f_at | R06251 | 2764 | tumor protein D52-like 2 | 4.88 | up | 0.03097 |
| rc_R06254_f_at | R06254 | 2765 | tumor protein D52-like 2 | 3.53 | up | 0.04865 |
| rc_R06400_at | R06400 | 2768 | EST | 3.03 | up | 0.03266 |
| rc_R06986_f_at | R06986 | 2776 | peptidylprolyl isomerase B (cyclophilin B) | 7.03 | up | 0.00628 |
| rc_R07172_i_at | R07172 | 2777 | EST | 5.54 | up | 0.01322 |
| rc_R15740_at | R15740 | 2791 | carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 | 3.36 | up | 0.00268 |
| rc_R16144_at | R16144 | 2794 | EST | 3.24 | up | 0.0087 |
| rc_R20817_s_at | R20817 | 2797 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) | 3.03 | up | 0.01091 |
| rc_R22565_at | R22565 | 2800 | EST | 3.52 | up | 0.04352 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | P value |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_R26744_at | R26744 | 2804 | midline 1 (Opitz/BBB syndrome) | 3.8 | up | 0.00266 |
| rc_R27016_s_at | R27016 | 2806 | myristoylated alanine-rich protein kinase C substrate | 3.53 | up | 0.03056 |
| rc_R27296_f_at | R27296 | 2807 | (MARCKS, 80K-L) | 3.41 | up | 0.00309 |
| rc_R28636_at | R28636 | 2809 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, | 3.06 | up | 0.03678 |
| rc_R31607_at | R31607 | 2813 | polypeptide 3 | 3.41 | up | 0.00163 |
| rc_R33498_s_at | R33498 | 2820 | EST | 3.5 | up | 0.03336 |
| rc_R39191_s_at | R39191 | 2834 | KIAA1020 protein | 5.18 | up | 0.03185 |
| rc_R39390_at | R39390 | 2837 | EST | 4.18 | up | 0.0004 |
| rc_R39610_s_at | R39610 | 2838 | calpain, large polypeptide L2 | 3.13 | up | 0.01863 |
| rc_R43952_at | R43952 | 2853 | homeo box B5 | 3.39 | up | 0.04829 |
| rc_R44617_f_at | R44617 | 2857 | MyoD family inhibitor | 6.54 | up | 0.02505 |
| rc_R44793_at | R44793 | 2859 | EST | 5.4 | up | 0.00329 |
| rc_R44839_at | R44839 | 2861 | i-beta-1,3-N-acetylglucosaminyltransferase | 5 | up | 0.01812 |
| rc_R45569_at | R45569 | 2864 | DKFZP547E1010 protein | 3.96 | up | 0.00259 |
| rc_R45994_f_at | R45994 | 2867 | EST | 6.48 | up | 0.00358 |
| rc_R46079_f_at | R46079 | 2868 | EST | 3.03 | up | 0.00755 |
| rc_R46337_s_at | R46337 | 2869 | secretory carrier membrane protein 3 | 3.01 | up | 0.00374 |
| rc_R48447_at | R48447 | 2871 | EST | 4.76 | up | 0.00533 |
| rc_R48473_f_at | R48473 | 2872 | EST | 3.46 | up | 0.01196 |
| rc_R48594_s_at | R48594 | 2875 | EST | 6.15 | up | 0.03831 |
| rc_R49395_s_at | R49395 | 2881 | EST | 3.31 | up | 0.00867 |
| rc_R49476_at | R49476 | 2883 | EST | 4.93 | up | 0.00763 |
| rc_R49482_at | R49482 | 2884 | EST | 3.27 | up | 0.0161 |
| rc_R49708_s_at | R49708 | 2886 | EST | 4.56 | up | 0.03767 |
| rc_R51908_s_at | R51908 | 2892 | EST | 3.16 | up | 0.0083 |
| rc_R52161_at | R52161 | 2893 | EST | 3.41 | up | 0.00053 |
| rc_R52649_at | R52649 | 2894 | EST | 4.69 | up | 0.00135 |
| rc_R53109_f_at | R53109 | 2899 | dimethylarginine dimethylaminohydrolase 2 | 3.31 | up | 0.02406 |
| rc_R54614_s_at | R54614 | 2902 | EST | 3.22 | up | 0.00334 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|---|---------|--------|------------------------------------|-------------|-----------|---------|
| rc_R56095_s_at | R56095 | 2906 | EST | 3.67 | up | 0.0158 |
| rc_R60512_s_at | R60512 | 2918 | KIAA0191 protein | 3.08 | up | 0.00856 |
| rc_R61374_at | R61374 | 2921 | EST | 4.33 | up | 0.01489 |
| rc_R61557_at | R61557 | 2922 | KIAA0100 gene product | 3.9 | up | 0.00292 |
| rc_R62456_at | R62456 | 2925 | EST | 3.44 | up | 0.00285 |
| rc_R66469_f_at | R66469 | 2937 | pleckstrin and Sec7 domain protein | 3.52 | up | 0.0272 |
| rc_R70005_at | R70005 | 2944 | EST | 4.98 | up | 0.00007 |
| rc_R70253_at | R70253 | 2945 | EST | 3.38 | up | 0.03125 |
| rc_R70532_at | R70532 | 2947 | EST | 3.44 | up | 0.02186 |
| rc_R70801_s_at | R70801 | 2950 | EST | 6.06 | up | 0.00291 |
| rc_R71395_at | R71395 | 2952 | EST | 4.12 | up | 0.03719 |
| rc_R72886_s_at | R72886 | 2956 | KIAA0422 protein | 5.5 | up | 0.00091 |
| rc_R73569_s_at | R73569 | 2960 | EST | 3.54 | up | 0.01962 |
| O-linked N-acetylglucosamine (GlcNAc) transferase | | | | | | |
| (UDP-N-acetylglucosamine:polypeptide-N- | | | | | | |
| acetylglucosaminyl transferase) | | | | | | |
| rc_R76782_s_at | R76782 | 2963 | acetylglucosaminyl transferase | 3.73 | up | 0.00094 |
| rc_R77451_i_at | R77451 | 2964 | EST | 3.67 | up | 0.00078 |
| rc_R79246_f_at | R79246 | 2969 | melanoma adhesion molecule | 6.06 | up | 0.00057 |
| rc_R91753_at | R91753 | 2983 | EST | 3.45 | up | 0.02391 |
| rc_R91819_at | R91819 | 2984 | EST | 12.81 | up | 0.00037 |
| rc_R92449_s_at | R92449 | 2985 | KIAA0323 protein | 4.34 | up | 0.00104 |
| rc_R96527_s_at | R96527 | 2999 | KIAA0253 protein | 4.62 | up | 0.00702 |
| rc_R96924_s_at | R96924 | 3001 | EST | 7.04 | up | 0.00012 |
| S67070_at | S67070 | 3023 | heat shock 27kD protein 2 | 3.12 | up | 0.01688 |
| S78187_at | S78187 | 3036 | cell division cycle 25B | 4.83 | up | 0.00547 |
| rc_T03438_s_at | T03438 | 3043 | EST | 3.79 | up | 0.02042 |
| rc_T03580_f_at | T03580 | 3046 | pyruvate kinase, muscle | 5.57 | up | 0.01344 |
| rc_T03749_at | T03749 | 3048 | KIAA1089 protein | 4.23 | up | 0.00776 |
| rc_T10316_s_at | T10316 | 3052 | EST | 3.2 | up | 0.04794 |
| rc_T10698_s_at | T10698 | 3054 | EST | 3.86 | up | 0.00195 |
| rc_T15852_f_at | T15852 | 3062 | EST | 5.21 | up | 0.00642 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_T16206_s_at | T16206 | 3065 | EST | 4.29 | up | 0.00868 |
| rc_T16226_at | T16226 | 3066 | EST | 7.23 | up | 0.00119 |
| rc_T16550_at | T16550 | 3072 | vacuolar protein sorting 45B (yeast homolog) | 5.88 | up | 0.00004 |
| rc_T16652_s_at | T16652 | 3073 | BCS1 (yeast homolog)-like | 3.63 | up | 0.00434 |
| rc_T16983_s_at | T16983 | 3074 | cleavage and polyadenylation specific factor 4, 30kD | 4.23 | up | 0.0106 |
| rc_T17066_s_at | T17066 | 3075 | SET domain, bifurcated, 1 | 5.14 | up | 0.00073 |
| rc_T17339_f_at | T17339 | 3076 | EST | 3.29 | up | 0.00669 |
| rc_T17353_s_at | T17353 | 3077 | EST | 3.52 | up | 0.02085 |
| rc_T23426_s_at | T23426 | 3079 | EST | 3.51 | up | 0.00674 |
| rc_T23465_at | T23465 | 3081 | EST | 3.64 | up | 0.00265 |
| rc_T23516_f_at | T23516 | 3083 | 3-phosphoglycerate dehydrogenase | 3.39 | up | 0.00551 |
| rc_T24068_s_at | T24068 | 3088 | EST | 8.65 | up | 0.00118 |
| rc_T26471_at | T26471 | 3094 | EST | 3.76 | up | 0.0165 |
| rc_T26646_f_at | T26646 | 3097 | X-ray repair complementing defective repair in Chinese hamster cells 1 | 3.49 | up | 0.02482 |
| rc_T30214_at | T30214 | 3099 | EST | 4.46 | up | 0.03654 |
| rc_T33489_s_at | T33489 | 3105 | EST | 4.6 | up | 0.00285 |
| rc_T33508_s_at | T33508 | 3106 | phosphatidylinositol-4-phosphate 5-kinase, type II, beta | 4.96 | up | 0.00064 |
| rc_T33619_s_at | T33619 | 3107 | EST | 3.36 | up | 0.01283 |
| rc_T33625_at | T33625 | 3108 | EST | 3.36 | up | 0.04096 |
| rc_T33859_at | T33859 | 3109 | KIAA0365 gene product | 3.9 | up | 0.0019 |
| T34377_at | T34377 | 3111 | potassium voltage-gated channel, shaker-related subfamily, beta member 2 | 4.55 | up | 0.00041 |
| rc_T40439_s_at | T40439 | 3115 | small nuclear ribonucleoprotein polypeptide B" | 3.06 | up | 0.02842 |
| rc_T41078_at | T41078 | 3121 | bromodomain adjacent to zinc finger domain, 2B | 3.08 | up | 0.03426 |
| rc_T47032_s_at | T47032 | 3124 | partner of RAC1 (arfaptin 2) | 6.09 | up | 0.00019 |
| rc_T47325_s_at | T47325 | 3125 | EST | 5.6 | up | 0.02923 |
| rc_T47969_s_at | T47969 | 3128 | ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) | 3.19 | up | 0.02283 |
| rc_T51972_at | T51972 | 3140 | EST | 3.44 | up | 0.00406 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|---|-------------|-----------|---------|
| rc_T53590_s_at | T53590 | 3144 | cytochrome P450, subfamily XIA (cholesterol side chain cleavage) | 5.09 | up | 0.00002 |
| rc_T55196_at | T55196 | 3147 | | 4.24 | up | 0.00046 |
| rc_T58607_at | T58607 | 3155 | | 6.83 | up | 0.03711 |
| rc_T59668_s_at | T59668 | 3160 | | 3.5 | up | 0.00083 |
| rc_T62521_at | T62521 | 3168 | lysyl oxidase | 4.1 | up | 0.00392 |
| rc_T62918_at | T62918 | 3169 | EST | 5.25 | up | 0.00687 |
| rc_T65957_f_at | T65957 | 3176 | ribosomal protein S3A | 3.94 | up | 0.04187 |
| rc_T66935_at | T66935 | 3179 | EST | 3.01 | up | 0.00123 |
| rc_T67053_f_at | T67053 | 3180 | EST | 5 | up | 0.01846 |
| rc_T77733_s_at | T77733 | 3219 | tubulin, gamma 1 | 4 | up | 0.00526 |
| rc_T78922_s_at | T78922 | 3222 | stem cell growth factor; lymphocyte secreted C-type | 3.89 | up | 0.00604 |
| rc_T79477_s_at | T79477 | 3223 | death-associated protein 6 | 4.4 | up | 0.00074 |
| rc_T81393_s_at | T81393 | 3228 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 | 3.32 | up | 0.0023 |
| rc_T88814_at | T88814 | 3242 | EST | 4.87 | up | 0.00001 |
| rc_T89703_at | T89703 | 3244 | EST | 5.27 | up | 0.00019 |
| rc_T90190_s_at | T90190 | 3247 | H1 histone family, member 2 | 4.88 | up | 0.00555 |
| rc_T94452_at | T94452 | 3257 | EST | 3.23 | up | 0.02245 |
| rc_T95057_f_at | T95057 | 3259 | EST | 6.46 | up | 0.00613 |
| rc_T97679_at | T97679 | 3266 | EST | 3.32 | up | 0.01566 |
| rc_T99312_at | T99312 | 3270 | EST | 3.22 | up | 0.00084 |
| U18018_at | U18018 | 3317 | ets variant gene 4 (E1A enhancer-binding protein, E1AF) | 3.9 | up | 0.0403 |
| U18321_at | U18321 | 3318 | death associated protein 3 | 3.14 | up | 0.00833 |
| U24704_at | U24704 | 3332 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 | 3.45 | up | 0.00037 |
| U26727_at | U26727 | 3337 | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) | 3.53 | up | 0.02913 |
| U30825_at | U30825 | 3343 | splicing factor, arginine/serine-rich 9 | 3.07 | up | 0.01928 |
| U45285_at | U45285 | 3364 | T-cell, immune regulator 1 | 5.75 | up | 0.00006 |
| U47025_s_at | U47025 | 3368 | phosphorylase, glycogen; brain | 4.47 | up | 0.00037 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| U51586_at | U51586 | 3386 | siach binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1 | 3.65 | up | 0.00403 |
| U55206_at | U55206 | 3392 | gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase) | 3.34 | up | 0.00315 |
| U59321_at | U59321 | 3398 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 | 3.12 | up | 0.02469 |
| U62392_at | U62392 | 3403 | zinc finger protein 193 | 3.56 | up | 0.0407 |
| U66661_at | U66661 | 3406 | gamma-aminobutyric acid (GABA) A receptor, epsilon | 3.55 | up | 0.0045 |
| U68142_at | U68142 | 3411 | RAB2, member RAS oncogene family-like SHC (Src homology 2 domain-containing) transforming protein 1 | 3.02 | up | 0.0296 |
| U73377_at | U73377 | 3417 | protein 1 | 4.64 | up | 0.00081 |
| U73379_at | U73379 | 3418 | ubiquitin carrier protein E2-C | 3.32 | up | 0.00808 |
| U75285_ma1_at | U75285 | 3422 | apoptosis inhibitor 4 (survivin) | 5.32 | up | 0.01127 |
| U85625_at | U85625 | 3448 | ribonuclease 6 precursor | 4 | up | 0.01664 |
| U90426_at | U90426 | 3453 | nuclear RNA helicase, DECD variant of DEAD box family | 3.24 | up | 0.00035 |
| U90551_at | U90551 | 3457 | H2A histone family, member L | 3.54 | up | 0.01523 |
| U90904_at | U90904 | 3458 | EST | 3.02 | up | 0.00381 |
| U91930_at | U91930 | 3460 | adaptor-related protein complex 3, delta 1 subunit | 3.68 | up | 0.00009 |
| rc_W02041_at | W02041 | 3466 | EST | 5.34 | up | 0.00027 |
| rc_W02695_at | W02695 | 3467 | EST | 3.1 | up | 0.04745 |
| rc_W04507_s_at | W04507 | 3469 | prefoldin 4 | 3.02 | up | 0.04091 |
| rc_W04550_at | W04550 | 3470 | EST | 4.01 | up | 0.00349 |
| rc_W15495_at | W15495 | 3474 | chromosome 21 open reading frame 5 | 3.09 | up | 0.00491 |
| W26716_at | W26716 | 3482 | non-histone chromosome protein 2 (S. cerevisiae)-like 1 | 5.47 | up | 0.00146 |
| W28362_at | W28362 | 3488 | KIAA0974 protein | 4.38 | up | 0.00322 |
| W28366_at | W28366 | 3489 | EST | 3.21 | up | 0.01007 |
| rc_W31906_at | W31906 | 3497 | secretogogin | 6.62 | up | 0.00926 |
| rc_W42627_f_at | W42627 | 3511 | EST | 4.37 | up | 0.00021 |
| rc_W42674_at | W42674 | 3512 | EST | 3.07 | up | 0.0261 |
| rc_W42778_at | W42778 | 3513 | EST | 3.27 | up | 0.02411 |
| rc_W42788_at | W42788 | 3514 | deoxynucleotidyltransferase, terminal | 3.24 | up | 0.02261 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| rc_W42957_at | W42957 | 3516 | calmodulin 2 (phosphorylase kinase, delta) | 5.79 | up | 0.03669 |
| rc_W44557_at | W44557 | 3518 | chromosome 1 open reading frame 2 | 4.1 | up | 0.00433 |
| rc_W45320_f_at | W45320 | 3523 | KRAB-associated protein 1 | 10.05 | up | 0.00002 |
| rc_W46286_s_at | W46286 | 3526 | EST | 3.68 | up | 0.00311 |
| rc_W46634_at | W46634 | 3530 | EST | 5.03 | up | 0.02152 |
| rc_W46810_s_at | W46810 | 3531 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2 | 3.17 | up | 0.03434 |
| rc_W46846_at | W46846 | 3532 | EST | 5.11 | up | 0.00025 |
| rc_W46947_at | W46947 | 3533 | EST | 3.42 | up | 0.04665 |
| rc_W47206_at | W47206 | 3535 | EST | 3.23 | up | 0.01931 |
| W49743_at | W49743 | 3540 | EST | 3.11 | up | 0.01121 |
| rc_W49791_at | W49791 | 3541 | plasminogen activator, tissue | 3.58 | up | 0.02438 |
| rc_W56642_at | W56642 | 3547 | EST | 3.15 | up | 0.00654 |
| rc_W57931_at | W57931 | 3549 | EST | 3.01 | up | 0.02661 |
| rc_W58081_at | W58081 | 3550 | neuroendocrine-specific protein C like (foocen) | 3.05 | up | 0.03767 |
| W58247_s_at | W58247 | 3551 | kinesin family member 4 | 3.08 | up | 0.00048 |
| rc_W60097_at | W60097 | 3556 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y | 4.82 | up | 0.04903 |
| rc_W60486_at | W60486 | 3558 | chromosome | 4.27 | up | 0.0046 |
| rc_W63608_at | W63608 | 3564 | EST | 3.33 | up | 0.02443 |
| W69302_at | W69302 | 3573 | EST | 4.37 | up | 0.00165 |
| rc_W69468_at | W69468 | 3574 | EST | 3.25 | up | 0.00055 |
| rc_W70336_at | W70336 | 3579 | EST | 4.46 | up | 0.00023 |
| rc_W72187_at | W72187 | 3582 | EST | 3.09 | up | 0.00134 |
| rc_W72276_at | W72276 | 3583 | EST | 3.56 | up | 0.0476 |
| rc_W73038_at | W73038 | 3588 | EST | 4.83 | up | 0.00902 |
| rc_W74536_s_at | W74536 | 3598 | advanced glycosylation end product-specific receptor | 3.07 | up | 0.00251 |
| rc_W78057_at | W78057 | 3600 | EST | 5.53 | up | 0.01231 |
| rc_W79421_at | W79421 | 3603 | EST | 3.57 | up | 0.00895 |
| rc_W79773_at | W79773 | 3605 | EST | 4.89 | up | 0.00034 |
| rc_W80730_at | W80730 | 3607 | EST | 3.35 | up | 0.01526 |
| rc_W80763_at | W80763 | 3608 | EST | 4.98 | up | 0.01026 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|------------------|---------|--------|--|-------------|-----------|---------|
| rc_W80852_at | W80852 | 3609 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | 6.37 | up | 0.00005 |
| rc_W81654_at | W81654 | 3616 | SRY (sex determining region Y)-box 13 | 6.06 | up | 0.00127 |
| rc_W84447_at | W84447 | 3617 | EST | 3.34 | up | 0.00986 |
| rc_W85875_at | W85875 | 3620 | EST | 4.91 | up | 0.01198 |
| rc_W86214_at | W86214 | 3625 | EST | 4.3 | up | 0.00194 |
| rc_W86748_at | W86748 | 3629 | EST | 5.09 | up | 0.01882 |
| rc_W90146_f_at | W90146 | 3644 | EST | 3.58 | up | 0.00322 |
| rc_W92608_s_at | W92608 | 3653 | BAI1-associated protein 3 | 4.84 | up | 0.00599 |
| rc_W94281_s_at | W94281 | 3658 | integral membrane protein 2C | 3.51 | up | 0.01689 |
| rc_W94885_at | W94885 | 3660 | EST | 6.53 | up | 0 |
| rc_W95841_at | W95841 | 3666 | EST | 3 | up | 0.00466 |
| X04347_s_at | X04347 | 3680 | heterogeneous nuclear ribonucleoprotein A1 | 3.34 | up | 0.00123 |
| X05610_at | X05610 | 3685 | collagen, type IV, alpha 2 | 6.04 | up | 0.00062 |
| X06700_s_at | X06700 | 3688 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | 3.58 | up | 0.02964 |
| X14487_mna1_s_at | X14487 | 3702 | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) | 3.19 | up | 0.01268 |
| X14850_at | X14850 | 3706 | H2A histone family, member X | 3.13 | up | 0.01523 |
| X17567_s_at | X17567 | 3719 | small nuclear ribonucleoprotein polypeptides B and B1 | 3.96 | up | 0.00317 |
| X53331_at | X53331 | 3727 | matrix Gla protein | 3.95 | up | 0.0151 |
| X54667_s_at | X54667 | 3731 | cystatin S, cystatin SN | 3.51 | up | 0.00187 |
| X54941_at | X54941 | 3732 | CDC28 protein kinase 1 | 3.99 | up | 0.0016 |
| X54942_at | X54942 | 3733 | CDC28 protein kinase 2 | 3.8 | up | 0.0035 |
| X56494_at | X56494 | 3738 | pyruvate kinase, muscle | 3.65 | up | 0.04795 |
| X57129_at | X57129 | 3743 | H1 histone family, member 2 | 4.63 | up | 0.00663 |
| X57809_s_at | X57809 | 3746 | immunoglobulin lambda locus | 3.64 | up | 0.02655 |
| X62153_s_at | X62153 | 3754 | minichromosome maintenance deficient (S. cerevisiae) 3 | 3.44 | up | 0.00704 |
| X62534_s_at | X62534 | 3755 | high-mobility group (nonhistone chromosomal) protein 2 | 3.39 | up | 0.0186 |
| X64364_at | X64364 | 3764 | basigin | 3.57 | up | 0.00902 |
| X66899_at | X66899 | 3772 | Ewing sarcoma breakpoint region 1 | 3.41 | up | 0.03777 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|----------------|---------|--------|--|-------------|-----------|---------|
| X69910_at | X69910 | 3787 | transmembrane protein (63kD), endoplasmic | 3.35 | up | 0.00898 |
| X74801_at | X74801 | 3791 | reticulum/Golgi intermediate compartment | 3.86 | up | 0.00453 |
| X79536_at | X79536 | 3804 | chaperonin containing TCP1, subunit 3 (gamma) | 3.06 | up | 0.00449 |
| X83425_at | X83425 | 3812 | heterogeneous nuclear ribonucleoprotein A1 | 3.66 | up | 0.02661 |
| X87212_at | X87212 | 3816 | Lutheran blood group (Aubergier b antigen included) cathepsin C | 3.45 | up | 0.02486 |
| X92896_at | X92896 | 3829 | DNA segment on chromosome X (unique) 9879 | 3.1 | up | 0.0405 |
| X99920_at | X99920 | 3843 | expressed sequence | 4.66 | up | 0.00113 |
| Y00705_at | Y00705 | 3850 | S100 calcium-binding protein A13 | 28.88 | up | 0.00003 |
| Y00764_at | Y00764 | 3851 | serine protease inhibitor, Kazal type 1 | 3.04 | up | 0.01294 |
| Y08302_at | Y08302 | 3852 | ubiquinol-cytochrome c reductase hinge protein | 3.48 | up | 0.00787 |
| Y08999_at | Y08999 | 3855 | dual specificity phosphatase 9 | 3.13 | up | 0.02376 |
| | | | actin related protein 2/3 complex, subunit 1A (41 kD) | | | |
| | | | eukaryotic translation elongation factor 1 delta (guanine | | | |
| Z21507_at | Z21507 | 3867 | nucleotide exchange protein) | 3.57 | up | 0.01898 |
| Z23090_at | Z23090 | 3868 | heat shock 27kD protein 1 | 3.69 | up | 0.00628 |
| Z24727_at | Z24727 | 3871 | tropomyosin 1 (alpha) | 3.64 | up | 0.00388 |
| Z37987_s_at | Z37987 | 3882 | glypican 3 | 10.66 | up | 0.02304 |
| rc_Z38299_at | Z38299 | 3887 | EST | 3.71 | up | 0.0036 |
| rc_Z38431_at | Z38431 | 3889 | EST | 3.09 | up | 0.0083 |
| rc_Z38444_at | Z38444 | 3891 | KIAA0923 protein | 3.38 | up | 0.02918 |
| rc_Z38462_at | Z38462 | 3892 | KIAA0938 protein | 4.69 | up | 0.0142 |
| rc_Z38904_at | Z38904 | 3896 | EST | 3.02 | up | 0.00814 |
| rc_Z39191_at | Z39191 | 3901 | EST | 3.47 | up | 0.00756 |
| rc_Z39200_at | Z39200 | 3902 | EST | 4.07 | up | 0.00075 |
| rc_Z39379_at | Z39379 | 3903 | EST | 3.77 | up | 0.00513 |
| rc_Z39429_at | Z39429 | 3906 | EST | 3.58 | up | 0.00416 |
| rc_Z39682_s_at | Z39682 | 3911 | KIAA0954 protein | 6.96 | up | 0.01966 |
| rc_Z40006_at | Z40006 | 3917 | EST | 3.54 | up | 0.00156 |
| rc_Z40883_r_at | Z40883 | 3924 | EST | 3.26 | up | 0.01863 |
| rc_Z41349_at | Z41349 | 3931 | EST | 3.45 | up | 0.01503 |

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | Fold Change | Direction | Pvalue |
|--------------|---------|--------|--|-------------|-----------|---------|
| rc_Z41747_at | Z41747 | 3936 | succinate dehydrogenase complex, subunit A, | 3.04 | up | 0.01336 |
| Z47727_at | Z47727 | 3940 | flavoprotein (Fp) | 3.28 | up | 0.00317 |
| Z74615_at | Z74615 | 3949 | polymerase (RNA) II (DNA directed) polypeptide K | 5.47 | up | 0.00283 |
| Z74616_s_at | Z74616 | 3950 | collagen, type I, alpha 1 collagen, type I, alpha 2 | 5.95 | up | 0.02212 |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | hcc | | | hcc | | | hcc | | |
|--|----------|--------|---|--------------------|---------|-------------|---------------|---------|----------------|-------------|---------|---------------|----------------|
| | | | | | p value | sample | | p value | sample | | p value | sample | |
| | | | | | | set 2: Mean | set 2: Median | | set 2: Std Dev | set 2: Mean | | set 2: Median | set 2: Std Dev |
| DEK oncogene (DNA binding) | | | | | | | | | | | | | |
| AA093497_s_at | AA093497 | 199 | binding | #N/A | #N/A | 180.58 | 107.64 | 165.71 | 52.11 | 48.84 | 26.51 | | |
| AA248283_at | AA248283 | 534 | EST | #N/A | #N/A | 67.18 | 45.86 | 55.18 | 21.63 | 18.96 | 11.71 | | |
| AA291456_s_at | AA291456 | 700 | EST | #N/A | #N/A | 828.34 | 830.24 | 196.63 | 671.21 | 509.58 | 629.13 | | |
| GAS2-related on chromosome 22 | | | | | | | | | | | | | |
| AA400643_s_at | AA400643 | 817 | chromosome 22 | 4.04 | 0.03751 | 118.72 | 123.18 | 137.15 | -43.6 | -33.96 | 60.39 | | |
| AA421079_at | AA421079 | 930 | EST | #N/A | #N/A | 37.17 | 34.26 | 18.5 | 15.27 | 16.75 | 15.28 | | |
| Notch (Drosophila) homolog 3 | | | | | | | | | | | | | |
| AA428172_f_at | AA428172 | 986 | 3 | 9.63 | 0.00195 | 335.57 | 374.9 | 231.52 | -9.64 | -15.61 | 56.16 | | |
| AA464043_s_at | AA464043 | 1255 | EST | 3.99 | 0.00056 | 116.97 | 115.99 | 53.49 | 14.27 | 10.06 | 25.86 | | |
| H19562_at | H19562 | 1896 | PTD010 protein | #N/A | #N/A | 522.13 | 432.65 | 256.94 | 393.61 | 326.53 | 182.71 | | |
| L08044_s_at | L08044 | 2149 | trefoil factor 3 (intestinal) | #N/A | #N/A | 214.6 | 108.17 | 238.79 | 107.82 | 58.55 | 184.16 | | |
| L29218_s_at | L29218 | 2190 | CDC-like kinase 2 | 6.51 | 0.00019 | 219.64 | 237.35 | 104.29 | 6.53 | -10.03 | 59.8 | | |
| L37747_s_at | L37747 | 2206 | lamin B1 | #N/A | #N/A | 43.42 | 28.65 | 37.33 | 5.97 | 5.1 | 7.57 | | |
| N34257_at | N34257 | 2495 | EST | #N/A | #N/A | 20.76 | 21.48 | 19.54 | -1.84 | -2.74 | 8.53 | | |
| R50692_at | R50692 | 2888 | KIAA0476 gene product | #N/A | #N/A | 197.89 | 187.87 | 101.08 | 148.53 | 151.12 | 63.03 | | |
| R60368_at | R60368 | 2917 | EST | #N/A | #N/A | 29.68 | 28.93 | 31.9 | -28.29 | -26.44 | 41.68 | | |
| R66475_at | R66475 | 2938 | EST | #N/A | #N/A | 45.68 | 32.34 | 34.37 | 7.64 | 8.26 | 6.3 | | |
| potassium voltage-gated channel, shaker-related subfamily, beta member 2 | | | | | | | | | | | | | |
| T34377_at | T34377 | 3111 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) | 4.55 | 0.00041 | 113.59 | 120.58 | 51.65 | 6.87 | 11.17 | 25.69 | | |
| KIAA0806 gene product | | | | | | | | | | | | | |
| U75968_s_at | U75968 | 3423 | helicase | #N/A | #N/A | 187.33 | 200.16 | 90.35 | 115.5 | 102.24 | 77.72 | | |
| W21426_at | W21426 | 3481 | EST | #N/A | #N/A | 63.36 | 64.93 | 20.23 | 45.59 | 40.39 | 19.89 | | |
| W28696_i_at | W28696 | 3491 | EST | #N/A | #N/A | 14.7 | 20.64 | 17.12 | 4.28 | 4.33 | 2.47 | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | | hcc sample set 2: | | hcc sample set 2: | | hcc sample set 2: | | normal set 2: | | normal set 2: | |
|--------------------------------|----------|--------|---------------------------|--------------------|---------|-------------------|--------|-------------------|--------|-------------------|---------|---------------|--------|---------------|--|
| | | | | set 2 | p value | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Median | Std Dev | |
| | | | | set 2 | p value | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Median | Std Dev | |
| H1 histone family, member | | | | | | | | | | | | | | | |
| X57129_at | X57129 | 3743 | 2 | 4.63 | 0.00663 | 137.13 | 137.75 | 87.31 | 8.38 | 5.39 | 28.3 | 8.38 | 5.39 | 28.3 | |
| rc_AA024658_at | AA024658 | 47 | ribosomal protein S19 | 7.55 | 0.00592 | 278.11 | 120.83 | 373.3 | 7.62 | 5.03 | 10.68 | 7.62 | 5.03 | 10.68 | |
| rc_AA029288_at | AA029288 | 65 | EST | 3.36 | 0.04908 | 134.53 | 56.15 | 209.69 | 4.09 | 3.35 | 8.39 | 4.09 | 3.35 | 8.39 | |
| rc_AA037828_at | AA037828 | 88 | KIAA0614 protein | #N/A | #N/A | 53.61 | 46.86 | 41.68 | 13.32 | 10.65 | 11.96 | 13.32 | 10.65 | 11.96 | |
| rc_AA040465_at | AA040465 | 95 | EST | 3.63 | 0.01806 | 229.8 | 210.67 | 180.94 | 47.15 | 45.53 | 5.48 | 47.15 | 45.53 | 5.48 | |
| rc_AA053660_at | AA053660 | 128 | EST | #N/A | #N/A | 543.66 | 223.47 | 685.44 | 95.24 | 79.97 | 42.99 | 95.24 | 79.97 | 42.99 | |
| cAMP responsive element | | | | | | | | | | | | | | | |
| rc_AA136332_at | AA136332 | 299 | binding protein 3 (luman) | #N/A | #N/A | 49.04 | 33.07 | 31.07 | -18.27 | -20.23 | 13.05 | -18.27 | -20.23 | 13.05 | |
| interferon regulatory factor 3 | | | | | | | | | | | | | | | |
| rc_AA149530_at | AA149530 | 324 | EST | #N/A | #N/A | 32.94 | 23.12 | 34.23 | 4.21 | 5.38 | 8.53 | 4.21 | 5.38 | 8.53 | |
| rc_AA149586_at | AA149586 | 325 | EST | #N/A | #N/A | 24.99 | 26.6 | 34.37 | 5.26 | 9.11 | 23.41 | 5.26 | 9.11 | 23.41 | |
| rc_AA206023_at | AA206023 | 427 | EST | #N/A | #N/A | 154.13 | 170.36 | 85.33 | 108.57 | 111.76 | 58.39 | 108.57 | 111.76 | 58.39 | |
| N-ethylmaleimide-sensitive | | | | | | | | | | | | | | | |
| rc_aa234530_s_at | AA234530 | 484 | factor | #N/A | #N/A | 143.67 | 135.48 | 82.59 | 51.33 | 42.9 | 35.02 | 51.33 | 42.9 | 35.02 | |
| rc_AA251909_at | AA251909 | 549 | EST | 3.59 | 0.01129 | 92.19 | 79.34 | 72.73 | 8.88 | 11.22 | 8.27 | 8.88 | 11.22 | 8.27 | |
| rc_AA262030_at | AA262030 | 605 | EST | #N/A | #N/A | 119.75 | 89.66 | 103.84 | 31.51 | 32.91 | 14.46 | 31.51 | 32.91 | 14.46 | |
| ribonuclease HI, large | | | | | | | | | | | | | | | |
| rc_AA262477_at | AA262477 | 608 | subunit | 4.57 | 0.00724 | 242.42 | 199.5 | 182.26 | 44.51 | 36.87 | 22.37 | 44.51 | 36.87 | 22.37 | |
| rc_AA283759_at | AA283759 | 671 | EST | #N/A | #N/A | 91.82 | 76.73 | 42.28 | 46.87 | 45.86 | 21.54 | 46.87 | 45.86 | 21.54 | |
| rc_AA291644_at | AA291644 | 701 | EST | 3.28 | 0.00033 | 114.73 | 117.29 | 44.59 | 32.77 | 30.24 | 21.1 | 32.77 | 30.24 | 21.1 | |
| rc_AA338760_at | AA338760 | 744 | EST | 3.96 | 0.01307 | 129.77 | 130.26 | 87.27 | 14.91 | 21.91 | 26.96 | 14.91 | 21.91 | 26.96 | |
| rc_AA398205_at | AA398205 | 789 | EST | 4.22 | 0.00059 | 125.4 | 107.84 | 63.85 | 15.01 | 7.37 | 26.26 | 15.01 | 7.37 | 26.26 | |
| tumor suppressor deleted in | | | | | | | | | | | | | | | |
| rc_AA401965_at | AA401965 | 833 | oral cancer-related 1 | 7.58 | 0.00089 | 932.74 | 924.02 | 593.69 | 120.58 | 93.29 | 109.41 | 120.58 | 93.29 | 109.41 | |
| rc_AA402272_at | AA402272 | 837 | EST | 3.73 | 0.02336 | 348.91 | 340 | 230.15 | 99.7 | 92.28 | 80.27 | 99.7 | 92.28 | 80.27 | |
| rc_AA404597_at | AA404597 | 854 | EST | #N/A | #N/A | 609.98 | 525.02 | 371.31 | 379.26 | 336.33 | 167.43 | 379.26 | 336.33 | 167.43 | |
| rc_AA417030_at | AA417030 | 914 | EST | 7.35 | 0.00555 | 200.3 | 168.21 | 135.63 | 6.42 | 7.5 | 7.77 | 6.42 | 7.5 | 7.77 | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | hcc | | | hcc | | | normal | | |
|------------------|----------|--------|--|------------------|---------|--------|--------|--------|--------|--------|---------|--------|--------|---------|
| | | | | change ln hcc | p value | sample | | hcc | sample | | hcc | sample | | normal |
| | | | | | | set 2 | set 2 | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| rc_AA423820_at | AA423820 | 940 | EST | #N/A | #N/A | 111.38 | 111.23 | 120.84 | 41.9 | 21.93 | 44.58 | 41.9 | 21.93 | 44.58 |
| rc_AA425852_i_at | AA425852 | 958 | EST | 3.82 | 0.0395 | 131.52 | 95.35 | 166.76 | 7.02 | 5.22 | 4.75 | 7.02 | 5.22 | 4.75 |
| rc_AA430032_at | AA430032 | 1009 | pituitary tumor-transforming 1 | 10.67 | 0.00052 | 377.69 | 320.44 | 294.49 | 26.8 | 15.31 | 35.24 | 26.8 | 15.31 | 35.24 |
| rc_AA430673_at | AA430673 | 1017 | EST | #N/A | #N/A | 45.74 | 34.15 | 44.8 | -1.21 | 3.63 | 15.26 | -1.21 | 3.63 | 15.26 |
| rc_AA443321_at | AA443321 | 1076 | EST | #N/A | #N/A | 33.93 | 32.89 | 11.76 | 10.79 | 9.65 | 7.26 | 10.79 | 9.65 | 7.26 |
| rc_AA443941_at | AA443941 | 1085 | tumor suppressing | #N/A | #N/A | 97.74 | 103.38 | 47.48 | 31.09 | 34.9 | 16.61 | 31.09 | 34.9 | 16.61 |
| rc_AA447223_at | AA447223 | 1100 | subtransferable candidate 1 | #N/A | #N/A | 31.66 | 18.91 | 31.1 | 4.45 | 3.74 | 6.5 | 4.45 | 3.74 | 6.5 |
| rc_aa449431_s_at | AA449431 | 1124 | translation initiation factor IF2 | 3.76 | 0.00571 | 94.41 | 95.64 | 54.08 | 17.4 | 16.96 | 5.38 | 17.4 | 16.96 | 5.38 |
| rc_AA454597_s_at | AA454597 | 1166 | EST | 4.23 | 0.00917 | 342.59 | 311.81 | 207.71 | 66.6 | 57.29 | 23.41 | 66.6 | 57.29 | 23.41 |
| rc_AA458882_at | AA458882 | 1205 | EST | #N/A | #N/A | 93.56 | 52.28 | 98.72 | 24.97 | 22.52 | 17.66 | 24.97 | 22.52 | 17.66 |
| rc_AA458934_at | AA458934 | 1208 | EST | #N/A | #N/A | 33.6 | 28.19 | 29.02 | 7.1 | 7.91 | 4.22 | 7.1 | 7.91 | 4.22 |
| rc_AA465342_at | AA465342 | 1271 | EST | 3.21 | 0.01378 | 131.07 | 109.99 | 95.4 | 30.07 | 33.06 | 23.97 | 30.07 | 33.06 | 23.97 |
| rc_AA477561_at | AA477561 | 1292 | EST | #N/A | #N/A | 146.3 | 127.03 | 97.99 | 63.83 | 76.56 | 37.87 | 63.83 | 76.56 | 37.87 |
| rc_AA491295_at | AA491295 | 1390 | calcium/calmodulin-dependent protein kinase kinase 2, beta | 3.71 | 0.0103 | 180.61 | 173.47 | 118.85 | 46.95 | 31.51 | 65.56 | 46.95 | 31.51 | 65.56 |
| rc_AA608545_at | AA608545 | 1462 | RAD51 (S. cerevisiae) homolog (E coli RecA homolog) | #N/A | #N/A | 70.5 | 57.51 | 53.36 | 7.76 | 8.92 | 6.17 | 7.76 | 8.92 | 6.17 |
| rc_AA620553_s_at | AA620553 | 1504 | flap structure-specific endonuclease 1 | 7.56 | 0.00101 | 262.87 | 232.63 | 201.66 | 14.44 | 4.85 | 38.53 | 14.44 | 4.85 | 38.53 |
| rc_AA621325_at | AA621325 | 1522 | HNK-1 sulfotransferase | #N/A | #N/A | 74.57 | 70.64 | 46.61 | 27.23 | 25.89 | 16.03 | 27.23 | 25.89 | 16.03 |
| rc_AA621780_at | AA621780 | 1530 | CGI-96 protein | #N/A | #N/A | 81.72 | 92.23 | 49.69 | 12.06 | 11.27 | 19.2 | 12.06 | 11.27 | 19.2 |
| rc_F02807_at | F02807 | 1781 | KIAA0838 protein | 5.67 | 0.02064 | 260.02 | 219.01 | 229.96 | 20.93 | 16.66 | 22.24 | 20.93 | 16.66 | 22.24 |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change ln hcc | hcc | | | hcc | | | hcc | | |
|--------------------------|---------|--------|-------------------------|-----------------------|---------|---------|--------|--------|---------|--------|--------|--------|---------|
| | | | | | sample | | hcc | sample | | hcc | sample | | hcc |
| | | | | | set 2 | p value | Mean | Median | Std Dev | set 2: | Mean | Median | Std Dev |
| rc_F04444_at | F04444 | 1788 | EST | 4.13 | 0.00944 | 371.21 | 360.5 | 186.45 | 119.68 | 121.27 | 109.82 | | |
| rc_F04524_s_at | F04524 | 1790 | stomatin-like protein 1 | #N/A | #N/A | 117.77 | 135.65 | 68.29 | 46.56 | 44.53 | 33.75 | | |
| rc_F08876_at | F08876 | 1797 | EST | 9.06 | 0 | 209.64 | 201.85 | 53.21 | -22.5 | -20.17 | 37.21 | | |
| rc_F10161_at | F10161 | 1811 | EST | #N/A | #N/A | 50.78 | 46.73 | 32.42 | 15.4 | 14.78 | 11.87 | | |
| rc_F10453_at | F10453 | 1819 | EST | 3.64 | 0.01878 | 135.07 | 138.53 | 85.7 | 27.28 | 14.2 | 54.04 | | |
| rc_H04649_at | H04649 | 1838 | EST | #N/A | #N/A | 180.25 | 158.18 | 164.34 | 50.86 | 41.2 | 33.9 | | |
| rc_H04793_at | H04793 | 1840 | DKFZP434F091 protein | #N/A | #N/A | 23.18 | 20 | 41.25 | -14.45 | -20.45 | 29 | | |
| rc_H59617_at | H59617 | 1964 | EST | 5.81 | 0.0115 | 212.68 | 209.19 | 157.42 | 19.24 | 21.65 | 16.88 | | |
| rc_H97012_at | H97012 | 2058 | EST | 3.51 | 0.03505 | 171.34 | 138.12 | 170.68 | 27.69 | 38.46 | 36.08 | | |
| rc_H98657_at | H98657 | 2068 | EST | #N/A | #N/A | 141.17 | 131.42 | 69.63 | 111.2 | 84.74 | 128.92 | | |
| rc_N23319_at | N23319 | 2454 | EST | #N/A | #N/A | 70.62 | 66.39 | 49.4 | 13.74 | 8.56 | 21.62 | | |
| rc_N23868_at | N23868 | 2459 | EST | #N/A | #N/A | 79.69 | 81.67 | 56.06 | 20.52 | 20.19 | 11.48 | | |
| rc_N45224_at | N45224 | 2516 | EST | #N/A | #N/A | 349.73 | 360.67 | 164.87 | 215.49 | 223.16 | 151.06 | | |
| rc_N48595_at | N48595 | 2528 | EST | #N/A | #N/A | 85.77 | 67.62 | 51.78 | 28.84 | 29.38 | 8.3 | | |
| rc_N75541_at | N75541 | 2692 | EST | 4.43 | 0.01059 | 182.83 | 131.35 | 183.41 | 34.1 | 15.82 | 56.07 | | |
| ras homolog gene family, | | | | | | | | | | | | | |
| rc_N90273_s_at | N90273 | 2713 | member H | #N/A | #N/A | 105.53 | 96.01 | 41.89 | 68.92 | 59.56 | 35.69 | | |
| rc_n93465_s_at | N93465 | 2735 | EST | #N/A | #N/A | 803.68 | 716.56 | 385.5 | 624.57 | 694.14 | 306.11 | | |
| rc_R39191_s_at | R39191 | 2834 | KIAA1020 protein | 5.18 | 0.03185 | 331.72 | 80.62 | 590.96 | 17.46 | 18.33 | 16.04 | | |
| rc_R44793_at | R44793 | 2859 | EST | 5.4 | 0.00329 | 155.86 | 121.83 | 125.26 | 10.1 | 7.86 | 16.54 | | |
| rc_R44817_at | R44817 | 2860 | EST | #N/A | #N/A | 594.46 | 602.82 | 206.15 | 255.91 | 249.29 | 69.09 | | |
| rc_R44896_at | R44896 | 2862 | KIAA0665 gene product | #N/A | #N/A | 67.08 | 57.13 | 34.18 | 19.1 | 20.75 | 23.04 | | |
| rc_R64137_s_at | R64137 | 2931 | EST | #N/A | #N/A | 31.25 | 24.23 | 21 | 2.9 | 2.65 | 6.94 | | |
| rc_R71395_at | R71395 | 2952 | EST | 4.12 | 0.03719 | 166.03 | 99.42 | 190.98 | 14.99 | 12.28 | 14.58 | | |
| rc_R72087_at | R72087 | 2955 | EST | #N/A | #N/A | 262.11 | 302.11 | 95 | 201.97 | 183.76 | 83.41 | | |
| rc_R91819_at | R91819 | 2984 | EST | 12.81 | 0.00037 | 467.79 | 364.2 | 426.16 | 11.34 | 9.35 | 36.49 | | |
| rc_T03749_at | T03749 | 3048 | KIAA1089 protein | 4.23 | 0.00776 | 103 | 97.55 | 74.34 | -5.18 | -6.08 | 13.69 | | |
| rc_T25744_s_at | T25744 | 3092 | EST | #N/A | #N/A | 72.74 | 73.3 | 37.84 | 15.56 | 12.65 | 13.18 | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | change in hcc | fold | | | hcc | | | hcc | | | normal | | |
|------------------|----------|--------|---|------------------|---------|---------|--------|--------|---------|--------|--------|--------|--------|--------|------|---------|
| | | | | | set 2 | p value | Mean | Median | Std Dev | set 2: | Mean | set 2: | Median | set 2: | Mean | Std Dev |
| | | | | | | | | | | | | | | | | |
| rc_T62918_at | T62918 | 3169 | EST | 5.25 | 0.00687 | 136.22 | 142.37 | 83.63 | -12.41 | -6.89 | 17.59 | | | | | |
| rc_T89731_at | T89731 | 3245 | EST | #N/A | #N/A | 63.59 | 65.07 | 20.47 | 5.75 | 3.83 | 11.8 | | | | | |
| rc_W32176_s_at | W32176 | 3498 | zinc metalloproteinase, STE24 (yeast, homolog) rab6 GTPase activating protein (GAP and centrosome-associated) | #N/A | #N/A | 550.53 | 614.92 | 234.79 | 290.18 | 277.95 | 129.45 | | | | | |
| rc_W47388_at | W47388 | 3536 | EST | #N/A | #N/A | 97.33 | 71 | 59.73 | 43.93 | 36.52 | 48.34 | | | | | |
| rc_W78057_at | W78057 | 3600 | EST | 5.53 | 0.01231 | 265.23 | 222.35 | 199.24 | 29.21 | 29.9 | 34.33 | | | | | |
| rc_W80763_at | W80763 | 3608 | EST | 4.98 | 0.01026 | 147.37 | 138.37 | 122.38 | 16.84 | 15.48 | 9.22 | | | | | |
| rc_W90146_f_at | W90146 | 3644 | EST | 3.58 | 0.00322 | 82.11 | 69.02 | 47.2 | 9.93 | 8.63 | 6.49 | | | | | |
| rc_Z38299_at | Z38299 | 3887 | EST | 3.71 | 0.0036 | 140.86 | 127.16 | 96.62 | 30.48 | 25.94 | 23.34 | | | | | |
| rc_Z38404_at | Z38404 | 3888 | EST | #N/A | #N/A | 59.77 | 56.71 | 37.29 | 29.82 | 30.16 | 9 | | | | | |
| rc_Z38462_at | Z38462 | 3892 | KIAA0938 protein | 4.69 | 0.0142 | 137.19 | 116.11 | 116.16 | -0.86 | 0.53 | 7.64 | | | | | |
| rc_Z38688_at | Z38688 | 3893 | EST | #N/A | #N/A | 49.85 | 46.83 | 42.25 | 21.38 | 13.4 | 29.47 | | | | | |
| rc_Z38729_at | Z38729 | 3894 | EST | #N/A | #N/A | 77.67 | 57.81 | 60.7 | -2.4 | -5.01 | 46.96 | | | | | |
| rc_Z40556_at | Z40556 | 3921 | CGI-96 protein | #N/A | #N/A | 176.19 | 76.96 | 285.02 | 59.62 | 55.07 | 16.66 | | | | | |
| rc_AA021549_at | AA021549 | 42 | EST | 3.17 | 0.00158 | 100.01 | 83.02 | 44.39 | 31.74 | 20.12 | 36.74 | | | | | |
| rc_AA026270_at | AA026270 | 56 | tyrosyl-tRNA synthetase | #N/A | #N/A | 269.96 | 261.31 | 191.51 | 76.85 | 76.68 | 45.22 | | | | | |
| rc_AA055896_at | AA055896 | 135 | collagen, type V, alpha 1 | 10.87 | 0.00907 | 414.16 | 454.82 | 330.75 | -3.14 | -5.8 | 33.88 | | | | | |
| rc_AA112979_s_at | AA112979 | 225 | vaccinia related kinase 1 | #N/A | #N/A | 37.93 | 31.05 | 16.86 | 8.54 | 8.02 | 2.59 | | | | | |
| rc_AA134063_at | AA134063 | 286 | EST | #N/A | #N/A | 25.71 | 13.84 | 34.35 | -5.21 | -6.17 | 6 | | | | | |
| rc_AA150053_at | AA150053 | 327 | EST | #N/A | #N/A | 270.14 | 248.87 | 144.92 | 101.87 | 88.37 | 73.73 | | | | | |
| rc_AA206914_at | AA206914 | 428 | EST | #N/A | #N/A | 89.35 | 94.1 | 46.27 | 66.34 | 69.2 | 26.35 | | | | | |
| rc_AA243133_at | AA243133 | 525 | serine/threonine kinase 15 | 7.03 | 0.00005 | 147.5 | 162.28 | 43.03 | 9.69 | 12.1 | 9.8 | | | | | |
| rc_AA243466_at | AA243466 | 527 | EST | #N/A | #N/A | 61.94 | 42.38 | 37.6 | 13.66 | 13.42 | 9.63 | | | | | |
| rc_AA243598_at | AA243598 | 531 | EST | #N/A | #N/A | 60.15 | 62.79 | 32.67 | 11.41 | 13.18 | 13.43 | | | | | |
| rc_AA252147_at | AA252147 | 551 | EST | #N/A | #N/A | 95.91 | 56.69 | 122.31 | 3.65 | -0.82 | 22.5 | | | | | |
| rc_AA255566_at | AA255566 | 570 | EST | #N/A | #N/A | 64.28 | 50.15 | 52.25 | 16.18 | 14.38 | 13.17 | | | | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | | hcc | | | hcc | | | hcc | | | normal | | |
|---------------------------|----------|--------|-------------------------|--------------------|---------|-------|---------|--------------------|----------------------|-----------------------|-----|-------------|---------------|----------------|-------------|---------------|----------------|
| | | | | | | set 2 | p value | sample set 2: Mean | sample set 2: Median | sample set 2: Std Dev | hcc | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| | | | | | | | | | | | | | | | | | |
| rc_AA279667_s_at | AA279667 | 629 | EST | #N/A | #N/A | #N/A | #N/A | 184.99 | 102.43 | 289.71 | | 8.06 | 7.61 | 23.78 | | | |
| rc_AA279943_at | AA279943 | 635 | EST | #N/A | #N/A | #N/A | #N/A | 137.05 | 63.54 | 232.2 | | -4.7 | -5.33 | 11.18 | | | |
| rc_AA290594_at | AA290594 | 691 | EST | #N/A | #N/A | #N/A | #N/A | 59.19 | 56.31 | 23.84 | | 21.4 | 18.8 | 23.98 | | | |
| rc_AA290776_s_at | AA290776 | 693 | EST | #N/A | #N/A | #N/A | #N/A | 524.07 | 516.6 | 88.67 | | 441.83 | 355.04 | 245.84 | | | |
| rc_AA292765_at | AA292765 | 712 | ZW10 interactor | 7.24 | 0.00498 | | | 202.52 | 192.15 | 142.78 | | 11.33 | 18.29 | 13.27 | | | |
| rc_AA398908_at | AA398908 | 801 | EST | 20.72 | 0.00114 | | | 629.56 | 433.87 | 551.97 | | -174.29 | -216.08 | 104.42 | | | |
| rc_AA405098_at | AA405098 | 855 | EST | 6.09 | 0.01224 | | | 221.56 | 130.95 | 237.73 | | -4.35 | -8.44 | 30.78 | | | |
| rc_AA406542_at | AA406542 | 878 | EST | #N/A | #N/A | #N/A | #N/A | 179.08 | 84.98 | 218.93 | | -1.99 | 1.49 | 12.75 | | | |
| rc_AA435738_at | AA435738 | 1042 | EST | #N/A | #N/A | #N/A | #N/A | 80.97 | 82 | 30.96 | | 50.41 | 51.29 | 33.08 | | | |
| rc_AA443585_at | AA443585 | 1077 | EST | #N/A | #N/A | #N/A | #N/A | 200.3 | 136.72 | 140.42 | | 118.18 | 97.38 | 102.71 | | | |
| Ts translation elongation | | | | | | | | | | | | | | | | | |
| rc_AA446596_at | AA446596 | 1092 | factor, mitochondrial | #N/A | #N/A | #N/A | #N/A | 103.35 | 97.42 | 153.31 | | 72.58 | 70.64 | 154.24 | | | |
| rc_AA447777_at | AA447777 | 1107 | EST | #N/A | #N/A | #N/A | #N/A | 258.37 | 212.57 | 171.93 | | 133.78 | 116.63 | 56.34 | | | |
| rc_AA453757_at | AA453757 | 1156 | EST | #N/A | #N/A | #N/A | #N/A | 128.41 | 118.8 | 40.54 | | 65.66 | 70.33 | 40.45 | | | |
| rc_AA459254_at | AA459254 | 1211 | EST | 6.22 | 0.00001 | | | 309.74 | 308.36 | 112.62 | | 51.84 | 43.51 | 37.57 | | | |
| chromosome-associated | | | | | | | | | | | | | | | | | |
| rc_AA459673_at | AA459673 | 1220 | polypeptide C | #N/A | #N/A | #N/A | #N/A | 32.11 | 31.27 | 15.41 | | 8.91 | 6.74 | 8.86 | | | |
| rc_AA476333_at | AA476333 | 1282 | EST | #N/A | #N/A | #N/A | #N/A | 52.26 | 34.54 | 55.5 | | 9.04 | 14.67 | 24.04 | | | |
| rc_AA496993_at | AA496993 | 1405 | EST | #N/A | #N/A | #N/A | #N/A | 91.01 | 73.62 | 80.93 | | 24.83 | 12.83 | 29.07 | | | |
| rc_AA504512_s_at | AA504512 | 1415 | KIAA0943 protein | 5.72 | 0.00384 | | | 316.32 | 322.55 | 180.22 | | 65.48 | 28.37 | 93.94 | | | |
| rc_AA609132_at | AA609132 | 1479 | EST | #N/A | #N/A | #N/A | #N/A | 67.33 | 42.61 | 65.11 | | 29.14 | 23.25 | 53.79 | | | |
| rc_AA609942_at | AA609942 | 1494 | EST | #N/A | #N/A | #N/A | #N/A | 89.98 | 66.8 | 71.4 | | 15.89 | 14.41 | 25.58 | | | |
| Fas-activated | | | | | | | | | | | | | | | | | |
| rc_F02254_s_at | F02254 | 1777 | serine/threonine kinase | 5.1 | 0.00329 | | | 376.8 | 341.06 | 145.28 | | 90 | 72.97 | 135.39 | | | |
| rc_H48459_s_at | H48459 | 1937 | KIAA0186 gene product | 3.1 | 0.02325 | | | 71.21 | 49.95 | 87.89 | | -29.4 | -30.17 | 6.19 | | | |
| rc_H87790_at | H87790 | 2018 | EST | #N/A | #N/A | #N/A | #N/A | 284.91 | 287.54 | 145.66 | | 466.07 | 547.34 | 192.71 | | | |
| rc_N34017_at | N34017 | 2494 | EST | #N/A | #N/A | #N/A | #N/A | 39.35 | 37.49 | 4.67 | | 5.47 | 7.05 | 10.01 | | | |
| rc_N35493_at | N35493 | 2502 | EST | #N/A | #N/A | #N/A | #N/A | 73.6 | 80.62 | 31.24 | | 19.03 | 18.75 | 17 | | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | hcc | | hcc | | hcc | | normal | | normal | |
|------------------|----------|--------|------------------------------|------------------|---------|--------|--------|--------|--------|---------|-------|--------|--------|---------|---------|
| | | | | change in hcc | p value | sample | | sample | | sample | | set 2: | | set 2: | |
| | | | | | | Mean | Median | Mean | Median | Std Dev | Mean | Mean | Median | Std Dev | Std Dev |
| rc_N63604_at | N63604 | 2601 | EST | #N/A | #N/A | 47.18 | 32.72 | 35 | 16.51 | 14.36 | 10.5 | | | | |
| rc_N63646_at | N63646 | 2602 | EST | #N/A | #N/A | 479.9 | 367.24 | 240.56 | 182.22 | 137.95 | 90.9 | | | | |
| | | | SRY (sex-determining | | | | | | | | | | | | |
| rc_N69014_s_at | N69014 | 2642 | region Y)-box 22 | #N/A | #N/A | 193.21 | 174.83 | 48.23 | 116.34 | 129.47 | 50.74 | | | | |
| rc_N69879_s_at | N69879 | 2651 | drebrin 1 | 3.15 | 0.01659 | 88.78 | 84.86 | 61.76 | 3.69 | -2.94 | 21.49 | | | | |
| rc_N69983_at | N69983 | 2652 | EST | #N/A | #N/A | 93.25 | 96.86 | 49.82 | 76.2 | 93.14 | 54.92 | | | | |
| rc_N70330_at | N70330 | 2656 | EST | #N/A | #N/A | 108.39 | 69.74 | 105.54 | 33.78 | 27.33 | 16.47 | | | | |
| rc_N74018_at | N74018 | 2684 | EST | #N/A | #N/A | 22.65 | 25.34 | 10.26 | 2.34 | 1.47 | 10.41 | | | | |
| rc_N89670_at | N89670 | 2709 | EST | #N/A | #N/A | 65.03 | 59.18 | 66.58 | 3.16 | -1.81 | 43.32 | | | | |
| rc_N93000_at | N93000 | 2727 | EST | #N/A | #N/A | 77.68 | 64.15 | 45.06 | 17.65 | 18.66 | 10.91 | | | | |
| rc_N99944_s_at | N99944 | 2749 | EST | 3.46 | 0.00104 | 211.02 | 200.61 | 102.49 | 60.05 | 50.12 | 29.73 | | | | |
| rc_R97176_at | R97176 | 3002 | EST | #N/A | #N/A | 143.07 | 152.08 | 86.96 | 53.41 | 58.26 | 38.91 | | | | |
| rc_T16226_at | T16226 | 3066 | EST | 7.23 | 0.00119 | 323.53 | 312.1 | 209.59 | 33.87 | 22.78 | 38.68 | | | | |
| rc_T32108_at | T32108 | 3103 | EST | #N/A | #N/A | 180.81 | 165.53 | 68.41 | 148.09 | 152.11 | 92.06 | | | | |
| rc_W15275_s_at | W15275 | 3472 | EST | #N/A | #N/A | 33.62 | 31.78 | 35.23 | 30.09 | 24.85 | 43.25 | | | | |
| rc_W31906_at | W31906 | 3497 | secretagogin | 6.62 | 0.00926 | 474.89 | 174.52 | 605.68 | 42.41 | 30.95 | 47.65 | | | | |
| rc_W46286_s_at | W46286 | 3526 | EST | 3.68 | 0.00311 | 154.73 | 166.08 | 72.64 | 23.51 | 22.85 | 61.89 | | | | |
| | | | DEAD/H (Asp-Glu-Ala- | | | | | | | | | | | | |
| | | | Asp/His) box polypeptide, Y | | | | | | | | | | | | |
| rc_W60097_at | W60097 | 3556 | chromosome | 4.82 | 0.04903 | 235.42 | 265.15 | 189.13 | 35.34 | 11.72 | 84.5 | | | | |
| | | | KDEL (Lys-Asp-Glu-Leu) | | | | | | | | | | | | |
| | | | endoplasmic reticulum | | | | | | | | | | | | |
| rc_W80852_at | W80852 | 3609 | protein retention receptor 3 | 6.37 | 0.00005 | 184.61 | 159.98 | 100.74 | 11.16 | 11.92 | 36.06 | | | | |
| | | | Wolf-Hirschhorn syndrome | | | | | | | | | | | | |
| rc_AA046745_at | AA046745 | 113 | candidate 1 | 3.33 | 0.00648 | 73.04 | 72.71 | 48.97 | 10.59 | 12.02 | 7.33 | | | | |
| rc_AA052941_at | AA052941 | 121 | EST | 3.36 | 0.00088 | 100.81 | 106.86 | 44.56 | 25.66 | 25.65 | 13.62 | | | | |
| rc_AA058589_f_at | AA058589 | 144 | EST | #N/A | #N/A | 44.63 | 51.66 | 34.1 | -9.37 | -10.9 | 8.66 | | | | |
| rc_AA126561_s_at | AA126561 | 249 | stanniocalcin | #N/A | #N/A | 51.44 | 44.19 | 31.6 | 7.16 | 7.73 | 8.55 | | | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | hcc | | | hcc | | | hcc | | |
|------------------|----------|--------|--|--------------------|---------|---------|--------|--------|---------|--------------------|--------------------|----------------------|-----------------------|
| | | | | | set 2 | p value | Mean | Median | Std Dev | sample set 2: Mean | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| | | | | | | | | | | | | | |
| rc_AA146849_s_at | AA146849 | 313 | target of myb1 (chicken) | 4.72 | 0.00326 | | 398.05 | 341.23 | 244.73 | 98.86 | 106.97 | | 86.19 |
| rc_AA149889_at | AA149889 | 326 | homolog | 8.55 | 0.00224 | | 240.81 | 312.86 | 143.89 | -0.24 | 8.25 | | 29.83 |
| rc_AA283711_s_at | AA283711 | 669 | neighbor of A-kinase anchoring protein 95 | #N/A | #N/A | | 382.91 | 380.33 | 210.95 | 221.7 | 203.51 | | 93.54 |
| rc_AA284153_at | AA284153 | 673 | ubiquitin carrier protein | #N/A | #N/A | | 117.98 | 127.81 | 72.86 | 53.98 | 43.58 | | 32.17 |
| rc_AA335191_f_at | AA335191 | 741 | EST | 6.47 | 0.01462 | | 512.64 | 199.99 | 673.92 | 43.84 | 33.21 | | 43.52 |
| | | | creatine kinase, brain | | | | | | | | | | |
| | | | TNF receptor-associated factor 1 | #N/A | #N/A | | 137.67 | 59.13 | 211.07 | 35.93 | 19.15 | | 31.32 |
| rc_AA402642_s_at | AA402642 | 840 | ATP-binding cassette, sub-family F (GCN20), member 2 | #N/A | #N/A | | 190.92 | 187.57 | 78.83 | 92.5 | 83.63 | | 49.3 |
| rc_AA427460_s_at | AA427460 | 972 | EST | #N/A | #N/A | | 25.39 | 21.98 | 9.32 | 5.32 | 4.23 | | 4.43 |
| rc_AA431429_at | AA431429 | 1021 | v-Ha-ras Harvey rat sarcoma viral oncogene homolog | | | | | | | | | | |
| rc_AA443316_s_at | AA443316 | 1075 | ubiquitin-conjugating enzyme E2L 3 | 3.4 | 0.00133 | | 138.89 | 124.06 | 70.22 | 40.07 | 41.12 | | 32.54 |
| rc_AA476260_at | AA476260 | 1280 | EST | #N/A | #N/A | | 61.23 | 69.49 | 40.45 | -32.66 | -15.85 | | 56.91 |
| rc_AA487058_at | AA487058 | 1352 | ubiquitin-conjugating enzyme E2L 3 | #N/A | #N/A | | 245.56 | 225.48 | 137.4 | 315.7 | 232.85 | | 213.47 |
| rc_AA521149_at | AA521149 | 1420 | EST | 3.33 | 0.00211 | | 113.43 | 106.74 | 60.79 | 28.44 | 29.54 | | 18.61 |
| rc_AA599244_at | AA599244 | 1448 | KIAA0530 protein | #N/A | #N/A | | 53.83 | 48.84 | 25.7 | 7.71 | 6.06 | | 7.11 |
| rc_AA599850_at | AA599850 | 1457 | EST | 3.55 | 0.03215 | | 122.91 | 75.32 | 123.52 | -1.23 | -2.33 | | 31.86 |
| rc_AA621530_at | AA621530 | 1526 | EST | 3.26 | 0.00298 | | 78.73 | 75.43 | 40.45 | 12.46 | 15.12 | | 13.43 |
| rc_AA621644_at | AA621644 | 1528 | EST | #N/A | #N/A | | 83.13 | 88.29 | 43.19 | 71.19 | 66.84 | | 29.87 |
| rc_C15078_i_at | C15078 | 1573 | EST | #N/A | #N/A | | 121.71 | 98.25 | 100.16 | 26.22 | 31.14 | | 60.2 |
| rc_D80710_f_at | D80710 | 1734 | integral type I protein | 3.17 | 0.04549 | | 153.76 | 74.74 | 166.28 | 22.95 | 28.29 | | 24.59 |
| rc_D80948_f_at | D80948 | 1738 | EST | #N/A | #N/A | | 70.05 | 77.71 | 32.11 | 41.25 | 43.53 | | 17.46 |
| rc_D81048_at | D81048 | 1739 | EST | #N/A | #N/A | | 150.18 | 149.32 | 51.77 | 86.08 | 85.08 | | 39.11 |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | | hcc sample set 2: | | | hcc sample set 2: | | | normal sample set 2: | | |
|----------------|---------|--------|--|--------------------|---------|-------------------|--------|---------|-------------------|---------|---------|----------------------|---------|---------|
| | | | | set 2 | p value | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Median | Std Dev |
| rc_F04320_s_at | F04320 | 1786 | (activator 1) 4 (37kD) | 6.29 | 0.00042 | 156.76 | 122.53 | 109.02 | 14.92 | 17.26 | 9.79 | 14.92 | 17.26 | 9.79 |
| rc_H14617_at | H14617 | 1884 | EST | #N/A | #N/A | 143.86 | 147.93 | 66.03 | 133.9 | 150.35 | 53.38 | 133.9 | 150.35 | 53.38 |
| rc_H26763_at | H26763 | 1907 | EST | #N/A | #N/A | 408.05 | 321.65 | 219.8 | 409.85 | 391.85 | 155.84 | 409.85 | 391.85 | 155.84 |
| rc_H68794_at | H68794 | 1984 | EST | 3.67 | 0.00327 | 215.75 | 176.78 | 110.42 | 65.56 | 54 | 51.09 | 65.56 | 54 | 51.09 |
| rc_H78211_at | H78211 | 2001 | EST | 7.5 | 0.02674 | 285.43 | 307.06 | 261.02 | -115.95 | -129.18 | 70.22 | -115.95 | -129.18 | 70.22 |
| rc_H95566_f_at | H95566 | 2050 | EST | #N/A | #N/A | 136.58 | 143.31 | 26.27 | 74.11 | 89.04 | 126.61 | 74.11 | 89.04 | 126.61 |
| rc_H99870_at | H99870 | 2082 | EST | #N/A | #N/A | 92.81 | 94.93 | 33.98 | 53.96 | 61.17 | 29.86 | 53.96 | 61.17 | 29.86 |
| rc_N62487_at | N62487 | 2591 | EST | #N/A | #N/A | 56.6 | 52.26 | 33.75 | 13.89 | 16.02 | 8.53 | 13.89 | 16.02 | 8.53 |
| rc_N67815_f_at | N67815 | 2627 | EST | 3.84 | 0.00439 | 351.55 | 356.17 | 99.35 | 104.07 | 151.77 | 86.01 | 104.07 | 151.77 | 86.01 |
| rc_N69084_i_at | N69084 | 2643 | EST | 3.11 | 0.0094 | 233.32 | 208.16 | 169.31 | 72.13 | 67.7 | 49.99 | 72.13 | 67.7 | 49.99 |
| rc_N73278_at | N73278 | 2672 | EST | #N/A | #N/A | 77.72 | 71.59 | 49.4 | 25.36 | 19.22 | 26.85 | 25.36 | 19.22 | 26.85 |
| rc_R06251_f_at | R06251 | 2764 | tumor protein D52-like 2 | 4.88 | 0.03097 | 466.88 | 341.39 | 380.43 | 74.25 | 66.72 | 64.11 | 74.25 | 66.72 | 64.11 |
| | | | carbohydrate (keratan sulfate Gal-6) | | | | | | | | | | | |
| rc_R15740_at | R15740 | 2791 | sulfotransferase 1 | 3.36 | 0.00268 | 117.43 | 100.03 | 64.73 | 31.77 | 21.3 | 33.53 | 31.77 | 21.3 | 33.53 |
| rc_R24507_at | R24507 | 2802 | EST | #N/A | #N/A | 31.61 | 16.41 | 30.69 | 3 | 3.45 | 5.62 | 3 | 3.45 | 5.62 |
| rc_R27296_f_at | R27296 | 2807 | EST | 3.41 | 0.00309 | 77.08 | 67.51 | 39.42 | 8.27 | 11.07 | 7.26 | 8.27 | 11.07 | 7.26 |
| rc_R30931_at | R30931 | 2810 | EST | #N/A | #N/A | 54.19 | 57.09 | 29.34 | 17.58 | 13.67 | 14.21 | 17.58 | 13.67 | 14.21 |
| rc_R45994_f_at | R45994 | 2867 | EST | 6.48 | 0.00358 | 730.52 | 598.82 | 420.14 | 145.88 | 160.69 | 163.03 | 145.88 | 160.69 | 163.03 |
| rc_R70253_at | R70253 | 2945 | EST | 3.38 | 0.03125 | 99.7 | 88.01 | 87.93 | -9.59 | -0.47 | 30.83 | -9.59 | -0.47 | 30.83 |
| rc_R72886_s_at | R72886 | 2956 | KIAA0422 protein | 5.5 | 0.00091 | 564.05 | 473.4 | 207.71 | 126.66 | 121.18 | 116.07 | 126.66 | 121.18 | 116.07 |
| rc_R96924_s_at | R96924 | 3001 | EST | 7.04 | 0.00012 | 336.8 | 329 | 106.3 | 51.01 | 52.94 | 54.09 | 51.01 | 52.94 | 54.09 |
| rc_T15852_f_at | T15852 | 3062 | EST | 5.21 | 0.00642 | 168.18 | 134.42 | 120.18 | -7.59 | 7.36 | 51.48 | -7.59 | 7.36 | 51.48 |
| | | | cleavage and polyadenylation specific factor 4, 30kD subunit | | | | | | | | | | | |
| rc_T16983_s_at | T16983 | 3074 | factor 4, 30kD subunit | 4.23 | 0.0106 | 262.26 | 268.2 | 155.86 | 65.64 | 45.67 | 74.28 | 65.64 | 45.67 | 74.28 |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | | hcc | | | hcc | | | normal | | |
|----------------|----------|--------|--|--------------------|---------|--------------------|----------------------|-----------------------|-----------------|-------------------|--------------------|--------------------|----------------------|-----------------------|
| | | | | set 2 | p value | sample set 2: Mean | sample set 2: Median | sample set 2: Std Dev | hcc set 2: Mean | hcc set 2: Median | hcc set 2: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| rc_T33865_f_at | T33865 | 3110 | RNA (guanine-7-) | #N/A | #N/A | 29.73 | 32.86 | 22.11 | -0.26 | 2.33 | 8.15 | | | |
| rc_T66935_at | T66935 | 3179 | methyltransferase EST | 3.01 | 0.00123 | 181.34 | 189.67 | 61.49 | 66.8 | 52.94 | 42.32 | | | |
| rc_T95057_f_at | T95057 | 3259 | EST | 6.46 | 0.00613 | 229.11 | 188.71 | 174.46 | 7.13 | 15.37 | 37.2 | | | |
| rc_W45320_f_at | W45320 | 3523 | KRAB-associated protein 1 | 10.05 | 0.00002 | 365.22 | 345.46 | 124.13 | -2.52 | 25.03 | 112.32 | | | |
| AF006041_at | AF006041 | 1549 | death-associated protein 6 | #N/A | #N/A | 174.22 | 170.16 | 37.64 | 74.91 | 58.55 | 50.31 | | | |
| D00596_at | D00596 | 1590 | thymidylate synthetase | 5.58 | 0.0098 | 200.17 | 128.11 | 170.5 | 20.16 | 20.43 | 12.43 | | | |
| D38491_at | D38491 | 1653 | KIAA0117 protein | #N/A | #N/A | 47.67 | 52.03 | 21.01 | 20.77 | 20.88 | 17.43 | | | |
| D63486_at | D63486 | 1712 | KIAA0152 gene product minichromosome | 3.56 | 0.00063 | 277.42 | 248.24 | 99.25 | 84.6 | 95.61 | 45.48 | | | |
| D84557_at | D84557 | 1749 | maintenance deficient (mis5, S. pombe) 6 | 3.97 | 0.0017 | 184.48 | 132.11 | 125.74 | 37.22 | 43.12 | 28.15 | | | |
| D86957_at | D86957 | 1754 | KIAA0202 protein | 3.08 | 0.02949 | 91.22 | 73.14 | 89.89 | 14.7 | 12.7 | 6.29 | | | |
| D86972_at | D86972 | 1755 | KIAA0218 gene product | #N/A | #N/A | 68.56 | 66.54 | 32.32 | 34.58 | 32.05 | 21.82 | | | |
| D90097_at | D90097 | 1768 | amylase, alpha 2B; pancreatic | #N/A | #N/A | 41.19 | 37.49 | 21.85 | 6.55 | 11.44 | 15.06 | | | |
| L29218_at | L29218 | 2190 | CDC-like kinase 2 | 3.82 | 0.00035 | 155.42 | 142.58 | 76.28 | 35.11 | 41.27 | 26.41 | | | |
| L38696_at | L38696 | 2208 | RNA-binding protein (autoantigenic) | #N/A | #N/A | 127.32 | 114.91 | 62.34 | 60.18 | 58.55 | 24.77 | | | |
| M11749_at | M11749 | 2240 | Thy-1 cell surface antigen | #N/A | #N/A | 83.1 | 65.86 | 64.52 | 26.05 | 28.95 | 20.56 | | | |
| M25753_at | M25753 | 2308 | cyclin B1 | #N/A | #N/A | 44.14 | 30.96 | 40.36 | -0.8 | 3.03 | 15.35 | | | |
| M32334_at | M32334 | 2333 | intercellular adhesion molecule 2 | #N/A | #N/A | 95.04 | 92.33 | 67.51 | 42.19 | 41.31 | 27.33 | | | |
| M55210_at | M55210 | 2353 | laminin, gamma 1 (formerly LAMB2) | 3.47 | 0.02551 | 137.63 | 115.85 | 102.71 | 27.07 | 29.17 | 12.36 | | | |
| M61916_at | M61916 | 2372 | laminin, beta 1 | 3.18 | 0.01171 | 75.1 | 67.4 | 61.41 | 7.19 | 7.98 | 8.99 | | | |

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | hcc | | | hcc | | | normal | normal | Std Dev |
|----------------|---------|--------|--|--------|---------|--------|--------|------|---------|---------|--------|---------|--------|---------|
| | | | | change | p value | sample | set 2: | Mean | sample | set 2: | Mean | set 2: | set 2: | |
| | | | | in hcc | | set 2: | Median | | set 2: | Std Dev | | Median | | |
| | | | stress-induced- | | | | | | | | | | | |
| | | | phosphoprotein 1 | | | | | | | | | | | |
| M86752_at | M86752 | 2412 | (Hsp70/Hsp90-organizing protein) | 5.15 | 0.02881 | 216.51 | 248.21 | | 192.98 | | 8.67 | 20.63 | | 39.03 |
| M87339_at | M87339 | 2415 | replication factor C (activator 1) 4 (37kD) | 4.59 | 0.00116 | 110.39 | 82.61 | | 79.29 | | 4.26 | 9.92 | | 16.79 |
| M94250_at | M94250 | 2426 | midkine (neurite growth-promoting factor 2) | 9.86 | 0.02104 | 690.32 | 193.74 | | 1414.43 | | -155.4 | -175.43 | | 101.89 |
| S72904_at | S72904 | 3031 | cytosolic ovarian carcinoma antigen 1 | #N/A | #N/A | 29.33 | 29.21 | | 18.34 | | 11.53 | 12.85 | | 7.55 |
| S78187_at | S78187 | 3036 | cell division cycle 25B | 4.83 | 0.00547 | 143.52 | 115.3 | | 109.13 | | 3.36 | -1.2 | | 26.9 |
| S78569_at | S78569 | 3037 | laminin, alpha 4 | #N/A | #N/A | 25.79 | 26.91 | | 21.66 | | 6.3 | 7.6 | | 9.38 |
| U38847_at | U38847 | 3357 | TAR (HIV) RNA-binding protein 1 | #N/A | #N/A | 83.43 | 70.23 | | 66.3 | | 15.7 | 17.43 | | 10.2 |
| U51477_at | U51477 | 3384 | diacylglycerol kinase, zeta (104kD) | #N/A | #N/A | 73.85 | 61.64 | | 31.81 | | 36.35 | 36.29 | | 23.02 |
| U59321_at | U59321 | 3398 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) | 3.12 | 0.02469 | 84.5 | 98.2 | | 70.13 | | 3.1 | -1.83 | | 19.73 |
| U66661_at | U66661 | 3406 | gamma-aminobutyric acid (GABA) A receptor, epsilon | 3.55 | 0.0045 | 97.79 | 83.66 | | 61.79 | | 16.58 | 14.81 | | 11.96 |
| U93237_rna2_at | U93237 | 3462 | multiple endocrine neoplasia I | #N/A | #N/A | 84.78 | 93.3 | | 24.25 | | 45.63 | 45.39 | | 17.66 |
| X92106_at | X92106 | 3822 | bleomycin hydrolase | #N/A | #N/A | 56.15 | 48.48 | | 36.93 | | 4.73 | 3.77 | | 11.78 |

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in hcc | hcc | | | hcc | | | normal | normal | normal |
|--------------------|----------|--------|--|--------------------|--------|---------|--------------------|----------------------|-----------------------|-------------|--------|--------|--------|
| | | | | | set 2 | p value | sample set 2: Mean | sample set 2: Median | sample set 2: Std Dev | set 2: Mean | | | |
| X92762_at | X92762 | 3828 | tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome) | #N/A | #N/A | 82.96 | 83.94 | 15.05 | 23.4 | 33.5 | 24.15 | | |
| Y09216_at | Y09216 | 3856 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 | #N/A | #N/A | 47.87 | 47.61 | 18.08 | 18.99 | 22.48 | 13.31 | | |
| M69013_at | M69013 | 2391 | guanine nucleotide binding protein (G protein), alpha 11 (Gq class) | #N/A | #N/A | 86.89 | 70.61 | 47.65 | 38.18 | 47.33 | 23.06 | | |
| AD000092_cds7_s_at | AD000092 | 1542 | RAD23 (S. cerevisiae) homolog A | #N/A | #N/A | 97.12 | 98.23 | 25.66 | 37.18 | 32.35 | 28.04 | | |
| X04654_s_at | X04654 | 3681 | small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) | #N/A | #N/A | 122.45 | 134.9 | 49.51 | 42.22 | 41.24 | 17.18 | | |
| M31211_s_at | M31211 | 2326 | myosin, light polypeptide 1, alkali; skeletal, fast protein kinase, interferon-inducible double stranded | #N/A | #N/A | 60.22 | 49.75 | 54.83 | -2.19 | -4.38 | 11.56 | | |
| U50648_s_at | U50648 | 3379 | RNA dependent | #N/A | #N/A | 214.34 | 192.86 | 122.38 | 105.38 | 92.58 | 43.12 | | |
| M74715_s_at | M74715 | 2395 | iduronidase, alpha-L-a disintegrin and metalloproteinase domain 15 (metargidin) | #N/A | #N/A | 122.69 | 121.95 | 72.58 | 41.88 | 24.48 | 43.99 | | |
| U41767_s_at | U41767 | 3360 | tropomyosin 2 (beta) | #N/A | #N/A | 196.76 | 147.11 | 113.93 | 83.03 | 66.93 | 68.33 | | |
| M12125_at | M12125 | 2241 | sulfolipase family 1A, phenol-prefering, member 3 | 7.13 | 0.0004 | 174.25 | 183.97 | 95.24 | 13.01 | 16.33 | 11.64 | | |
| U20499_at | U20499 | 3321 | | #N/A | #N/A | 141.35 | 126.33 | 135.57 | 48.34 | 54.37 | 24.69 | | |

Table 8B. Genes and ESTs expressed only in normal liver compared to hepatocellular carcinoma.

| Affy ID | Genbank | Seq ID | Known Gene Name | hcc fold | | | hcc | | | hcc | | | normal | | | normal | | |
|------------------|----------|--------|---|----------|---------|-------------|---------------|---------|-------------|---------------|---------|-------------|-------------|----------------|----------------|----------------|----------------|----------------|
| | | | | change | p value | set 2: Mean | sample Median | std Dev | set 2: Mean | sample Median | std Dev | set 2: Mean | set 2: Mean | set 2: Std Dev | set 2: Std Dev | set 2: Std Dev | set 2: Std Dev | set 2: Std Dev |
| rc_AA010205_at | AA010205 | 23 | EST | 5.71 | 0.00014 | 26.95 | 20.06 | 32.19 | 187.55 | 154.99 | 92.13 | 187.55 | 154.99 | 92.13 | 187.55 | 154.99 | 92.13 | 92.13 |
| rc_AA013095_s_at | AA013095 | 33 | potassium voltage-gated channel, shaker-related | #N/A | #N/A | 5.12 | 7.9 | 12.98 | 18.56 | 15.83 | 8.24 | 18.56 | 15.83 | 8.24 | 18.56 | 15.83 | 8.24 | 8.24 |
| rc_AA046747_at | AA046747 | 114 | EST | 4.77 | 0.00023 | -0.57 | 3.68 | 23.81 | 113.78 | 88.54 | 66.41 | 113.78 | 88.54 | 66.41 | 113.78 | 88.54 | 66.41 | 66.41 |
| rc_AA074885_at | AA074885 | 161 | macrophage receptor with | 10.88 | 0.00087 | 35.67 | 58.01 | 44.34 | 652.03 | 761.74 | 300.57 | 652.03 | 761.74 | 300.57 | 652.03 | 761.74 | 300.57 | 300.57 |
| rc_AA099225_at | AA099225 | 206 | EST | 6.59 | 0.00064 | 10.9 | 9.75 | 15.11 | 212.68 | 163.45 | 194.31 | 212.68 | 163.45 | 194.31 | 212.68 | 163.45 | 194.31 | 194.31 |
| rc_AA253410_at | AA253410 | 564 | EST | #N/A | #N/A | 3.66 | 1.48 | 10.67 | 49.37 | 26.82 | 45.2 | 49.37 | 26.82 | 45.2 | 49.37 | 26.82 | 45.2 | 45.2 |
| rc_AA281796_at | AA281796 | 650 | mannose-P-dolichol utilization | #N/A | #N/A | 95.74 | 105.86 | 45.46 | 170.88 | 165.02 | 41.87 | 170.88 | 165.02 | 41.87 | 170.88 | 165.02 | 41.87 | 41.87 |
| rc_AA282541_at | AA282541 | 661 | EST | #N/A | #N/A | 17.21 | 11.75 | 13.38 | 31.31 | 29.9 | 13.53 | 31.31 | 29.9 | 13.53 | 31.31 | 29.9 | 13.53 | 13.53 |
| rc_AA285053_at | AA285053 | 681 | EST | 5 | 0.00718 | 36.49 | 20.15 | 49.24 | 238.16 | 242.27 | 169.12 | 238.16 | 242.27 | 169.12 | 238.16 | 242.27 | 169.12 | 169.12 |
| rc_AA287566_at | AA287566 | 690 | KIAA0187 gene product | 6.99 | 0.00023 | 18.67 | 14.05 | 35.71 | 246.24 | 201.66 | 228.64 | 246.24 | 201.66 | 228.64 | 246.24 | 201.66 | 228.64 | 228.64 |
| rc_AA404248_at | AA404248 | 847 | EST | #N/A | #N/A | 24.05 | 30.59 | 15.83 | 40.92 | 35.06 | 17.49 | 40.92 | 35.06 | 17.49 | 40.92 | 35.06 | 17.49 | 17.49 |
| rc_AA448002_at | AA448002 | 1113 | putative type II membrane | 14.14 | 0 | 39.9 | 38.99 | 13.33 | 594.13 | 528.63 | 282.58 | 594.13 | 528.63 | 282.58 | 594.13 | 528.63 | 282.58 | 282.58 |
| rc_AA460661_at | AA460661 | 1229 | EST | 5.46 | 0.00151 | 20.05 | 8.57 | 39.04 | 184.62 | 198.21 | 108.17 | 184.62 | 198.21 | 108.17 | 184.62 | 198.21 | 108.17 | 108.17 |
| rc_AA487576_at | AA487576 | 1357 | EST | #N/A | #N/A | 11.67 | 2.42 | 27.75 | 26.05 | 25.27 | 11.13 | 26.05 | 25.27 | 11.13 | 26.05 | 25.27 | 11.13 | 11.13 |
| rc_AA621235_at | AA621235 | 1517 | EST | #N/A | #N/A | 65.79 | 68.63 | 35.33 | 114.75 | 113.36 | 65.35 | 114.75 | 113.36 | 65.35 | 114.75 | 113.36 | 65.35 | 65.35 |
| rc_F09979_at | F09979 | 1809 | EST | #N/A | #N/A | 61.21 | 6.31 | 128.69 | 226.47 | 116.41 | 288.21 | 226.47 | 116.41 | 288.21 | 226.47 | 116.41 | 288.21 | 288.21 |
| rc_F10380_at | F10380 | 1816 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase | #N/A | #N/A | 43.64 | 47.09 | 18.15 | 106.49 | 93.71 | 83.35 | 106.49 | 93.71 | 83.35 | 106.49 | 93.71 | 83.35 | 83.35 |
| rc_H57056_at | H57056 | 1953 | EST | #N/A | #N/A | -1.79 | -7.37 | 11.38 | 35.07 | 38.32 | 17.88 | 35.07 | 38.32 | 17.88 | 35.07 | 38.32 | 17.88 | 17.88 |
| rc_H58673_at | H58673 | 1959 | EST | 15.49 | 0.00002 | 34.96 | 26.37 | 38.53 | 652.47 | 677.55 | 376.36 | 652.47 | 677.55 | 376.36 | 652.47 | 677.55 | 376.36 | 376.36 |
| rc_H59136_at | H59136 | 1962 | EST | 6.63 | 0.00033 | 33.12 | 21.17 | 42.92 | 250.23 | 229.94 | 129.12 | 250.23 | 229.94 | 129.12 | 250.23 | 229.94 | 129.12 | 129.12 |
| H66367_at | H66367 | 1977 | EST | 3.84 | 0.00133 | 37.14 | 35.15 | 26.61 | 155.38 | 149.31 | 70.77 | 155.38 | 149.31 | 70.77 | 155.38 | 149.31 | 70.77 | 70.77 |
| H72650_at | H72650 | 1994 | EST | #N/A | #N/A | 78.97 | 93.74 | 40.9 | 122 | 125 | 42.24 | 122 | 125 | 42.24 | 122 | 125 | 42.24 | 42.24 |
| rc_H87765_at | H87765 | 2017 | KIAA0626 gene product | 3.94 | 0.00123 | 10.11 | 10.07 | 4.23 | 94.26 | 93.78 | 60.64 | 94.26 | 93.78 | 60.64 | 94.26 | 93.78 | 60.64 | 60.64 |
| M10943_at | M10943 | 2234 | metallothionein 1F (functional) | 6.23 | 0.00007 | 35.67 | 28.76 | 22.4 | 217.65 | 186.71 | 86.73 | 217.65 | 186.71 | 86.73 | 217.65 | 186.71 | 86.73 | 86.73 |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, | 3.82 | 0.00131 | -15.66 | -12.63 | 23.86 | 93.07 | 86.04 | 61.35 | 93.07 | 86.04 | 61.35 | 93.07 | 86.04 | 61.35 | 61.35 |
| M63967_at | M63967 | 2378 | aldehyde dehydrogenase 5 | 3.88 | 0.00274 | 40.43 | 30.04 | 29.05 | 164.38 | 178.74 | 87.39 | 164.38 | 178.74 | 87.39 | 164.38 | 178.74 | 87.39 | 87.39 |

Table 8B. Genes and ESTs expressed only in normal liver compared to hepatocellular carcinoma.

| Affy ID | Genbank | Seq ID | Known Gene Name | hcc fold change | p value | hcc sample | | | hcc normal | | | normal set 2: Median | normal set 2: Std Dev |
|----------------|---------|--------|----------------------------------|-----------------|---------|-------------|---------------|----------------|-------------|----------------|-------------|----------------------|-----------------------|
| | | | | | | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Mean | set 2: Std Dev | set 2: Mean | | |
| rc_N22404_at | N22404 | 2450 | EST | 3.44 | 0.02267 | 56.69 | 35.82 | 73.26 | 193.63 | 130.09 | 162.83 | | |
| rc_N34919_at | N34919 | 2499 | EST | #N/A | #N/A | 19.32 | 19.72 | 14.37 | 52.96 | 44.23 | 24.23 | | |
| rc_N54604_at | N54604 | 2570 | EST | #N/A | #N/A | 45.27 | 14.34 | 81.45 | 133.06 | 119.1 | 109.95 | | |
| rc_N65959_at | N65959 | 2612 | EST | 3.38 | 0.00785 | 37.8 | 28.94 | 31.45 | 142.87 | 149.26 | 79.26 | | |
| rc_N67105_at | N67105 | 2624 | EST | 4.69 | 0.00194 | 12.46 | 10.45 | 12.64 | 143.36 | 102.9 | 121.4 | | |
| rc_N69114_at | N69114 | 2644 | nuclear receptor subfamily 1, | #N/A | #N/A | 12.69 | 5.95 | 15.01 | 72.29 | 73.28 | 57.34 | | |
| rc_N74624_at | N74624 | 2688 | collectin sub-family member 10 | #N/A | #N/A | 39.43 | 35.17 | 24.21 | 71.81 | 62.09 | 43.57 | | |
| N99542_at | N99542 | 2747 | orosomucoid 1 | 3.53 | 0.00607 | 61.09 | 67.97 | 39.3 | 226.06 | 187.68 | 146.11 | | |
| rc_R09053_at | R09053 | 2783 | EST | 3.45 | 0.03074 | 64.12 | 36.33 | 102.03 | 186.87 | 204.61 | 113.19 | | |
| rc_R73816_at | R73816 | 2961 | EST | 7.05 | 0.01287 | 35.12 | 13.76 | 100.6 | 462.31 | 374.67 | 450.91 | | |
| rc_R99591_at | R99591 | 3016 | CD5 antigen-like (scavenger | 7.41 | 0.00043 | 124.14 | 139.76 | 50.35 | 1035.39 | 904.92 | 691.83 | | |
| rc_T58756_at | T58756 | 3156 | receptor cysteine rich family) | 16.61 | 0 | -1.02 | 1.06 | 24.36 | 390.04 | 386.76 | 164.41 | | |
| T68083_at | T68083 | 3185 | short-chain | #N/A | #N/A | 96.34 | 59.71 | 104.53 | 263.22 | 280.22 | 136.48 | | |
| rc_T68711_at | T68711 | 3188 | EST | 35.98 | 0.0003 | 29.03 | -33.95 | 176.15 | 1388.67 | 1074.67 | 890.91 | | |
| rc_W48860_at | W48860 | 3537 | EST | #N/A | #N/A | 37.25 | 31.7 | 27.5 | 52.69 | 41.31 | 21.1 | | |
| rc_W78093_at | W78093 | 3601 | X-prolyl aminopeptidase | #N/A | #N/A | 408.58 | 397.88 | 102.27 | 518.77 | 518.8 | 211.32 | | |
| rc_W85890_at | W85890 | 3623 | (aminopeptidase P) 2, | #N/A | #N/A | 60.91 | 60.47 | 23.73 | 70.98 | 66.52 | 24.66 | | |
| rc_W90018_f_at | W90018 | 3642 | EST | #N/A | #N/A | 21.51 | 1.31 | 56.9 | 59.32 | 53.19 | 41.68 | | |
| X54380_at | X54380 | 3730 | pregnancy-zone protein | 7.71 | 0.00069 | 15.11 | 8.07 | 27.07 | 274.41 | 255.4 | 203.47 | | |
| Z48475_at | Z48475 | 3943 | glucokinase (hexokinase 4) | 4.6 | 0.01693 | 65.99 | 51.37 | 146.72 | 305.23 | 239.52 | 155.98 | | |
| Z49269_at | Z49269 | 3945 | subfamily A (Cys-Cys), member 14 | 7.24 | 0.01047 | 138.63 | 66.95 | 201.93 | 526.13 | 532.29 | 166.67 | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | change | in metas | p value | metastatic: | | | normal | | |
|------------------|----------|--------|----------------------|-------|---------|---------|----------|---------|-------------|--------|---------|--------|--------|---------|
| | | | | | | | | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| rc_AA007160_at | AA007160 | 16 | EST | 6 | 0.01035 | 171.32 | 175.07 | 138.03 | 9.1 | 8.6 | 12.54 | | | |
| | | | diphtheria toxin | | | | | | | | | | | |
| | | | resistance protein | | | | | | | | | | | |
| | | | required for | | | | | | | | | | | |
| | | | diphthamide | | | | | | | | | | | |
| | | | biosynthesis | | | | | | | | | | | |
| | | | (Saccharomyces)-like | | | | | | | | | | | |
| AA009913_at | AA009913 | 21 | 2 | #N/A | #N/A | 69.53 | 81.03 | 27.69 | 16.81 | 18.22 | 13.51 | | | |
| rc_AA011134_at | AA011134 | 29 | EST | 28.79 | 0.00602 | 1157.47 | 566.78 | 1448.16 | -72.57 | -51.2 | 69.3 | | | |
| | | | DKFZP434G032 | | | | | | | | | | | |
| rc_AA024482_at | AA024482 | 45 | protein | #N/A | #N/A | 207.37 | 118.58 | 230.63 | -1.3 | -3.13 | 13.6 | | | |
| rc_AA026030_at | AA026030 | 53 | EST | 11.01 | 0.01649 | 566.65 | 284.32 | 828.49 | 3.02 | 4.66 | 40.87 | | | |
| | | | tyrosyl-tRNA | | | | | | | | | | | |
| rc_AA026270_at | AA026270 | 56 | synthetase | #N/A | #N/A | 201.1 | 224.51 | 50.82 | 76.85 | 76.68 | 45.22 | | | |
| | | | glutamate-cysteine | | | | | | | | | | | |
| | | | ligase (gamma- | | | | | | | | | | | |
| | | | glutamylcysteine | | | | | | | | | | | |
| | | | synthetase), | | | | | | | | | | | |
| rc_AA035540_at | AA035540 | 81 | regulatory (30.8kD) | #N/A | #N/A | 39.84 | 34.37 | 13.29 | 13.59 | 12.27 | 8.96 | | | |
| rc_AA040465_at | AA040465 | 95 | EST | 3.25 | 0.00146 | 161.91 | 125.35 | 72.19 | 47.15 | 45.53 | 5.48 | | | |
| rc_AA043944_at | AA043944 | 100 | EST | #N/A | #N/A | 52.9 | 29.13 | 46.43 | 3.69 | 3.15 | 7.26 | | | |
| rc_AA053033_at | AA053033 | 124 | EST | 7.83 | 0.00379 | 212.61 | 135.28 | 160.82 | 3.41 | -1.28 | 19.74 | | | |
| | | | cadherin 17, LI | | | | | | | | | | | |
| rc_AA053102_s_at | AA053102 | 125 | cadherin (liver- | | | | | | | | | | | |
| rc_AA053248_i_at | AA053248 | 126 | intestine) | 26.63 | 0.01745 | 1053.43 | 972.71 | 785.51 | 4.92 | 4.94 | 9.04 | | | |
| rc_AA053660_at | AA053660 | 128 | EST | 7.01 | 0.00003 | 2234.44 | 1595.15 | 1053.3 | 341.06 | 304.8 | 189.89 | | | |
| rc_AA055805_s_at | AA055805 | 132 | EST | 15.98 | 0.00003 | 1573.49 | 1340 | 820.5 | 95.24 | 79.97 | 42.99 | | | |
| | | | EST | 42.83 | 0.00142 | 1270.03 | 1026.97 | 1179.12 | -11.11 | -10.85 | 20.27 | | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: metastatic: | | | normal | | |
|------------------|----------|--------|---|-------------|---------|-------------------------|---------|---------|-------------|---------------|----------------|
| | | | | in metas | p value | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA055811_s_at | AA055811 | 133 | glycoprotein A33 (transmembrane) | 6.86 | 0.02152 | 236.18 | 196.53 | 171.06 | 14.84 | 17.82 | 17.5 |
| rc_AA055896_at | AA055896 | 135 | collagen, type V, alpha 1 | 18.16 | 0.00146 | 540.67 | 538.43 | 382 | -3.14 | -5.8 | 33.88 |
| rc_AA084343_at | AA084343 | 178 | EST | #N/A | #N/A | 133.86 | 126.19 | 19.99 | 84.58 | 76.82 | 41.45 |
| | | | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | | | | | | | | |
| rc_AA100719_s_at | AA100719 | 212 | vaccinia related kinase 1 | 50.88 | 0.00081 | 1405.2 | 1264.79 | 1137.97 | -17.03 | -22.23 | 16.43 |
| rc_AA112979_s_at | AA112979 | 225 | mitotic spindle coiled-coil related protein | #N/A | #N/A | 25.08 | 24.98 | 13.02 | 8.54 | 8.02 | 2.59 |
| rc_AA115979_at | AA115979 | 232 | EST | #N/A | #N/A | 74.58 | 89.38 | 66.52 | 22.91 | 13.67 | 29.42 |
| rc_AA126041_at | AA126041 | 244 | EST | #N/A | #N/A | 42.91 | 33.83 | 16.2 | 26.42 | 28.92 | 9.81 |
| AA127712_at | AA127712 | 255 | EST | 6.59 | 0.03706 | 332.45 | 208.85 | 296.68 | -29.54 | -28.71 | 104.37 |
| | | | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) | | | | | | | | |
| rc_AA128553_f_at | AA128553 | 260 | EST | #N/A | #N/A | 87.35 | 102.82 | 24.17 | 114.91 | 108.16 | 30.28 |
| rc_AA131162_s_at | AA131162 | 266 | EST | 4.68 | 0.00042 | 117.43 | 123.78 | 39.05 | 11.86 | 13.57 | 19.83 |
| rc_AA134968_at | AA134968 | 289 | EST | 12.11 | 0.00079 | 322.34 | 208.47 | 256.66 | 10.04 | 7.96 | 15.53 |
| rc_AA150053_at | AA150053 | 327 | EST | 3.71 | 0.00102 | 309.61 | 304.16 | 82.48 | 101.87 | 88.37 | 73.73 |
| | | | matrix metalloproteinase 23B | | | | | | | | |
| rc_AA151428_s_at | AA151428 | 335 | serine protease, umbilical endothelium | 7.15 | 0.00056 | 174.77 | 131.66 | 104.51 | 3.23 | 10.67 | 24.39 |
| rc_AA156243_at | AA156243 | 340 | | 41.44 | 0.00139 | 1255.4 | 547.15 | 1189.26 | 9.32 | 11.44 | 9.39 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: metastatic: | | | | normal | | | |
|------------------|----------|--------|--------------------------|-------------|---------|-------------------------|---------|---------|--------|--------|---------|--------|---------|
| | | | | in metas | p value | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Std Dev |
| rc_AA157857_s_at | AA157857 | 350 | keratin 19 | #N/A | #N/A | 2728.74 | 2917.98 | 1076.95 | -13.21 | -14.4 | 15.84 | -13.21 | 15.84 |
| rc_AA159525_at | AA159525 | 354 | EST | 49.39 | 0.00062 | 1309.05 | 1107.08 | 965.67 | -32.72 | -28.32 | 20.11 | -32.72 | 20.11 |
| rc_AA161043_at | AA161043 | 356 | tetraspan 1 | 18.8 | 0.00015 | 1477.19 | 932.02 | 1467.59 | 70.82 | 58.62 | 42.88 | 70.82 | 42.88 |
| rc_AA171760_at | AA171760 | 367 | EST | 17.86 | 0 | 645.43 | 578.38 | 312.37 | 28.03 | 16.24 | 57.21 | 28.03 | 57.21 |
| | | | polyglutamine binding | | | | | | | | | | |
| rc_AA179787_at | AA179787 | 380 | protein 1 | 6.44 | 0.00206 | 191.33 | 171.71 | 138.9 | -11.56 | -12.46 | 42.46 | -11.56 | 42.46 |
| rc_AA179845_at | AA179845 | 381 | EST | 5.77 | 0.01414 | 280.06 | 335.41 | 172.62 | 37.43 | 37.69 | 14.87 | 37.43 | 14.87 |
| rc_AA181600_at | AA181600 | 384 | EST | 5.38 | 0.03316 | 166.88 | 94.16 | 153.49 | -40.51 | -47.81 | 24.34 | -40.51 | 24.34 |
| rc_AA196790_at | AA196790 | 421 | EST | 7.64 | 0.00287 | 239.45 | 275.18 | 142.37 | 22.91 | 26.8 | 10.54 | 22.91 | 10.54 |
| rc_AA211483_at | AA211483 | 435 | EST | 44.07 | 0.00175 | 1300.23 | 1303.61 | 1051.58 | -29.25 | -34.99 | 17.49 | -29.25 | 17.49 |
| rc_AA227926_at | AA227926 | 460 | EST | 6.81 | 0.01701 | 228.91 | 120.1 | 243.92 | 16.24 | 14.21 | 6.86 | 16.24 | 6.86 |
| rc_AA232508_at | AA232508 | 464 | EST | #N/A | #N/A | 464 | 533.98 | 266.87 | 170.48 | 156.89 | 104.75 | 170.48 | 104.75 |
| | | | general transcription | | | | | | | | | | |
| | | | factor IIIC, polypeptide | | | | | | | | | | |
| | | | 1 (alpha subunit, | | | | | | | | | | |
| rc_AA233290_at | AA233290 | 469 | 220kD) | #N/A | #N/A | 56.54 | 43.91 | 22.15 | 28.32 | 31.59 | 25.36 | 28.32 | 25.36 |
| rc_AA234096_at | AA234096 | 479 | EST | 23.72 | 0.00018 | 607.06 | 420.34 | 366.53 | -3.47 | 1.73 | 30.91 | -3.47 | 30.91 |
| rc_AA234346_at | AA234346 | 480 | EST | #N/A | #N/A | 36.98 | 39.47 | 12.81 | 6.21 | 6.79 | 19.99 | 6.21 | 19.99 |
| rc_AA234362_at | AA234362 | 481 | EST | 3.89 | 0.03524 | 116.26 | 75.37 | 105.77 | -1.86 | -4.2 | 16.67 | -1.86 | 16.67 |
| | | | survival of motor | | | | | | | | | | |
| | | | neuron protein | | | | | | | | | | |
| rc_AA234365_at | AA234365 | 482 | interacting protein 1 | #N/A | #N/A | 56.37 | 42.6 | 34.73 | 12.96 | 16.93 | 12.99 | 12.96 | 12.99 |
| rc_AA234706_at | AA234706 | 488 | EST | #N/A | #N/A | 68.33 | 53.21 | 21.55 | 49.66 | 39.76 | 42.06 | 49.66 | 42.06 |
| rc_AA235707_at | AA235707 | 500 | EST | 9.17 | 0.00005 | 189.42 | 161.88 | 57.05 | -18.19 | -19.06 | 14.8 | -18.19 | 14.8 |
| | | | ecotropic viral | | | | | | | | | | |
| rc_AA236533_s_at | AA236533 | 514 | integration site 1 | 4.01 | 0.02882 | 106.15 | 76.05 | 78.18 | -16.45 | -14.04 | 8.52 | -16.45 | 8.52 |
| rc_AA243173_at | AA243173 | 526 | EST | 8.75 | 0.00003 | 384.86 | 482.53 | 162.08 | 41.66 | 40.74 | 27.31 | 41.66 | 27.31 |
| | | | apoptosis inhibitor 4 | | | | | | | | | | |
| rc_AA252994_at | AA252994 | 557 | (survivin) | 3.55 | 0.00075 | 152.63 | 140.53 | 31.01 | 50.23 | 40.59 | 35.61 | 50.23 | 35.61 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastatic: metastatic: | | | normal | | | | |
|---------------------|----------|--------|------------------------|-------------------------|---------|-------------------------|---------|---------|-------------|---------------|----------------|--|--|
| | | | | | | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | | |
| adaptor-related | | | | | | | | | | | | | |
| protein complex 1, | | | | | | | | | | | | | |
| AA253330_s_at | AA253330 | 562 | gamma 1 subunit | 3.87 | 0.00708 | 219.95 | 186.12 | 141.92 | 47.32 | 51.59 | 30.28 | | |
| rc_AA253473_at | AA253473 | 567 | EST | 15.23 | 0.00171 | 375.2 | 435.68 | 216.18 | -4.38 | -3.19 | 12.35 | | |
| rc_AA255566_at | AA255566 | 570 | EST | #N/A | #N/A | 63.43 | 65.2 | 30.17 | 16.18 | 14.38 | 13.17 | | |
| rc_AA256642_at | AA256642 | 582 | EST | 11.17 | 0.00035 | 266.31 | 275.43 | 135.85 | 0.78 | -1.34 | 15.74 | | |
| WW domain binding | | | | | | | | | | | | | |
| protein 4 (formin | | | | | | | | | | | | | |
| rc_AA258836_at | AA258836 | 601 | binding protein 21) | #N/A | #N/A | 41.9 | 44.58 | 13.6 | 26.08 | 23.64 | 10.4 | | |
| rc_AA262943_at | AA262943 | 611 | EST | 13.42 | 0.00234 | 430.7 | 207.29 | 511.01 | -1.08 | -6.93 | 19.06 | | |
| neuroblastoma- | | | | | | | | | | | | | |
| rc_AA281214_s_at | AA281214 | 643 | amplified protein | #N/A | #N/A | 130.98 | 133.63 | 68.42 | 69.89 | 53.91 | 39.31 | | |
| rc_AA282505_at | AA282505 | 659 | EST | #N/A | #N/A | 461.54 | 478.83 | 622.39 | -41.45 | -17 | 98.17 | | |
| putative G protein- | | | | | | | | | | | | | |
| rc_AA291259_at | AA291259 | 697 | coupled receptor | #N/A | #N/A | 112.28 | 45.1 | 113.44 | 1.53 | 1.88 | 6.06 | | |
| AA291456_s_at | AA291456 | 700 | EST | 3.96 | 0.03633 | 1808.4 | 1273.75 | 1481.84 | 671.21 | 509.58 | 629.13 | | |
| rc_AA292765_at | AA292765 | 712 | ZW10 interactor | 7.14 | 0.02623 | 230.83 | 166.72 | 232.16 | 11.33 | 18.29 | 13.27 | | |
| rc_AA292931_at | AA292931 | 715 | EST | 3.97 | 0.00067 | 230.65 | 260.43 | 79.42 | 57.32 | 61.89 | 18.62 | | |
| AA295819_s_at | AA295819 | 722 | EST | 8 | 0.01793 | 230.14 | 251.43 | 146.89 | -14.93 | -20.8 | 19.72 | | |
| rc_AA331393_at | AA331393 | 739 | EST | 16.73 | 0.00848 | 600.02 | 315.98 | 598.52 | 5.08 | 3.88 | 9.43 | | |
| rc_AA335191_f_at | AA335191 | 741 | creatine kinase, brain | 47.35 | 0.00419 | 3540.65 | 3971.43 | 3135.19 | 43.84 | 33.21 | 43.52 | | |
| mutY (E. coli) | | | | | | | | | | | | | |
| rc_AA349792_s_at | AA349792 | 759 | homolog | #N/A | #N/A | 525.17 | 553.97 | 245.2 | 221.5 | 212.24 | 98.86 | | |
| rc_AA372018_at | AA372018 | 768 | EST | 14.3 | 0.00178 | 363.44 | 220.03 | 261.04 | -2.44 | -3.09 | 8.36 | | |
| differentially | | | | | | | | | | | | | |
| expressed in | | | | | | | | | | | | | |
| hematopoietic | | | | | | | | | | | | | |
| AA372630_s_at | AA372630 | 769 | lineages | 25.49 | 0.01743 | 2094.32 | 436.62 | 3873.61 | 6.67 | 4.87 | 7.16 | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: metastatic: | | | normal | | |
|----------------|----------|--------|--|-------------|---------|-------------------------|---------|---------|-------------|---------------|----------------|
| | | | | in metas | p value | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| AA384184_s_at | AA384184 | 774 | DKFZP586B0519 protein laminin receptor 1 (67kD, ribosomal protein SA) | 3.38 | 0.01209 | 476.17 | 411.64 | 148.86 | 181.02 | 188.54 | 135.4 |
| rc_AA394121_at | AA394121 | 778 | protein SA) | 23.78 | 0.00099 | 788.51 | 677.33 | 612.74 | 0.21 | -8.38 | 31.59 |
| rc_AA398908_at | AA398908 | 801 | EST | 38.69 | 0.01089 | 1678.58 | 1796.68 | 1500.48 | -174.29 | -216.08 | 104.42 |
| rc_AA399226_at | AA399226 | 803 | tight junction protein 3 (zona occludens 3) tumor suppressor deleted in oral cancer- related 1 | 3.59 | 0.02002 | 89.54 | 78.97 | 63.98 | -5.01 | -6.48 | 11.33 |
| rc_AA401965_at | AA401965 | 833 | related 1 | #N/A | #N/A | 384.12 | 271.95 | 444.06 | 120.58 | 93.29 | 109.41 |
| rc_AA404597_at | AA404597 | 854 | EST | #N/A | #N/A | 624.37 | 495.56 | 274.8 | 379.26 | 336.33 | 167.43 |
| rc_AA405715_at | AA405715 | 862 | hypothetical protein | 4.68 | 0.00898 | 152.23 | 138.92 | 96.78 | 24.47 | 27.3 | 11.75 |
| rc_AA406542_at | AA406542 | 878 | EST | 8.27 | 0.00724 | 230.18 | 170.94 | 206.8 | -1.99 | 1.49 | 12.75 |
| rc_AA410469_at | AA410469 | 883 | EST | 6.3 | 0.00103 | 337.03 | 250.11 | 264.1 | 50.51 | 42.79 | 60.18 |
| rc_AA419217_at | AA419217 | 923 | DKFZP586E1422 protein anterior gradient 2 (Xenopus laevis) | 6.77 | 0.00045 | 276.53 | 215.37 | 172.25 | 36.93 | 36.7 | 21.88 |
| rc_AA421562_at | AA421562 | 934 | homolog | 56.3 | 0.0041 | 2556.78 | 792 | 3323.39 | 14.22 | 15.72 | 6.54 |
| rc_AA422086_at | AA422086 | 938 | EST | 10.71 | 0.03418 | 828.27 | 598.22 | 800.79 | 39.48 | 34.98 | 23.29 |
| rc_AA422150_at | AA422150 | 939 | cytochrome P540 family member | 17.14 | 0.00108 | 664.26 | 609.99 | 475.91 | 28.76 | 27.53 | 22.47 |
| rc_AA424487_at | AA424487 | 945 | predicted from ESTs | 38.41 | 0.00002 | 2689.32 | 1863.02 | 1900.51 | 67.92 | 61.95 | 46.24 |
| rc_AA424881_at | AA424881 | 949 | EST | 6.3 | 0.00556 | 158.13 | 155.45 | 82.63 | -16.85 | -22.15 | 20.49 |
| rc_AA425279_at | AA425279 | 951 | quiescin Q6 | 6.15 | 0.00083 | 221.93 | 181.8 | 167.44 | 18.33 | 22.33 | 44.81 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastatic: | | | normal | | | | |
|-----------------------|----------|--------|--------------------------|-------------------------|---------|-------------|---------|---------|--------|--------|---------|--|--|
| | | | | | | Mean | Median | Std Dev | Mean | Median | Std Dev | | |
| serine/threonine | | | | | | | | | | | | | |
| kinase 24 (Ste20, | | | | | | | | | | | | | |
| rc_AA425401_at | AA425401 | 954 | yeast homolog) | 3.22 | 0.00625 | 246.6 | 166.4 | 175.99 | 76.4 | 78.33 | 43.72 | | |
| rc_AA425852_i_at | AA425852 | 958 | EST | 4.8 | 0.03874 | 149.8 | 125.7 | 128.03 | 7.02 | 5.22 | 4.75 | | |
| ATP-binding cassette, | | | | | | | | | | | | | |
| sub-family F (GCN20), | | | | | | | | | | | | | |
| rc_AA427460_s_at | AA427460 | 972 | member 2 | #N/A | #N/A | 215.08 | 135.22 | 216.95 | 92.5 | 83.63 | 49.3 | | |
| AA427468_s_at | AA427468 | 973 | claudin 4 | 84.43 | 0 | 5646.4 | 5344.98 | 1581.19 | 72.58 | 64.85 | 87.74 | | |
| rc_AA427636_at | AA427636 | 976 | EST | 19.23 | 0.00145 | 511.98 | 500.83 | 299.69 | 6.19 | 3.7 | 15.84 | | |
| serine protease | | | | | | | | | | | | | |
| rc_AA429009_at | AA429009 | 994 | inhibitor, Kunitz type 1 | 30.04 | 0.00001 | 1010.32 | 1100.19 | 472.23 | -2.97 | -24.67 | 62.21 | | |
| cisplatin resistance | | | | | | | | | | | | | |
| rc_AA429890_s_at | AA429890 | 1004 | associated | 12.51 | 0.00053 | 1225.72 | 590.09 | 992.47 | 90.02 | 67.23 | 59.35 | | |
| rc_AA430674_at | AA430674 | 1018 | EST | 15.11 | 0.00293 | 454.82 | 306.15 | 378.36 | -71.57 | -82.03 | 59.56 | | |
| rc_AA436616_at | AA436616 | 1056 | EST | 3.18 | 0.04402 | 79.96 | 91.35 | 62.83 | -0.73 | 3.24 | 15.36 | | |
| rc_AA442763_at | AA442763 | 1072 | cyclin B2 | 5.09 | 0.02168 | 136.16 | 109.91 | 91.52 | -14.64 | -15.1 | 13.08 | | |
| v-Ha-ras Harvey rat | | | | | | | | | | | | | |
| sarcoma viral | | | | | | | | | | | | | |
| rc_AA443316_s_at | AA443316 | 1075 | oncogene homolog | 4.13 | 0.01729 | 191.06 | 173.3 | 113.42 | 40.07 | 41.12 | 32.54 | | |
| tumor suppressing | | | | | | | | | | | | | |
| subtransferable | | | | | | | | | | | | | |
| rc_AA443941_at | AA443941 | 1085 | candidate 1 | 3.57 | 0.01685 | 137.02 | 138.22 | 83.35 | 31.09 | 34.9 | 16.61 | | |
| rc_AA447687_at | AA447687 | 1104 | EST | 11.42 | 0.00362 | 306.28 | 178.65 | 244.12 | -16.27 | -14.45 | 8.55 | | |
| rc_AA447991_at | AA447991 | 1112 | EST | 4.99 | 0.00173 | 279.79 | 234.63 | 161.24 | 64.49 | 40.73 | 53.34 | | |
| rc_AA449456_at | AA449456 | 1126 | EST | 6.29 | 0.00087 | 847.4 | 775.81 | 377.99 | 160.93 | 178.76 | 112.71 | | |
| rc_AA451877_at | AA451877 | 1138 | EST | 8.63 | 0.00489 | 239.55 | 157.3 | 244.02 | -27.28 | -27.59 | 18.28 | | |
| rc_AA454597_s_at | AA454597 | 1166 | EST | 3.63 | 0.0067 | 268.15 | 274.94 | 167.72 | 66.6 | 57.29 | 23.41 | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: metastatic: | | | normal normal | | |
|---|----------|--------|-----------------------|-------------|---------|-------------------------|---------|---------|---------------|---------------|----------------|
| | | | | in metas | p value | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| KIAA0144 gene | | | | | | | | | | | |
| AA454908_s_at | AA454908 | 1171 | product | 9.3 | 0.00539 | 320.03 | 253.32 | 238.5 | -33.7 | -46.73 | 73.56 |
| rc_AA457235_at | AA457235 | 1200 | EST | #N/A | #N/A | 481.26 | 138.32 | 573.73 | 11.06 | 17.32 | 15.26 |
| rc_AA459254_at | AA459254 | 1211 | EST | 5.36 | 0.0259 | 403.69 | 194.85 | 401.21 | 51.84 | 43.51 | 37.57 |
| rc_AA460666_at | AA460666 | 1231 | EST | #N/A | #N/A | 56.19 | 58.13 | 26.29 | -24.55 | -17.23 | 20.98 |
| rc_AA463861_at | AA463861 | 1251 | EST | 24.79 | 0.00096 | 672.22 | 311.71 | 641.54 | -22.02 | -20.04 | 16.5 |
| rc_AA464962_at | AA464962 | 1264 | EST | #N/A | #N/A | 61.02 | 56.4 | 30.98 | 20.99 | 14.37 | 19.64 |
| rc_AA465342_at | AA465342 | 1271 | EST | #N/A | #N/A | 113.36 | 100.15 | 87.62 | 30.07 | 33.06 | 23.97 |
| rc_AA465660_at | AA465660 | 1273 | LIM domain binding 1 | #N/A | #N/A | 171.26 | 118.15 | 103.39 | 124.59 | 105.93 | 56.71 |
| tumor necrosis factor receptor superfamily, member 12 | | | | | | | | | | | |
| (translocating chain-association | | | | | | | | | | | |
| rc_AA476749_s_at | AA476749 | 1286 | membrane protein) | #N/A | #N/A | 53.23 | 44.04 | 18.16 | 25.5 | 29.62 | 11.96 |
| rc_AA477561_at | AA477561 | 1292 | EST | #N/A | #N/A | 160.87 | 104.95 | 133.7 | 63.83 | 76.56 | 37.87 |
| rc_AA478556_at | AA478556 | 1303 | EST | #N/A | #N/A | 172.35 | 136.55 | 120.49 | 143.25 | 134.62 | 109.1 |
| rc_AA482546_s_at | AA482546 | 1336 | KIAA0124 protein | 4.41 | 0.00604 | 181.72 | 113.91 | 140.73 | 38.26 | 30.26 | 32.72 |
| chromosome 6 open reading frame 1 | | | | | | | | | | | |
| rc_AA491208_at | AA491208 | 1388 | reading frame 1 | #N/A | #N/A | 159.88 | 143.86 | 80.49 | 123.37 | 131.81 | 47.97 |
| rc_AA599244_at | AA599244 | 1448 | KIAA0530 protein | 3.39 | 0.01246 | 77.48 | 78.85 | 37.98 | 7.71 | 6.06 | 7.11 |
| rc_AA599585_at | AA599585 | 1454 | EST | #N/A | #N/A | 66.17 | 48.91 | 48.12 | -12.47 | -17.55 | 21.82 |
| rc_AA609013_s_at | AA609013 | 1477 | dipeptidase 1 (renal) | 10.17 | 0.00109 | 1185.55 | 1222.89 | 634.13 | 114.31 | 98.91 | 75.22 |
| rc_AA609795_at | AA609795 | 1492 | EST | #N/A | #N/A | 74.38 | 34 | 77.76 | -41.44 | -45.5 | 28.82 |
| rc_AA620497_s_at | AA620497 | 1503 | EST | #N/A | #N/A | 147.72 | 165.83 | 66.02 | 95.91 | 76.7 | 80.33 |
| rc_AA620995_at | AA620995 | 1512 | EST | 3.74 | 0.03414 | 100.71 | 80.15 | 101.95 | 3.5 | 1.8 | 3.77 |
| rc_AA621277_at | AA621277 | 1520 | EST | 3.81 | 0.00194 | 81.18 | 74.81 | 30.84 | -0.15 | 1.98 | 12.84 |
| AB002304_at | AB002304 | 1534 | KIAA0306 protein | #N/A | #N/A | 584.5 | 621.94 | 136.64 | 313.99 | 298.88 | 88.6 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic: | | | normal | | |
|----------------|----------|--------|---|--------|----------|---------|-------------|--------|---------|--------|--------|---------|
| | | | | change | in metas | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| AB002349_at | AB002349 | 1537 | KIAA0351 gene product | #N/A | #N/A | #N/A | 65.63 | 52.11 | 32.26 | 49.37 | 46.52 | 37.93 |
| AB006782_at | AB006782 | 1541 | lectin, galactoside- binding, soluble, 9 | #N/A | #N/A | #N/A | 475.47 | 430.44 | 192.68 | 222.25 | 213.37 | 51.25 |
| AF003521_at | AF003521 | 1545 | jagged 2 | 11.26 | 0.00008 | 0.00008 | 426 | 330.95 | 309.91 | 15.48 | -3.6 | 91.81 |
| C00808_s_at | C00808 | 1553 | EST | #N/A | #N/A | #N/A | 122.57 | 118.32 | 53.36 | 91.65 | 87.87 | 32.51 |
| C14228_f_at | C14228 | 1567 | EST | #N/A | #N/A | #N/A | 39.93 | 33.15 | 13.59 | -0.51 | 2.85 | 8.61 |
| rc_C15078_i_at | C15078 | 1573 | EST | #N/A | #N/A | #N/A | 115.08 | 73.82 | 91.34 | 26.22 | 31.14 | 60.2 |
| rc_C21248_at | C21248 | 1585 | pituitary tumor- transforming 1 | 3.85 | 0.00456 | 0.00456 | 100.24 | 96.81 | 47.17 | -1.7 | -11.27 | 28.49 |
| D13435_at | D13435 | 1605 | phosphatidylinositol glycan, class F | #N/A | #N/A | #N/A | 80.8 | 88.58 | 41.56 | 34.85 | 41.76 | 18.11 |
| D14520_at | D14520 | 1613 | basic transcription element binding | 4.93 | 0.00004 | 0.00004 | 151.12 | 135.19 | 57.24 | 25.67 | 17.28 | 25.67 |
| rc_D20906_at | D20906 | 1627 | protein 2 | 5.18 | 0.02189 | 0.02189 | 210.11 | 151.67 | 185.24 | 14.87 | 11.71 | 27.2 |
| D21063_at | D21063 | 1628 | minichromosome maintenance deficient | 3.83 | 0.00983 | 0.00983 | 91.18 | 55.12 | 60.89 | -51.33 | -62.63 | 28.4 |
| D50914_at | D50914 | 1673 | (S. cerevisiae) 2 (mitotin) | 4.74 | 0.00752 | 0.00752 | 116.55 | 91.64 | 89.27 | -17.4 | -17.86 | 16.97 |
| D63486_at | D63486 | 1712 | KIAA0124 protein | 6.33 | 0.00078 | 0.00078 | 543.91 | 676.55 | 287.16 | 84.6 | 95.61 | 45.48 |
| D63880_at | D63880 | 1715 | KIAA0152 gene product | 4.26 | 0.00253 | 0.00253 | 93.03 | 103.26 | 41.4 | -2.12 | -4.45 | 9.38 |
| D79992_at | D79992 | 1724 | KIAA0170 gene product | #N/A | #N/A | #N/A | 35.23 | 42.16 | 14.88 | 22 | 18.09 | 11.9 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | change in metas | p value | metastatic: | | | normal | | |
|----------------|---------|--------|-------------------------|------|--|--------------------|---------|-------------|--------|---------|--------|--------|---------|
| | | | | | | | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| | | | KIAA0175 gene | | | | | | | | | | |
| D79997_at | D79997 | 1725 | product | | | #N/A | #N/A | 55.25 | 42.49 | 53.87 | 8.57 | 6.15 | 13.07 |
| rc_D80710_f_at | D80710 | 1734 | integral type I protein | | | 7.08 | 0.00213 | 253.6 | 303.7 | 149.08 | 22.95 | 28.29 | 24.59 |
| rc_D80948_f_at | D80948 | 1738 | EST | | | #N/A | #N/A | 82.4 | 67.39 | 42.83 | 41.25 | 43.53 | 17.46 |
| D83735_at | D83735 | 1747 | calponin 2 | | | 10.42 | 0.00001 | 486.85 | 436.55 | 172.25 | 42.54 | 43.06 | 57.58 |
| | | | trinucleotide repeat | | | | | | | | | | |
| | | | containing 11 (THR- | | | | | | | | | | |
| | | | associated protein, | | | | | | | | | | |
| D83783_at | D83783 | 1748 | 230 kDa subunit) | | | 6.55 | 0.00176 | 236.64 | 156.39 | 216.64 | 23.23 | 19.65 | 27.84 |
| | | | minichromosome | | | | | | | | | | |
| D84557_at | D84557 | 1749 | maintenance deficient | | | #N/A | #N/A | 142.92 | 125.75 | 102.81 | 37.22 | 43.12 | 28.15 |
| | | | (mis5, S. pombe) 6 | | | | | | | | | | |
| D87073_at | D87073 | 1759 | zinc finger protein 142 | | | #N/A | #N/A | 40.84 | 34.37 | 13.36 | 33.34 | 33.07 | 21.13 |
| D88154_at | D88154 | 1766 | (clone pHZ-49) | | | 4.18 | 0.00051 | 117.8 | 129.16 | 47.7 | 23.85 | 18.99 | 17.79 |
| rc_F02330_at | F02330 | 1778 | villin-like | | | #N/A | #N/A | 199.08 | 170.47 | 83.95 | 178.42 | 195.54 | 58.6 |
| rc_F03811_f_at | F03811 | 1784 | EST | | | #N/A | #N/A | 638.66 | 598.46 | 142.63 | 235.37 | 232.6 | 47.16 |
| | | | KIAA0440 protein | | | | | | | | | | |
| | | | replication factor C | | | | | | | | | | |
| rc_F04320_s_at | F04320 | 1786 | (activator 1) 4 (37kD) | | | 3.63 | 0.01119 | 90.37 | 115.96 | 49.41 | 14.92 | 17.26 | 9.79 |
| | | | Kell blood group | | | | | | | | | | |
| | | | precursor (McLeod | | | | | | | | | | |
| rc_F04531_s_at | F04531 | 1791 | phenotype) | | | 7.79 | 0.03205 | 311.05 | 366.72 | 262.03 | 16.22 | 20.65 | 13.52 |
| rc_F09394_s_at | F09394 | 1803 | KIAA0715 protein | | | 22.89 | 0.01753 | 865.39 | 696.47 | 631.83 | -49.72 | -50.25 | 35.81 |
| | | | procollagen-proline, 2- | | | | | | | | | | |
| | | | oxoglutarate 4- | | | | | | | | | | |
| | | | dioxygenase (proline 4- | | | | | | | | | | |
| | | | hydroxylase), alpha | | | | | | | | | | |
| rc_F09788_at | F09788 | 1808 | polypeptide II | | | 4.14 | 0.00003 | 104.92 | 112.31 | 27.67 | 19.92 | 20.29 | 13.83 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: | | | normal | | |
|----------------|---------|--------|---|-------------|---------|-------------|---------|---------|-------------|---------------|----------------|
| | | | | in metas | p value | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_H03629_s_at | H03629 | 1834 | desmin | #N/A | #N/A | 52.19 | 58.52 | 35.47 | -1.96 | -2.94 | 8.58 |
| rc_H09281_at | H09281 | 1863 | EST | 6 | 0.00966 | 147.11 | 187.25 | 71.67 | -2.97 | -0.54 | 11.7 |
| rc_H11760_f_at | H11760 | 1878 | EST | #N/A | #N/A | 70.59 | 62.53 | 58.16 | 9.96 | 8.19 | 11.54 |
| | | | E74-like factor 4 (ets domain transcription factor) | | | | | | | | |
| rc_H24269_s_at | H24269 | 1902 | factor | #N/A | #N/A | 51.79 | 47.58 | 24.25 | 15.19 | 16.8 | 12.36 |
| | | | gamma-aminobutyric acid (GABA) B receptor, 1 | | | | | | | | |
| H43286_s_at | H43286 | 1929 | receptor, 1 | 5.02 | 0.01972 | 377.04 | 222.91 | 315.96 | 57.02 | 63.58 | 24.25 |
| | | | H2A histone family, member Y | | | | | | | | |
| rc_H43646_at | H43646 | 1930 | member Y | 4.6 | 0.00147 | 413.02 | 424.34 | 219.27 | 92.12 | 91.3 | 52.41 |
| H53657_s_at | H53657 | 1945 | adenylate cyclase 3 | 3.98 | 0.0045 | 140.07 | 111.99 | 74.77 | 31.33 | 31.74 | 15.29 |
| rc_H57709_s_at | H57709 | 1956 | ribosomal protein L31 | #N/A | #N/A | 47.56 | 34.17 | 56.68 | 4.55 | 2.44 | 52.46 |
| | | | solute carrier family 2 (facilitated glucose transporter), member 1 | | | | | | | | |
| rc_H58873_s_at | H58873 | 1961 | 1 | 57.98 | 0.00063 | 4996.66 | 4603.55 | 4107.24 | 69.89 | 70.74 | 58.94 |
| rc_H59617_at | H59617 | 1964 | EST | 3.3 | 0.04588 | 116.07 | 71.39 | 101 | 19.24 | 21.65 | 16.88 |
| rc_H78211_at | H78211 | 2001 | EST | 6.73 | 0.02488 | 211.51 | 183.81 | 208.45 | -115.95 | -129.18 | 70.22 |
| rc_H98657_at | H98657 | 2068 | EST | #N/A | #N/A | 179.15 | 192.17 | 32.25 | 111.2 | 84.74 | 128.92 |
| | | | creatine kinase, mitochondrial 1 (ubiquitous) | | | | | | | | |
| J04469_at | J04469 | 2111 | | 7.9 | 0.00705 | 212.04 | 143.89 | 162.12 | -17.21 | -18.81 | 12.68 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | change in metas | p value | metastatic: | | | normal | | |
|-------------|---------|--------|--|-------|---------|--------------------|---------|-------------|--------|---------|--------|--------|---------|
| | | | | | | | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| J05257_at | J05257 | 2118 | dipeptidase 1 (renal) IMP (inosine monophosphate) | 12.02 | 0.02099 | 429.91 | 300.76 | 352.56 | -21.05 | -21.78 | 30.67 | | |
| J05272_at | J05272 | 2119 | dehydrogenase 1 mucin 1, | #N/A | #N/A | 269.89 | 205 | 173.64 | 126.69 | 106.27 | 82.73 | | |
| J05582_s_at | J05582 | 2121 | transmembrane ribosomal protein S6 | 5.39 | 0.00056 | 114 | 114.74 | 42.09 | -6.01 | -4.53 | 13.68 | | |
| L07597_at | L07597 | 2146 | kinase, 90kD, polypeptide 1 | #N/A | #N/A | 36.09 | 29.39 | 44.43 | -12.04 | -10.72 | 11.97 | | |
| L08044_s_at | L08044 | 2149 | trefoil factor 3 (intestinal) | 21.42 | 0.01674 | 2956.22 | 1618.2 | 3127.19 | 107.82 | 58.55 | 184.16 | | |
| L11669_at | L11669 | 2157 | tetracycline transporter-like protein matrix | 6.75 | 0.00101 | 218.77 | 261.77 | 115.8 | 26.26 | 25.92 | 17.48 | | |
| L23808_at | L23808 | 2179 | metalloproteinase 12 (macrophage elastase) | 6.18 | 0.02195 | 175.24 | 161.83 | 132.75 | -9.99 | -8.2 | 8.11 | | |
| L35035_at | L35035 | 2201 | ribose 5-phosphate isomerase A (ribose 5- phosphate epimerase) | #N/A | #N/A | 64.36 | 69.69 | 40.9 | 11.52 | 12.58 | 6.43 | | |
| L35545_at | L35545 | 2202 | endothelial cell protein C/activated protein C receptor | #N/A | #N/A | 66.65 | 55.46 | 68.13 | 7.75 | 5.68 | 11.48 | | |
| L38696_at | L38696 | 2208 | RNA-binding protein (autoantigenic) | 3.7 | 0.00093 | 230.48 | 161.69 | 118.85 | 60.18 | 58.55 | 24.77 | | |
| L41351_at | L41351 | 2214 | protease, serine, 8 (prostasin) | 6.34 | 0.01132 | 214.13 | 104.95 | 189.28 | 10.88 | 9.6 | 22.68 | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: | | | normal | | |
|-------------|---------|--------|--|-------------|---------|-------------|---------|---------|--------|---------|---------|
| | | | | #N/A | p value | Mean | Median | Std Dev | Mean | Median | Std Dev |
| L42583_f_at | L42583 | 2215 | keratin 6A | #N/A | #N/A | 116.33 | 111.15 | 91.3 | 60.92 | 51.12 | 22.52 |
| M12125_at | M12125 | 2241 | tropomyosin 2 (beta) | 10.83 | 0.00191 | 291.63 | 158.55 | 229.08 | 13.01 | 16.33 | 11.64 |
| M15205_at | M15205 | 2265 | thymidine kinase 1, | 3.75 | 0.00159 | 153.15 | 150.31 | 66.27 | 41.98 | 35.02 | 29.02 |
| M16364_s_at | M16364 | 2269 | soluble creatine kinase, brain carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | 12.69 | 0.03633 | 683.38 | 491.19 | 929.94 | -72.18 | -70.9 | 40.37 |
| M18728_at | M18728 | 2285 | kalikrein 1, renal/pancreas/salivar y endogenous retroviral protease melanoma adhesion molecule carcinoembryonic antigen-related cell adhesion molecule 5 transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) replication factor C (activator 1) 4 (37kD) midkine (neurite growth-promoting factor 2) | 44.82 | 0.00291 | 1390.62 | 1362.73 | 1031.01 | -9.17 | -13.17 | 11.83 |
| M25629_at | M25629 | 2307 | | #N/A | #N/A | 47.43 | 40.22 | 29.15 | -2.42 | 2.12 | 15.6 |
| M27826_at | M27826 | 2313 | | 26.36 | 0.00342 | 993.89 | 833.56 | 816.33 | 5.88 | 7.04 | 32.2 |
| M29277_at | M29277 | 2316 | | 3.91 | 0.00112 | 269.54 | 313.13 | 82.76 | 80.09 | 81.21 | 48.32 |
| M29540_at | M29540 | 2317 | | 36.57 | 0.0116 | 1516.55 | 1083.69 | 1372.55 | -1.09 | -3.15 | 11.75 |
| M31523_at | M31523 | 2329 | | #N/A | #N/A | 59.78 | 62.53 | 10.63 | 18.65 | 21.63 | 8.94 |
| M87339_at | M87339 | 2415 | | 4.07 | 0.00316 | 93.72 | 78.1 | 56.58 | 4.26 | 9.92 | 16.79 |
| M94250_at | M94250 | 2426 | | 10.39 | 0.01818 | 442.2 | 188.32 | 624.9 | -155.4 | -175.43 | 101.89 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic: | | | | normal | | | |
|----------------|---------|--------|---|--------|----------|---------|-------------|--------|-------------|--------|--------|---------|--------|--------|
| | | | | change | in metas | | metastatic: | | metastatic: | | set 2: | | set 2: | |
| | | | | | | | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Median |
| M94345_at | M94345 | 2427 | capping protein (actin filament), gelsolin-like | 22.38 | 0.00003 | 503.47 | 539.15 | 179.05 | -7.51 | -10.35 | 22.75 | | | |
| M94362_at | M94362 | 2428 | lamin B2 | #N/A | #N/A | 175.16 | 154.32 | 75.52 | 79.2 | 81.73 | 34.64 | | | |
| | | | pregnancy specific beta-1-glycoprotein | | | | | | | | | | | |
| M94891_s_at | M94891 | 2429 | 4, pregnancy specific beta-1-glycoprotein 7 | #N/A | #N/A | 221.09 | 197.74 | 80.32 | 178.23 | 166.98 | 61.33 | | | |
| | | | hydroxymethylbilane synthase | | | | | | | | | | | |
| M95623_cds1_at | M95623 | 2431 | EST | #N/A | #N/A | 67.65 | 72.44 | 22.29 | 6.67 | 0.88 | 24.92 | | | |
| rc_N22015_at | N22015 | 2448 | EST | 46.61 | 0.00025 | 1225.51 | 887.65 | 1106.3 | -5.3 | -6.84 | 18.82 | | | |
| rc_N35376_at | N35376 | 2501 | EST | #N/A | #N/A | 39.01 | 35.99 | 19.81 | 28.53 | 29.44 | 8.2 | | | |
| | | | v-myb avian myeloblastosis viral oncogene homolog | | | | | | | | | | | |
| rc_N49284_s_at | N49284 | 2537 | EST | 11.82 | 0.01981 | 510.82 | 523.45 | 423.41 | -36.17 | -50.08 | 50.71 | | | |
| rc_N54265_s_at | N54265 | 2563 | EST | #N/A | #N/A | 45.56 | 44.98 | 19.91 | 17.71 | 26.43 | 25.36 | | | |
| rc_N54395_at | N54395 | 2565 | EST | #N/A | #N/A | 49.95 | 46.84 | 48.26 | -16.14 | -17.71 | 6.65 | | | |
| | | | DEAD/H (Asp-Glu-Ala-Asp/His) box | | | | | | | | | | | |
| rc_N62675_s_at | N62675 | 2594 | polypeptide 16 | 3.61 | 0.04034 | 109.44 | 104.65 | 108.08 | 6.49 | 15.91 | 35.18 | | | |
| rc_N63165_at | N63165 | 2598 | EST | #N/A | #N/A | 68.04 | 62.1 | 44.7 | 30.07 | 26.23 | 13.84 | | | |
| rc_N64616_at | N64616 | 2611 | EST | 3.11 | 0.0074 | 68.89 | 75.8 | 32.12 | -0.83 | 9.77 | 28.69 | | | |
| rc_N66951_at | N66951 | 2621 | EST | 5.54 | 0.02442 | 451.16 | 432.45 | 381.81 | 59.83 | 75.27 | 32.75 | | | |
| | | | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | | | | | | | | | | | |
| rc_N72116_s_at | N72116 | 2668 | EST | 9.01 | 0.00051 | 338.43 | 314.06 | 196.66 | 32.57 | 29.68 | 20.1 | | | |
| rc_N73846_at | N73846 | 2680 | EST | 3.27 | 0.00012 | 78.37 | 79.7 | 20.06 | 14.43 | 14.3 | 17.21 | | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastatic: metastatic: | | | | normal normal | | | |
|----------------|---------|--------|--|-------------|----------|---------|-------------------------|---------|---------|--------|---------------|---------|------|---------|
| | | | | in metas | in metas | | Mean | Median | Std Dev | Mean | Median | Std Dev | Mean | Std Dev |
| rc_N89670_at | N89670 | 2709 | EST | 4.26 | 0.00002 | 115.98 | 108.4 | 29.79 | 3.16 | -1.81 | 43.32 | | | |
| rc_N92659_at | N92659 | 2721 | EST | #N/A | #N/A | 31.19 | 37.23 | 14.14 | 5.91 | 4.05 | 5.63 | | | |
| rc_N92734_at | N92734 | 2722 | EST | #N/A | #N/A | 45.63 | 39.49 | 14.19 | 27.31 | 25.45 | 10.41 | | | |
| | | | protein tyrosine phosphatase type IVA, member 3 | | | | | | | | | | | |
| rc_N93798_at | N93798 | 2738 | EST | 4.65 | 0.00118 | 557.51 | 523.56 | 229.03 | 139.69 | 122.61 | 84.93 | | | |
| rc_R06251_f_at | R06251 | 2764 | EST | 5.57 | 0.00037 | 343.86 | 381.79 | 95.11 | 74.25 | 66.72 | 64.11 | | | |
| rc_R06866_s_at | R06866 | 2774 | EST | 5.18 | 0.00187 | 148.48 | 114.86 | 102.01 | 18.26 | 15.16 | 17.11 | | | |
| | | | tumor protein D52-like | | | | | | | | | | | |
| rc_R26744_at | R26744 | 2804 | EST | 4.32 | 0.00532 | 112.54 | 90 | 76.53 | -0.2 | -3.06 | 24.42 | | | |
| rc_R27296_f_at | R27296 | 2807 | EST | #N/A | #N/A | 41.82 | 39.83 | 32.72 | 8.27 | 11.07 | 7.26 | | | |
| rc_R33498_s_at | R33498 | 2820 | EST | 41.34 | 0.00001 | 1839.74 | 1920.41 | 1082.84 | 46.45 | 33.01 | 43.64 | | | |
| rc_R36109_at | R36109 | 2823 | EST | #N/A | #N/A | 47.54 | 48.43 | 19.9 | 25.67 | 20.25 | 34.73 | | | |
| | | | calcium channel, voltage-dependent, beta 3 subunit | | | | | | | | | | | |
| rc_R36947_s_at | R36947 | 2825 | EST | 4.11 | 0.00006 | 101.82 | 109.62 | 28.57 | -0.61 | 0.94 | 37.6 | | | |
| | | | protein similar to E.coli yhdg and R. capsulatus nifR3 | | | | | | | | | | | |
| rc_R38511_s_at | R38511 | 2832 | EST | 5.19 | 0.00015 | 131.5 | 147.54 | 44.02 | 21.3 | 23.75 | 9.22 | | | |
| rc_R39191_s_at | R39191 | 2834 | EST | 4.69 | 0.00456 | 130.93 | 145.31 | 62.13 | 17.46 | 18.33 | 16.04 | | | |
| | | | KIAA1020 protein | | | | | | | | | | | |
| rc_R40057_at | R40057 | 2839 | EST | #N/A | #N/A | 47.6 | 46.28 | 36.57 | 0.83 | -0.8 | 7.91 | | | |
| | | | prominin (mouse)-like | | | | | | | | | | | |
| rc_R44479_at | R44479 | 2855 | EST | 4.14 | 0.0181 | 97.01 | 105.95 | 60.51 | 7.08 | 5.99 | 7.62 | | | |
| rc_R44817_at | R44817 | 2860 | EST | #N/A | #N/A | 600.1 | 550.42 | 309.14 | 255.91 | 249.29 | 69.09 | | | |
| | | | KIAA0552 gene product | | | | | | | | | | | |
| | | | Fc fragment of IgG, low affinity IIIa, receptor for (CD16) | | | | | | | | | | | |
| rc_R49047_at | R49047 | 2878 | EST | #N/A | #N/A | 44.49 | 36.71 | 14.37 | 15.43 | 14.16 | 14.13 | | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic: | | normal | | | | |
|----------------|---------|--------|-------------------------|--------|----------|---------|-------------|--------|--------|---------|---------|--------|--|
| | | | | change | in metas | | metastatic: | | normal | | | | |
| | | | | | | | Mean | Median | Mean | Median | | | |
| | | | ubiquitin specific | | | | | | | | | | |
| rc_R54935_l_at | R54935 | 2903 | protease 7 (herpes | #N/A | #N/A | #N/A | 75.76 | 81.15 | 31.57 | 17.77 | 14 | 18.86 | |
| rc_R55470_at | R55470 | 2904 | virus-associated) | 3.59 | 0.00515 | 256.38 | 225.69 | 73.42 | 138.22 | 75.29 | 73.42 | 53.04 | |
| R56678_at | R56678 | 2908 | EST | 3.81 | 0.02242 | 98.37 | 78.38 | 75.74 | 75.74 | 2.67 | 5 | 5.82 | |
| rc_R59093_at | R59093 | 2911 | EST | #N/A | #N/A | 57.79 | 33.48 | 73.58 | 73.58 | 12.26 | 10.21 | 7.73 | |
| rc_R63925_at | R63925 | 2929 | EST | #N/A | #N/A | 70.52 | 60.93 | 15.36 | 15.36 | 49.82 | 52.73 | 13.77 | |
| R69700_at | R69700 | 2943 | EST | 6.71 | 0.0021 | 387.34 | 393.81 | 94.86 | 94.86 | 79.33 | 57.85 | 129.97 | |
| rc_R71395_at | R71395 | 2952 | EST | 10.42 | 0.00422 | 318.75 | 274.93 | 227.75 | 227.75 | 14.99 | 12.28 | 14.58 | |
| R76363_at | R76363 | 2962 | EST | #N/A | #N/A | 47.81 | 38.04 | 24.76 | 24.76 | 12.67 | 16.94 | 13.17 | |
| rc_R85266_at | R85266 | 2977 | EST | #N/A | #N/A | 53.4 | 54.53 | 25.44 | 25.44 | 48.68 | 39.83 | 33.9 | |
| rc_R91819_at | R91819 | 2984 | EST | 8.95 | 0.00009 | 263.33 | 219.91 | 135.67 | 135.67 | 11.34 | 9.35 | 36.49 | |
| | | | matrix | | | | | | | | | | |
| | | | metalloproteinase 12 | | | | | | | | | | |
| | | | (macrophage | | | | | | | | | | |
| rc_R92994_s_at | R92994 | 2990 | elastase) | 11.05 | 0.00248 | 312.14 | 252.62 | 248.32 | 248.32 | 11.43 | 6.64 | 11.52 | |
| rc_R95966_l_at | R95966 | 2997 | EST | 11.22 | 0.00682 | 482.68 | 436.3 | 446.39 | 446.39 | -106.64 | -160.75 | 127.91 | |
| rc_R96924_s_at | R96924 | 3001 | EST | 6.18 | 0.03417 | 451.59 | 490.51 | 339.66 | 339.66 | 51.01 | 52.94 | 54.09 | |
| | | | | | | | | | | | | | |
| S78187_at | S78187 | 3036 | cell division cycle 25B | 8.07 | 0.00009 | 198.51 | 218.04 | 74.52 | 74.52 | 3.36 | -1.2 | 26.9 | |
| rc_T03438_s_at | T03438 | 3043 | EST | 8.18 | 0.00032 | 300.09 | 229.6 | 218.02 | 218.02 | 31.03 | 28.88 | 15.86 | |
| rc_T03541_at | T03541 | 3045 | EST | #N/A | #N/A | 455.39 | 418.21 | 288.45 | 288.45 | 155.27 | 155.62 | 50.93 | |
| rc_T15473_at | T15473 | 3058 | muscle specific gene | 5.81 | 0.02404 | 189.25 | 139.11 | 184.39 | 184.39 | -5.65 | -10.77 | 15.89 | |
| | | | cleavage and | | | | | | | | | | |
| | | | polyadenylation | | | | | | | | | | |
| | | | specific factor 4, 30kD | | | | | | | | | | |
| rc_T16983_s_at | T16983 | 3074 | subunit | 5.23 | 0.00075 | 268.21 | 300.53 | 81.43 | 81.43 | 65.64 | 45.67 | 74.28 | |
| rc_T25744_s_at | T25744 | 3092 | EST | #N/A | #N/A | 79.78 | 68.72 | 52.01 | 52.01 | 15.56 | 12.65 | 13.18 | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: metastatic: | | | normal | | |
|----------------|---------|--------|--|-------------|---------|-------------------------|---------|---------|--------|--------|---------|
| | | | | in metas | p value | Mean | Median | Std Dev | Mean | Median | Std Dev |
| rc_T30193_s_at | T30193 | 3098 | protease, serine, 8 | 8.39 | 0.00043 | 1912.22 | 1228.46 | 1739.5 | 214.88 | 175.57 | 127.28 |
| rc_T30222_at | T30222 | 3100 | (prolactin) | #N/A | #N/A | 35.41 | 34.75 | 27.14 | 8.47 | 9.56 | 17.71 |
| rc_T32108_at | T32108 | 3103 | EST | 6.96 | 0.00723 | 1095.16 | 593.52 | 923.47 | 148.09 | 152.11 | 92.06 |
| rc_T47601_at | T47601 | 3126 | EST | 4.05 | 0.00878 | 199.79 | 219.84 | 62.16 | 84.5 | 28.33 | 122.16 |
| rc_T53404_at | T53404 | 3143 | EST | 10.68 | 0.00582 | 654.13 | 475.25 | 687.49 | 48.3 | 0.6 | 93.06 |
| rc_T66935_at | T66935 | 3179 | EST | 3.97 | 0.00188 | 253.93 | 230.32 | 129.66 | 66.8 | 52.94 | 42.32 |
| rc_T89601_r_at | T89601 | 3243 | EST | #N/A | #N/A | 839.07 | 747.51 | 231.92 | 410.07 | 342.22 | 200.88 |
| rc_T91116_at | T91116 | 3252 | EST | 4.01 | 0.02721 | 133.54 | 61.72 | 126.12 | 16.62 | 11.42 | 13.64 |
| rc_T96060_at | T96060 | 3263 | EST | #N/A | #N/A | 910.76 | 225.75 | 1282.67 | 67.92 | 70.44 | 91.72 |
| U01062_at | U01062 | 3273 | inositol 1,4,5-trisphosphate receptor, type 3 | 7.41 | 0 | 160.46 | 164.36 | 23.91 | -16.8 | -26.61 | 26.44 |
| U01147_at | U01147 | 3275 | active BCR-related gene | 3.22 | 0.00103 | 97.43 | 84.12 | 41.43 | 27.15 | 22.94 | 17 |
| U03398_at | U03398 | 3282 | tumor necrosis factor (ligand) superfamily, member 9 | #N/A | #N/A | 116.17 | 88.07 | 59.5 | 115.08 | 92.7 | 93.14 |
| U04313_at | U04313 | 3284 | protease inhibitor 5 (maspin) | 4.54 | 0.02986 | 132.77 | 69.67 | 115.99 | -0.34 | -2.59 | 9.7 |
| U07969_s_at | U07969 | 3289 | cadherin 17, LI cadherin (liver-intestine) | 10.78 | 0.02002 | 428.65 | 383.68 | 390.23 | 15.78 | 12.82 | 12.06 |
| U16306_at | U16306 | 3312 | chondroitin sulfate proteoglycan 2 (versican) | #N/A | #N/A | 48.35 | 56.91 | 35.99 | 8.07 | 4.58 | 16.58 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic: metastatic: | | | | normal | | | |
|-----------------|---------|--------|--|--------|----------|---------|-------------------------|--------|---------|--------|--------|---------|--|--|
| | | | | change | in metas | | Mean | Median | Std Dev | Mean | Median | Std Dev | | |
| | | | | | | | | | | | | | | |
| U17760_ma1_at | U17760 | 3315 | laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD)) | 3.54 | 0.01853 | 103.13 | 111.96 | 72.83 | 6.99 | -3.15 | 21.08 | | | |
| U20499_at | U20499 | 3321 | sulfotransferase family 1A, phenol-preferring, member 3 | 5.5 | 0.00299 | 316.7 | 231.67 | 222.02 | 48.34 | 54.37 | 24.69 | | | |
| U21049_at | U21049 | 3325 | epithelial protein up-regulated in carcinoma, membrane associated protein 17 | 7.53 | 0.01667 | 202.38 | 248.15 | 119.31 | -14.32 | -12.21 | 19.43 | | | |
| U38847_at | U38847 | 3357 | TAR (HIV) RNA-binding protein 1 | #N/A | #N/A | 72.74 | 66.76 | 36.14 | 15.7 | 17.43 | 10.2 | | | |
| U40990_at | U40990 | 3359 | potassium voltage-gated channel, KQT-like subfamily, member 1 | 3.18 | 0.00093 | 128.02 | 142.31 | 43.16 | 40.88 | 42.64 | 23.09 | | | |
| U48705_ma1_s_at | U48705 | 3370 | discoidin domain receptor family, member 1 | 5.94 | 0.01323 | 178.04 | 200.63 | 102.82 | -1.87 | -6.25 | 25.81 | | | |
| U51095_at | U51095 | 3382 | caudal type homeobox transcription factor 1 | 4.76 | 0.02664 | 130.81 | 143.82 | 93.4 | 5.83 | 5.55 | 8.97 | | | |
| U53786_at | U53786 | 3390 | envoplakin | #N/A | #N/A | 221.51 | 73.95 | 249.37 | -20.54 | -20.08 | 16.22 | | | |
| U66661_at | U66661 | 3406 | gamma-aminobutyric acid (GABA) A receptor, epsilon | #N/A | #N/A | 55.33 | 44.93 | 29.26 | 16.58 | 14.81 | 11.96 | | | |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastatic: Mean | metastatic: Median | metastatic: Std Dev | normal Mean | normal Median | normal Std Dev |
|----------------|---------|--------|--|-------------------------|---------|---------------------|-----------------------|------------------------|----------------|------------------|-------------------|
| U75968_s_at | U75968 | 3423 | DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 11 (S.cerevisiae CHL1- like helicase) O-linked N- acetylglucosamine (GlcNAc) transferase (UDP-N- acetylglucosamine:pol ypeptide-N- acetylglucosaminyl transferase) | #N/A | #N/A | 195.48 | 155.37 | 89.8 | 115.5 | 102.24 | 77.72 |
| U77413_at | U77413 | 3427 | pyridoxal (pyridoxine, vitamin B6) kinase EST | #N/A | #N/A | 59.38 | 59.78 | 48.05 | 1.2 | 5.23 | 13.8 |
| U89606_at | U89606 | 3452 | leukemia inhibitory factor (cholinergic differentiation factor) | 3.58 | 0.00322 | 103.6 | 97.56 | 58.85 | 15.19 | 18.94 | 24.5 |
| rc_W02695_at | W02695 | 3467 | EST | #N/A | #N/A | 129.58 | 99.52 | 100.52 | 30.69 | 33.06 | 16.14 |
| rc_W46451_s_at | W46451 | 3529 | EST | #N/A | #N/A | 120.95 | 76.95 | 88.42 | 36.63 | 40.09 | 21.06 |
| rc_W60968_at | W60968 | 3559 | EphB2 | #N/A | #N/A | 125.7 | 144.72 | 48.22 | 51.99 | 55.29 | 21.11 |
| rc_W67251_s_at | W67251 | 3570 | EST | 6.13 | 0.01463 | 204.71 | 182.17 | 127.82 | 21.77 | 23.88 | 12.17 |
| rc_W73189_at | W73189 | 3589 | EST | 3.69 | 0.02909 | 113.63 | 144.75 | 67.73 | 20.7 | 23.2 | 15.44 |
| rc_W78057_at | W78057 | 3600 | EST | 9.06 | 0.0034 | 397.29 | 374.78 | 305.93 | 29.21 | 29.9 | 34.33 |
| rc_W90146_f_at | W90146 | 3644 | EST | 6.23 | 0.01558 | 170.66 | 147.78 | 126.32 | 9.93 | 8.63 | 6.49 |
| rc_W92449_at | W92449 | 3652 | protease inhibitor 5 (maspin) | 31.67 | 0.00011 | 715.17 | 491.5 | 459.71 | -40.13 | -40.74 | 17.76 |
| rc_W93726_s_at | W93726 | 3656 | HSPC113 protein | 16.48 | 0.00014 | 355.41 | 304.26 | 149.69 | -14.2 | -14.8 | 10.59 |
| W95348_at | W95348 | 3663 | EST | 10.89 | 0.01065 | 555.52 | 492.63 | 563.86 | 26.59 | 29.36 | 21.03 |
| rc_W95477_at | W95477 | 3664 | EST | 26.51 | 0.00161 | 941.08 | 566.6 | 1130.33 | 17.15 | 18.75 | 12.83 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic: | | | normal | | |
|-------------|---------|--------|--|--------|----------|---------|-------------|--------|---------|-------------|---------------|----------------|
| | | | | change | in metas | | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| | | | small nuclear ribonucleoprotein | | | | | | | | | |
| X04654_s_at | X04654 | 3681 | 70kD polypeptide (RNP antigen) | #N/A | #N/A | #N/A | 98.11 | 89.35 | 38.15 | 42.22 | 41.24 | 17.18 |
| X13956_at | X13956 | 3701 | EST | 3.2 | 0.00321 | 0.00321 | 79.19 | 75.13 | 39.53 | 15.11 | 18.02 | 14.55 |
| X14850_at | X14850 | 3706 | H2A histone family, member X | 4.11 | 0.0001 | 0.0001 | 118.41 | 97.53 | 52.6 | 11.6 | 13.26 | 30.46 |
| | | | v-abl Abelson murine leukemia viral oncogene homolog 1 | | | | | | | | | |
| X16416_at | X16416 | 3713 | oncogene homolog 1 | #N/A | #N/A | #N/A | 82.49 | 90.74 | 16.7 | 36.59 | 38 | 14.59 |
| X54667_s_at | X54667 | 3731 | cystatin S, cystatin SN | 8.53 | 0.00059 | 0.00059 | 273.96 | 169.94 | 217.11 | -10.09 | -15.68 | 74.89 |
| X57348_s_at | X57348 | 3744 | stratifin matrix | 12.53 | 0.0013 | 0.0013 | 308.28 | 241.69 | 194.79 | -63.66 | -76.43 | 44.95 |
| | | | metalloproteinase 11 (stromelysin 3) | | | | | | | | | |
| X57766_at | X57766 | 3745 | cadherin 3, P-cadherin (placental) | #N/A | #N/A | #N/A | 166.25 | 142.96 | 124.34 | 63.38 | 62.13 | 25.48 |
| X63629_at | X63629 | 3762 | interferon, alpha-inducible protein 27 | 3.02 | 0.01654 | 0.01654 | 67.22 | 76.67 | 29.17 | -4.24 | -6.82 | 16.9 |
| X67325_at | X67325 | 3775 | sodium channel, nonvoltage-gated 1 | 9.67 | 0.03245 | 0.03245 | 962.87 | 412.22 | 1361.55 | 26.81 | 48.73 | 69.77 |
| | | | alpha cadherin 17, LI | | | | | | | | | |
| X76180_at | X76180 | 3795 | cadherin (liver-intestine) | 11.68 | 0 | 0 | 320.05 | 268.84 | 127.86 | 22.38 | 23.9 | 15.02 |
| X83228_at | X83228 | 3810 | FXD domain-containing ion transport regulator 3 | 10.58 | 0.02147 | 0.02147 | 342.12 | 423.87 | 282.49 | -8.87 | -6.9 | 8.55 |
| X93036_at | X93036 | 3830 | transport regulator 3 | 42.36 | 0.00167 | 0.00167 | 1322.91 | 783.61 | 1219 | -83.87 | -85.84 | 40.53 |

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastatic: | | | normal | | | |
|---|--------------------------------------|--------|--|---|---------|-------------|--------|---------|-------------|---------------|----------------|-------|
| | | | | in metas | p value | Mean | Median | Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | |
| X99133_at Y00503_at | X99133 Y00503 | 3842 | lipocalin 2 (oncogene 24p3) | 6.27 | 0.0453 | 284.56 | 129.1 | 434.01 | -28.39 | -19.41 | 26.24 | |
| | | 3849 | | 14.19 | 0.00217 | 362.5 | 427.85 | 240.73 | 7.02 | 10.74 | 10.98 | |
| Y10807_s_at rc_Z39191_at rc_Z39569_at rc_Z41415_at | Y10807 Z39191 Z39569 Z41415 | 3860 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2 | 4.28 | 0.00124 | 393.27 | 449.97 | 142.94 | 96 | 90.42 | 44.52 | |
| | | 3901 | | EST | 8.84 | 0.00011 | 442.36 | 371.88 | 228.18 | 46.98 | 49.3 | 33.31 |
| | | 3909 | | EST | #N/A | #N/A | 166.55 | 125.78 | 217.77 | -9.57 | -12.15 | 17.32 |
| | | 3933 | | EST | #N/A | #N/A | 199.73 | 88.96 | 271.2 | 10.38 | 6.64 | 11.47 |
| | | | | SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) | | | | | | | | |
| Z46629_at | Z46629 | 3938 | sex-reversal) | #N/A | #N/A | 39.69 | 40.61 | 13.99 | 6.21 | 8.06 | 9.16 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | normal | | | normal | | |
|------------------|----------|--------|----------------------------|-------------|---------|-----------|-----------|------------|-------------|---------------|----------------|-------------|---------------|----------------|
| | | | | in metas | p value | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA001902_at | AA001902 | 5 | KIAA0305 gene product | #N/A | #N/A | 14.88 | 17.06 | 8.8 | 29.11 | 28.6 | 23.36 | | | |
| rc_AA001903_i_at | AA001903 | 6 | EST | #N/A | #N/A | 6.64 | 0.97 | 14.07 | 26.52 | 28.7 | 13.21 | | | |
| rc_AA004669_at | AA004669 | 9 | EST | #N/A | #N/A | 8.66 | 10.77 | 8.65 | 33.32 | 25.36 | 31.12 | | | |
| | | | copper chaperone for | | | | | | | | | | | |
| rc_AA004707_at | AA004707 | 10 | superoxide dismutase | #N/A | #N/A | 217.76 | 217.72 | 144.41 | 502.14 | 479.38 | 161.01 | | | |
| | | | retinol-binding protein 4, | | | | | | | | | | | |
| rc_AA005202_at | AA005202 | 12 | interstitial | 3.18 | 0.00106 | 43.46 | 41.24 | 9.66 | 163.36 | 107.5 | 110.2 | | | |
| | | | peroxisomal membrane | | | | | | | | | | | |
| rc_AA009719_at | AA009719 | 20 | protein 2 (22kD) | 47.12 | 0.00008 | -50.14 | -51.69 | 47.17 | 1370.32 | 1503.99 | 715.62 | | | |
| rc_AA010205_at | AA010205 | 23 | EST | 7.41 | 0 | 14.43 | 17.64 | 14.87 | 187.55 | 154.99 | 92.13 | | | |
| rc_AA010360_at | AA010360 | 24 | EST | 6.55 | 0.00027 | 12.5 | 14.77 | 8.62 | 169.99 | 135.98 | 129.2 | | | |
| rc_AA010619_at | AA010619 | 27 | EST | 8.55 | 0.00057 | 21.58 | 5.47 | 42.99 | 279.66 | 268.6 | 154.98 | | | |
| | | | potassium voltage-gated | | | | | | | | | | | |
| | | | channel, shaker-related | | | | | | | | | | | |
| rc_AA013095_s_at | AA013095 | 33 | subfamily, beta member 1, | #N/A | #N/A | 7.81 | 3.06 | 19.71 | 18.56 | 15.83 | 8.24 | | | |
| rc_AA015768_at | AA015768 | 34 | EST | 15.3 | 0.00008 | 12.22 | 14.2 | 11.71 | 417.95 | 472.1 | 248.15 | | | |
| rc_AA016021_at | AA016021 | 35 | ubiquitin-like 3 | #N/A | #N/A | 13.88 | 16.21 | 13.21 | 65.65 | 51.44 | 46.44 | | | |
| rc_AA017146_at | AA017146 | 36 | EST | 10.1 | 0.00052 | 30.35 | 22.85 | 50.05 | 414.24 | 435.09 | 193.39 | | | |
| rc_AA018867_at | AA018867 | 39 | EST | 42.87 | 0.00002 | 45.29 | 29.28 | 52.68 | 1944.56 | 2160.33 | 1142.41 | | | |
| rc_AA019715_at | AA019715 | 41 | EST | #N/A | #N/A | 8.03 | 8.03 | 6.49 | 15.9 | 14.58 | 7.82 | | | |
| | | | suppressor of Ty | | | | | | | | | | | |
| rc_AA024511_at | AA024511 | 46 | (S.cerevisiae) 3 homolog | #N/A | #N/A | 7.82 | 3.08 | 12.06 | 62.54 | 58.34 | 27.73 | | | |
| rc_AA024866_at | AA024866 | 49 | EST | #N/A | #N/A | 10.89 | 7.87 | 8.56 | 31.16 | 30.56 | 14.26 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | normal | | | normal | | |
|---|----------|--------|-----------------------|-------------|---------|-----------|--------|------------|-------------|---------------|----------------|-------------|---------------|----------------|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA025930_at | AA025930 | 52 | EST | 3.59 | 0.00372 | 33.24 | 25.62 | 26.11 | 115.2 | 110.13 | 45.17 | | | |
| microvascular endothelial differentiation gene 1 | | | | | | | | | | | | | | |
| AA027766_at | AA027766 | 58 | EST | #N/A | #N/A | 16.71 | 16.37 | 7.36 | 25.05 | 26.19 | 13.26 | | | |
| AA028976_at | AA028976 | 63 | EST | #N/A | #N/A | 9.46 | 10.28 | 18.91 | 72.06 | 47.28 | 55.89 | | | |
| rc_AA031360_s_at | AA031360 | 67 | EST | #N/A | #N/A | 13.46 | 12.87 | 10.49 | 26.25 | 24.36 | 9.3 | | | |
| rc_AA032250_at | AA032250 | 73 | EST | 3.56 | 0.0009 | 10.56 | 13.86 | 9.55 | 84.44 | 83.69 | 50.06 | | | |
| rc_AA034365_at | AA034365 | 76 | EST | #N/A | #N/A | 119.56 | 39.46 | 171.27 | 216.28 | 159.86 | 152.39 | | | |
| rc_AA039616_at | AA039616 | 90 | EST | 9.36 | 0.00009 | 2.48 | -4.83 | 14.2 | 238.71 | 224.42 | 125.28 | | | |
| rc_AA040087_at | AA040087 | 92 | EST | 4.13 | 0.00123 | 34.99 | 27.32 | 18.99 | 156.63 | 148.88 | 90.44 | | | |
| rc_AA040291_at | AA040291 | 94 | KIAA0669 gene product | 3.55 | 0.00308 | 12.98 | 12.72 | 16.36 | 101.69 | 98.94 | 80.43 | | | |
| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) | | | | | | | | | | | | | | |
| AA041208_at | AA041208 | 96 | EST | #N/A | #N/A | 234.76 | 302.34 | 215.51 | 448.34 | 390 | 234.61 | | | |
| rc_AA043790_at | AA043790 | 99 | EST | #N/A | #N/A | 5.63 | 7.44 | 12.94 | 32.16 | 31.34 | 10.66 | | | |
| AA044095_at | AA044095 | 102 | EST | #N/A | #N/A | 29.41 | 18.4 | 35.04 | 31.85 | 24.92 | 38.98 | | | |
| Autosomal Highly Conserved Protein | | | | | | | | | | | | | | |
| AA044842_at | AA044842 | 105 | EST | 5.21 | 0.0009 | 16.66 | 16.52 | 18 | 167.15 | 159.32 | 123.77 | | | |
| rc_AA045481_at | AA045481 | 107 | EST | #N/A | #N/A | 28.81 | 21.88 | 17.14 | 71.32 | 63.94 | 38.49 | | | |
| rc_AA046457_at | AA046457 | 111 | EST | 3.2 | 0.00513 | 77.66 | 80.71 | 27.66 | 304.54 | 264.9 | 233.62 | | | |
| rc_AA046747_at | AA046747 | 114 | EST | 4.82 | 0.00022 | -5.19 | -4.2 | 10.73 | 113.78 | 88.54 | 66.41 | | | |
| AA047151_at | AA047151 | 116 | EST | 7.13 | 0.00007 | 17.55 | 17.5 | 10.09 | 188.62 | 185.41 | 80.5 | | | |
| rc_AA053917_at | AA053917 | 131 | EST | #N/A | #N/A | -18.24 | -11.6 | 21.61 | 56.08 | 38.68 | 82.71 | | | |
| rc_AA055992_at | AA055992 | 136 | calumenin | 3.51 | 0.00604 | 80.45 | 65.8 | 47.34 | 276.06 | 265.13 | 141.34 | | | |
| AA056319_at | AA056319 | 139 | EST | #N/A | #N/A | 21.89 | 17.62 | 12.89 | 29.23 | 26.53 | 11.96 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|--------------------------|----------|--------|-------------------------------|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA056482_at | AA056482 | 141 | EST | 4.82 | 0.00199 | 10.09 | 19.17 | 14.96 | 135.83 | 132.94 | 97.88 |
| SEC24 (S. cerevisiae) | | | | | | | | | | | |
| rc_AA056735_at | AA056735 | 142 | D related gene family, member | #N/A | #N/A | 4.59 | 10.03 | 14.42 | 29.84 | 28.43 | 10.97 |
| macrophage receptor with | | | | | | | | | | | |
| rc_AA074885_at | AA074885 | 161 | collagenous structure | 11.05 | 0.00786 | 79.55 | 25.58 | 153.64 | 652.03 | 761.74 | 300.57 |
| rc_AA075298_at | AA075298 | 163 | EST | #N/A | #N/A | 46.45 | 36.93 | 42.61 | 129.13 | 121.57 | 70.36 |
| rc_AA076672_at | AA076672 | 172 | EST | #N/A | #N/A | 86.18 | 87.53 | 60.88 | 122.82 | 105.84 | 54.8 |
| rc_AA084286_at | AA084286 | 176 | paternally expressed gene 3 | #N/A | #N/A | -2.06 | 0.32 | 14.88 | 30.7 | 26.84 | 20.69 |
| rc_AA084318_at | AA084318 | 177 | EST | #N/A | #N/A | 9.73 | 3.97 | 17.06 | 30.63 | 32.37 | 11.48 |
| rc_AA086201_at | AA086201 | 185 | EST | 5.8 | 0.00012 | 21.29 | 24.75 | 14.37 | 177.39 | 182.95 | 95.51 |
| AA092376_at | AA092376 | 196 | 15 kDa selenoprotein | #N/A | #N/A | 16.78 | 14.2 | 28.1 | 59.07 | 57.94 | 24.97 |
| AA092596_at | AA092596 | 197 | bone morphogenetic protein | 3.46 | 0.02532 | 30.18 | 22.69 | 61.67 | 148.47 | 171.15 | 77.57 |
| AA092716_at | AA092716 | 198 | HLA-B associated transcript- | 13.97 | 0.00009 | 62.83 | 63.53 | 42.33 | 952.09 | 817.41 | 545.31 |
| rc_AA098864_at | AA098864 | 205 | EST | #N/A | #N/A | 30.42 | 31.06 | 18.38 | 56.43 | 52.57 | 21.3 |
| rc_AA099225_at | AA099225 | 206 | EST | 7.33 | 0.00062 | 4.37 | 1.35 | 6.08 | 212.68 | 163.45 | 194.31 |
| rc_AA099571_at | AA099571 | 209 | MD-2 protein | #N/A | #N/A | 10.12 | 4.61 | 19.11 | 55.77 | 62.72 | 31.71 |
| rc_AA102098_at | AA102098 | 218 | EST | #N/A | #N/A | -1.8 | -5.18 | 15.21 | 21.79 | 20.01 | 6.78 |
| rc_AA102571_at | AA102571 | 220 | EST | #N/A | #N/A | 8.7 | 12.32 | 15.12 | 17.15 | 15.33 | 7.6 |
| acyl-Coenzyme A | | | | | | | | | | | |
| rc_AA112209_s_at | AA112209 | 223 | dehydrogenase, long chain | 3.37 | 0.00084 | 29.77 | 28.31 | 11.33 | 116 | 100.18 | 66.07 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | metastati metastati | | normal | | normal | |
|------------------|----------|--------|---------------------------------|-------------|---------|-----------|--------|---------------------|-----|--------|---------|---------------|----------------|
| | | | | in metas | p value | c: Mean | Median | c: Std | Dev | Mean | Std Dev | set 2: Median | set 2: Std Dev |
| rc_AA115933_s_at | AA115933 | 231 | KIAA1098 protein | #N/A | #N/A | 8.62 | 6.46 | 10.77 | | 33.88 | 16.63 | 34.38 | 16.63 |
| rc_AA116075_at | AA116075 | 234 | EST | #N/A | #N/A | 29.71 | 23.88 | 10 | | 62.94 | 25.13 | 64.79 | 25.13 |
| rc_AA121140_at | AA121140 | 235 | EST | 3.33 | 0.00058 | 6.67 | 5.82 | 3.73 | | 74.84 | 31.9 | 83.56 | 31.9 |
| rc_AA121257_at | AA121257 | 236 | EST | #N/A | #N/A | 21.76 | 21.21 | 32.49 | | 42.39 | 11.55 | 43.62 | 11.55 |
| rc_AA126059_at | AA126059 | 246 | EST | 3.08 | 0.00706 | 102.34 | 104.33 | 40.8 | | 380.92 | 316.4 | 280.71 | 316.4 |
| rc_AA127514_at | AA127514 | 253 | EST | 3.4 | 0.00045 | 11.36 | 10.76 | 6.8 | | 74.71 | 36.07 | 76.5 | 36.07 |
| | | | schwannomin interacting | | | | | | | | | | |
| rc_AA127646_at | AA127646 | 254 | protein 1 | #N/A | #N/A | 6.76 | -0.26 | 12.36 | | 44.24 | 20.02 | 41.48 | 20.02 |
| | | | sequence-specific single- | | | | | | | | | | |
| | | | stranded-DNA-binding | | | | | | | | | | |
| rc_AA128177_at | AA128177 | 258 | protein | #N/A | #N/A | 11.71 | 6.05 | 16.96 | | 44.4 | 33.54 | 33.57 | 33.54 |
| rc_AA129465_f_at | AA129465 | 263 | EST | #N/A | #N/A | 7.9 | 10.16 | 24.29 | | 61.62 | 34.37 | 59.75 | 34.37 |
| | | | meningioma expressed | | | | | | | | | | |
| | | | antigen 6 (coiled-coil proline- | | | | | | | | | | |
| rc_AA133214_s_at | AA133214 | 276 | rich) | #N/A | #N/A | 3.16 | 7.46 | 14.35 | | 65.17 | 51.18 | 56.11 | 51.18 |
| | | | calcitonin receptor-like | | | | | | | | | | |
| | | | receptor activity modifying | | | | | | | | | | |
| rc_AA133215_at | AA133215 | 277 | protein 1 | 4.55 | 0.02092 | 76.1 | 37.86 | 72.97 | | 250.94 | 64.2 | 266.82 | 64.2 |
| rc_AA133457_at | AA133457 | 280 | EST | #N/A | #N/A | 233.92 | 279.32 | 161.44 | | 456.09 | 114 | 475.45 | 114 |
| rc_AA136333_at | AA136333 | 300 | zinc finger protein | #N/A | #N/A | 17.23 | 17.21 | 5.7 | | 45.55 | 25.1 | 39.88 | 25.1 |
| rc_AA136611_at | AA136611 | 303 | EST | #N/A | #N/A | 9.05 | 6.82 | 8.39 | | 48.23 | 13.53 | 42.67 | 13.53 |
| rc_AA136940_at | AA136940 | 305 | EST | #N/A | #N/A | 40.81 | 41.78 | 20.7 | | 79.13 | 41.89 | 73.37 | 41.89 |
| AA143019_at | AA143019 | 309 | EST | 6.75 | 0.00109 | -0.4 | -5.82 | 18.62 | | 192.42 | 136.81 | 176.13 | 136.81 |
| rc_AA147626_at | AA147626 | 316 | EST | #N/A | #N/A | 37.93 | 20.43 | 44.09 | | 82.38 | 37.45 | 75.98 | 37.45 |
| | | | DKFZP586A0522 protein | 21.82 | 0 | 15.59 | 14.85 | 24.51 | | 610.52 | 288.9 | 685.45 | 288.9 |
| | | | flavin containing | | | | | | | | | | |
| rc_AA148480_s_at | AA148480 | 318 | monooxygenase 5 | 19.64 | 0 | 18.26 | 14.26 | 14.85 | | 521.95 | 247.99 | 407.11 | 247.99 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|---------------------------------|----------|--------|------------------|----------------------------|---------|-----------|--------|---------------|----------------|--------|-------------------|
| | | | | | | c: Mean | Median | c: Std Dev | set 2: Mean | Median | set 2: Std Dev |
| rc_AA148539_at | AA148539 | 319 | EST | #N/A | #N/A | 9.96 | 9.87 | 8.65 | 28.88 | 25.89 | 6.73 |
| rc_AA149253_at | AA149253 | 323 | EST | 5.12 | 0.00863 | 78.65 | 75.3 | 61.14 | 401.77 | 301.06 | 333.03 |
| rc_AA150205_at | AA150205 | 328 | EST | #N/A | #N/A | -1.1 | -1.72 | 9.15 | 8.12 | 7.44 | 9.59 |
| rc_AA150284_at | AA150284 | 329 | EST | #N/A | #N/A | 28.51 | 25.35 | 17.97 | 41.67 | 43.94 | 18.29 |
| rc_AA151243_at | AA151243 | 334 | EST | #N/A | #N/A | 1.13 | -0.17 | 14.55 | 43.61 | 42.74 | 11.08 |
| S-adenosylhomocysteine | | | | | | | | | | | |
| AA157401_at | AA157401 | 346 | hydrolase-like 1 | #N/A | #N/A | 15.44 | 13.27 | 14.06 | 61.17 | 65.58 | 27.48 |
| rc_AA167550_at | AA167550 | 361 | EST | #N/A | #N/A | 4.38 | 7.64 | 6.98 | 28.69 | 26.29 | 16.06 |
| rc_AA171529_at | AA171529 | 365 | EST | #N/A | #N/A | -1.76 | -4.58 | 6.37 | 51.3 | 47.89 | 33.98 |
| AA174202_at | AA174202 | 375 | EST | #N/A | #N/A | 55.99 | 38.87 | 72.55 | 120.99 | 128.88 | 62.33 |
| rc_AA179004_at | AA179004 | 377 | EST | 14.34 | 0.00008 | -33.2 | -28.97 | 78.62 | 503.76 | 495.87 | 326.16 |
| rc_AA182030_at | AA182030 | 387 | EST | 8.32 | 0.00018 | 14.05 | 16.82 | 12.13 | 222.23 | 220.01 | 117.56 |
| STAT induced STAT | | | | | | | | | | | |
| rc_AA182568_at | AA182568 | 388 | inhibitor-2 | 10.92 | 0.00099 | 23.5 | 18.15 | 21.15 | 501.87 | 386.2 | 478.02 |
| rc_AA187437_at | AA187437 | 389 | EST | #N/A | #N/A | 33.59 | 47.3 | 26.91 | 62.23 | 63 | 25.01 |
| protein phosphatase 2 | | | | | | | | | | | |
| (formerly 2A), regulatory | | | | | | | | | | | |
| subunit A (PR 65), beta | | | | | | | | | | | |
| rc_AA191310_s_at | AA191310 | 397 | isoform | 7.28 | 0 | 26.23 | 29.87 | 6.93 | 206.65 | 209.15 | 77.34 |
| rc_AA193671_at | AA193671 | 405 | KIAA0580 protein | #N/A | #N/A | 40.18 | 43.2 | 23.51 | 64.83 | 38.29 | 71.28 |
| eukaryotic translation | | | | | | | | | | | |
| initiation factor 4A, isoform 2 | | | | | | | | | | | |
| AA195179_s_at | AA195179 | 415 | EST | #N/A | #N/A | 30.71 | 38.24 | 25.48 | 85.7 | 87.87 | 42.11 |
| rc_AA195463_at | AA195463 | 416 | EST | #N/A | #N/A | 5.44 | 6.92 | 3.77 | 51.81 | 64.76 | 26.85 |
| rc_AA195515_at | AA195515 | 417 | EST | #N/A | #N/A | 7.27 | 3.56 | 8.61 | 51.59 | 49.91 | 23.13 |
| rc_AA195657_at | AA195657 | 419 | EST | 6.44 | 0.00016 | 5.72 | 7.44 | 9.74 | 157.7 | 136.21 | 100.68 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | metastati metastati | | | normal | | |
|---|----------|--------|----------------------|-------------|---------|-----------|--------|------------|---------------------|----------------------|-----------------------|--------|--|--|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | | |
| intercellular adhesion molecule 1 (CD54), human | | | | | | | | | | | | | | |
| rc_AA197311_s_at | AA197311 | 422 | rhinovirus receptor | 6.07 | 0.00053 | -19.49 | 1.63 | 43.72 | 154.69 | 175.76 | 83.19 | | | |
| rc_AA199603_at | AA199603 | 423 | EST | #N/A | #N/A | 14.97 | 24.27 | 28.57 | 54.95 | 55.7 | 19.61 | | | |
| rc_AA211370_at | AA211370 | 432 | EST | #N/A | #N/A | 27.26 | 29.44 | 16.5 | 44.85 | 45.87 | 21.25 | | | |
| rc_AA211418_at | AA211418 | 434 | EST | #N/A | #N/A | 65.81 | 70.1 | 37.84 | 223.56 | 214.42 | 151.4 | | | |
| rc_AA223902_at | AA223902 | 450 | EST | 9.91 | 0.00003 | 7.98 | -3.32 | 28.42 | 292.86 | 294.78 | 156.98 | | | |
| rc_AA226925_at | AA226925 | 452 | EST | #N/A | #N/A | 11.94 | 9.22 | 7.55 | 49.69 | 48.29 | 27.49 | | | |
| rc_AA227480_s_at | AA227480 | 456 | pim-2 oncogene | 3.31 | 0.02413 | 48 | 62.07 | 33.49 | 195.79 | 162.34 | 182.76 | | | |
| histone deacetylase 6 | | | | | | | | | | | | | | |
| rc_AA227968_at | AA227968 | 461 | epoxide hydrolase 2, | #N/A | #N/A | 177.49 | 137.57 | 94.86 | 349.29 | 340.4 | 101.81 | | | |
| cytoplasmic | | | | | | | | | | | | | | |
| rc_AA232114_s_at | AA232114 | 463 | EST | 24.34 | 0.00007 | 63.09 | 46.66 | 60.38 | 1455.28 | 1626.11 | 664.36 | | | |
| rc_AA233126_at | AA233126 | 466 | EST | #N/A | #N/A | 48.86 | 59.64 | 33.59 | 88.56 | 74.17 | 35.35 | | | |
| rc_AA233152_at | AA233152 | 467 | EST | 12.95 | 0 | -29.09 | -28.01 | 34.42 | 299.54 | 291.48 | 156.26 | | | |
| AA233225_at | AA233225 | 468 | MRS1 protein | #N/A | #N/A | 25.16 | 30.66 | 26.03 | 54.1 | 55.8 | 22.69 | | | |
| histidine ammonia-lyase | | | | | | | | | | | | | | |
| rc_AA233369_at | AA233369 | 471 | EST | 9.06 | 0.0008 | 49.39 | 47.92 | 39.8 | 425.35 | 405.81 | 214.85 | | | |
| rc_AA233763_at | AA233763 | 472 | EST | 4.61 | 0.00004 | 25.29 | 36.26 | 17.49 | 146.52 | 139.66 | 60.53 | | | |
| sperm associated antigen 7 | | | | | | | | | | | | | | |
| rc_AA233797_at | AA233797 | 473 | EST | #N/A | #N/A | 54.72 | 50.23 | 11.36 | 116.14 | 127.3 | 54.24 | | | |
| rc_AA233837_at | AA233837 | 474 | EST | 4.79 | 0.0034 | 18.96 | 19.45 | 40.67 | 214.77 | 118.28 | 278.62 | | | |
| CCAAT/enhancer binding protein (C/EBP), delta | | | | | | | | | | | | | | |
| AA234634_f_at | AA234634 | 486 | EST | 7.48 | 0.03318 | 158.16 | 49.12 | 223.12 | 621.92 | 588.94 | 332.64 | | | |
| AA234687_at | AA234687 | 487 | EST | #N/A | #N/A | -8.8 | -12.38 | 20.12 | 61.87 | 47.79 | 57.62 | | | |
| rc_AA234717_at | AA234717 | 489 | EST | #N/A | #N/A | 10.99 | 5.01 | 20.04 | 50.22 | 53.32 | 31.32 | | | |
| AA234817_at | AA234817 | 490 | EST | 6.22 | 0.00099 | 31.51 | 20.97 | 34.92 | 222.41 | 156.99 | 133.06 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|------------------|----------|--------|---|----------------------------|---------|-----------|--------|---------------|----------------|--------|-------------------|
| | | | | | | c: Mean | Median | c: Std Dev | set 2: Mean | Median | set 2: Std Dev |
| rc_AA234831_at | AA234831 | 491 | EST | 3.42 | 0.00206 | 23.54 | 21.62 | 28.81 | 112.19 | 119 | 49.23 |
| rc_AA235288_at | AA235288 | 494 | PTPL1-associated RhoGAP | 3.7 | 0.00643 | 34.06 | 30.95 | 14.36 | 169.9 | 113.81 | 138.05 |
| rc_AA235507_at | AA235507 | 498 | golgi autoantigen, golgin | 3.28 | 0.00249 | 22.14 | 37.31 | 26.61 | 111.91 | 126.75 | 58.39 |
| rc_AA242822_at | AA242822 | 524 | subfamily a, 5 | | #N/A | 9.44 | 13.66 | 8.25 | 27.21 | 25.96 | 16.64 |
| rc_AA243654_at | AA243654 | 532 | EST | | #N/A | 0.67 | 3.93 | 11.08 | 69.19 | 62.85 | 48.63 |
| rc_AA247453_at | AA247453 | 533 | EST | | 3.09 | 0.0015 | 32.38 | 37.86 | 21.04 | 120.43 | 133.44 |
| rc_AA250958_f_at | AA250958 | 538 | EST | #N/A | #N/A | 53.41 | 53.63 | 22.55 | 99.74 | 114.71 | 55.23 |
| rc_AA251114_at | AA251114 | 539 | prostate cancer overexpressed gene 1 | 6.6 | 0.00039 | 28.47 | 18.55 | 28.89 | 219.81 | 202.99 | 87.55 |
| rc_AA251776_at | AA251776 | 545 | jun D proto-oncogene | #N/A | #N/A | 30.8 | 23.59 | 32.23 | 51.25 | 46.83 | 15.96 |
| rc_AA251845_at | AA251845 | 548 | EST | | #N/A | 269.35 | 283.55 | 60.62 | 477.47 | 411.47 | 377.99 |
| rc_AA253410_at | AA253410 | 564 | EST | | #N/A | 18.46 | 7.23 | 42.79 | 49.37 | 26.82 | 45.2 |
| rc_AA255546_at | AA255546 | 569 | EST | | 4 | 0.00301 | 61.04 | 67.88 | 31.64 | 260.34 | 224.12 |
| rc_AA255903_at | AA255903 | 573 | CD39-like 4 | 5.67 | 0.01687 | 72.5 | 39.23 | 108.92 | 383.56 | 374.1 | 211.92 |
| rc_AA256341_at | AA256341 | 578 | EST | 7.37 | 0.00091 | 17.81 | 2.34 | 28.59 | 280.57 | 324.08 | 170.98 |
| rc_AA256990_at | AA256990 | 585 | EST | #N/A | #N/A | 8.43 | 11.36 | 27.79 | 15.63 | 16.56 | 6.89 |
| rc_AA257057_s_at | AA257057 | 586 | EST | 8.11 | 0.00379 | 42.36 | 16.78 | 47.02 | 451.86 | 462.6 | 343.05 |
| rc_AA258158_at | AA258158 | 588 | EST | #N/A | #N/A | 7.91 | 2.43 | 17.94 | 44.84 | 34.32 | 35.63 |
| rc_AA258353_at | AA258353 | 593 | EST | 5.28 | 0.00193 | 71.76 | 84 | 37.77 | 347.7 | 363.14 | 106.2 |
| rc_AA259064_at | AA259064 | 602 | EST | 13.15 | 0.00001 | 15.32 | -1.37 | 28.67 | 401.93 | 394.99 | 178.23 |
| rc_AA278670_at | AA278670 | 616 | EST | #N/A | #N/A | 7.44 | 11.47 | 12.63 | 54.24 | 49.98 | 28.69 |
| rc_AA278824_at | AA278824 | 619 | EST | #N/A | #N/A | 26.85 | 31.59 | 11.72 | 83.48 | 91.25 | 30.24 |
| rc_AA278853_at | AA278853 | 621 | EST | #N/A | #N/A | 10.28 | 11.7 | 21.49 | 42.68 | 43.68 | 17.64 |
| rc_AA279158_i_at | AA279158 | 623 | EST | #N/A | #N/A | 50 | 46.97 | 19.41 | 87.9 | 72.44 | 38.36 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | change In metas | p value | metastati | | metastati | | normal | | normal | |
|---|----------|--------|----------------------------|-------|---------|--------------------|---------|-----------|-----------|------------|--------|--------|---------|--------|---------|
| | | | | #N/A | #N/A | #N/A | #N/A | c: Mean | c: Median | c: Std Dev | Mean | Median | Std Dev | Mean | Std Dev |
| rc_AA279341_at | AA279341 | 625 | EST | #N/A | #N/A | #N/A | #N/A | 67.56 | 80.37 | 50.19 | 132.89 | 118.11 | 67.28 | | |
| rc_AA279916_at | AA279916 | 633 | EST | #N/A | #N/A | #N/A | #N/A | 61.08 | 56.18 | 25.7 | 115.24 | 102.89 | 58.77 | | |
| spleen focus forming virus (SFFV) proviral integration | | | | | | | | | | | | | | | |
| rc_AA280413_s_at | AA280413 | 638 | oncogene spi1 | 4.46 | 0.02062 | 64.05 | 69.15 | 51.55 | 339.15 | 51.55 | 339.15 | 353.53 | 235.59 | | |
| rc_AA281545_at | AA281545 | 645 | EST | 3.64 | 0.00002 | 6.52 | -0.81 | 16.89 | 87.27 | 16.89 | 87.27 | 85.27 | 34.29 | | |
| seven in absentia | | | | | | | | | | | | | | | |
| rc_AA281770_at | AA281770 | 649 | (Drosophila) homolog 1 | 3.96 | 0.00094 | 7.67 | 4.72 | 15.41 | 103.75 | 15.41 | 103.75 | 79.4 | 70.74 | | |
| rc_AA281796_at | AA281796 | 650 | mannose-P-dolichol | 3.3 | 0.04108 | 65.08 | 53.58 | 57.86 | 170.88 | 57.86 | 170.88 | 165.02 | 41.87 | | |
| rc_AA282541_at | AA282541 | 661 | utilization defect 1 | #N/A | #N/A | 7.18 | 5.97 | 14.25 | 31.31 | 14.25 | 31.31 | 29.9 | 13.53 | | |
| rc_AA282956_at | AA282956 | 664 | EST | #N/A | #N/A | 0.28 | -9.07 | 30.81 | 59.89 | 30.81 | 59.89 | 51.54 | 35.5 | | |
| rc_AA283066_at | AA283066 | 666 | EST | #N/A | #N/A | 21.18 | 25.64 | 13.39 | 67.44 | 13.39 | 67.44 | 59.46 | 35.89 | | |
| phosphatidylethanolamine N- methyltransferase | | | | | | | | | | | | | | | |
| rc_AA284795_at | AA284795 | 678 | EST | 10.03 | 0.00019 | 44.8 | 62.07 | 44.12 | 514.93 | 44.12 | 514.93 | 591.52 | 206.4 | | |
| rc_AA285053_at | AA285053 | 681 | EST | 6.95 | 0.00125 | 12.65 | 14.54 | 23.53 | 238.16 | 23.53 | 238.16 | 242.27 | 169.12 | | |
| rc_AA286710_at | AA286710 | 683 | lymphocyte adaptor protein | #N/A | #N/A | 37.88 | 39.15 | 30.32 | 82.93 | 30.32 | 82.93 | 86.15 | 45.58 | | |
| rc_AA287566_at | AA287566 | 690 | KIAA0187 gene product | 9.07 | 0.00013 | 4.86 | 6.24 | 7.4 | 246.24 | 7.4 | 246.24 | 201.66 | 228.64 | | |
| rc_AA291293_at | AA291293 | 698 | EST | #N/A | #N/A | 17.35 | 18.07 | 17.24 | 33.6 | 17.24 | 33.6 | 33.3 | 5.56 | | |
| AA292440_s_at | AA292440 | 709 | DKFZP566B133 protein | #N/A | #N/A | 122.1 | 125.27 | 37.73 | 370.32 | 37.73 | 370.32 | 318.31 | 181.37 | | |
| AA296821_at | AA296821 | 723 | EST | #N/A | #N/A | 15.47 | 10.65 | 21.91 | 57.72 | 21.91 | 57.72 | 71.28 | 33.61 | | |
| AA298180_at | AA298180 | 726 | EST | 3.11 | 0.00747 | 19.6 | 25.9 | 18.83 | 109.91 | 18.83 | 109.91 | 84.28 | 88.07 | | |
| rc_AA312946_s_at | AA312946 | 731 | EST | 9.21 | 0.00106 | 12.32 | 13.78 | 12.24 | 300.22 | 12.24 | 300.22 | 304.56 | 213.18 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | metastati | | normal | | normal | |
|-------------------------|----------|--------|----------------------|-------------|---------|-----------|--------|------------|-------------|---------------|----------------|--------|--|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | | |
| fatty-acid-Coenzyme A | | | | | | | | | | | | | |
| AA316272_at | AA316272 | 734 | ligase, long-chain 3 | #N/A | #N/A | 34.62 | 38.08 | 17.08 | 71.9 | 73.01 | 73.01 | 27.47 | |
| AA328684_at | AA328684 | 737 | EST | #N/A | #N/A | 49.88 | 48.15 | 31.41 | 115.97 | 114.66 | 114.66 | 46.25 | |
| rc_AA342918_at | AA342918 | 750 | EST | #N/A | #N/A | 23.67 | 31.68 | 25.77 | 69.4 | 73.71 | 73.71 | 18.13 | |
| rc_AA343142_at | AA343142 | 751 | EST | 20.87 | 0.00003 | -12.34 | -21.46 | 30.45 | 610.64 | 636.83 | 636.83 | 438.33 | |
| complement component 8, | | | | | | | | | | | | | |
| rc_AA344866_s_at | AA344866 | 752 | gamma polypeptide | 7.28 | 0.00206 | 292.65 | 305.28 | 176.61 | 1845.16 | 1679.29 | 1679.29 | 561.04 | |
| rc_AA363203_s_at | AA363203 | 761 | EST | #N/A | #N/A | 35.7 | 40.27 | 34.51 | 78.45 | 75.11 | 75.11 | 47.8 | |
| rc_AA365691_at | AA365691 | 763 | EST | #N/A | #N/A | 48.01 | 47.17 | 25.37 | 28.69 | 26.73 | 26.73 | 13.89 | |
| rc_AA381125_at | AA381125 | 772 | EST | 15.48 | 0 | 17.66 | 13.82 | 13.2 | 412.26 | 344.45 | 344.45 | 217.56 | |
| AA397841_at | AA397841 | 780 | EST | 8.21 | 0 | 7.72 | 3.33 | 18.47 | 214.17 | 189.93 | 189.93 | 116.41 | |
| rc_AA397904_at | AA397904 | 781 | EST | #N/A | #N/A | 22.74 | 18.55 | 19.05 | 59.75 | 54.83 | 54.83 | 32.24 | |
| rc_AA397919_at | AA397919 | 785 | EST | #N/A | #N/A | 108.63 | 144.35 | 84.25 | 243.79 | 199.62 | 199.62 | 185.4 | |
| growth factor receptor- | | | | | | | | | | | | | |
| rc_AA398124_s_at | AA398124 | 787 | bound protein 14 | 7.82 | 0.00009 | 3.4 | 5.86 | 7.61 | 189.27 | 167.23 | 167.23 | 110.44 | |
| rc_AA398280_at | AA398280 | 792 | EST | 12.43 | 0.00134 | -114.74 | -71.05 | 103.33 | 433.45 | 423.73 | 423.73 | 356.61 | |
| rc_AA398386_at | AA398386 | 793 | EST | 5.71 | 0.00007 | 10.59 | 16.25 | 21.59 | 153.16 | 164.38 | 164.38 | 83.94 | |
| rc_AA398423_at | AA398423 | 795 | EST | 8.26 | 0.00063 | -17.3 | -16.19 | 23.92 | 230.91 | 250.5 | 250.5 | 156.29 | |
| rc_AA398674_at | AA398674 | 798 | thrombospondin 1 | #N/A | #N/A | -27.87 | 14.49 | 146.65 | 137.87 | 96.14 | 96.14 | 119.21 | |
| rc_AA400030_at | AA400030 | 806 | EST | 3.98 | 0.00088 | 8.99 | 12.21 | 11.35 | 97.83 | 115.15 | 115.15 | 52.04 | |
| rc_AA400080_at | AA400080 | 807 | EST | #N/A | #N/A | 25.33 | 23.57 | 27.54 | 61.21 | 60.21 | 60.21 | 29.91 | |
| rc_AA400258_at | AA400258 | 812 | EST | 11.89 | 0.00478 | 85.31 | 36.81 | 139.93 | 827.48 | 884.35 | 884.35 | 562.14 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | metastati | | normal | | set 2: Median | set 2: Std Dev |
|---|----------|--------|---------------------|----------------------------|---------|-----------|-----------|---------------|----------------|---------|--------|------------------|-------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | | | | |
| tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein | | | | | | | | | | | | | |
| AA400333_at | AA400333 | 815 | interacting protein | #N/A | #N/A | 27.22 | 27.33 | 24.37 | | 62.54 | 58.6 | 31.69 | |
| rc_AA400934_at | AA400934 | 824 | EST | 4.98 | 0.02013 | 75.44 | 67.21 | 77.7 | | 305.09 | 307.45 | 125.76 | |
| calcitonin receptor-like receptor activity modifying protein 3 | | | | | | | | | | | | | |
| rc_AA400979_at | AA400979 | 825 | protein 3 | 6.65 | 0.01051 | 48.89 | 21.04 | 80.4 | | 276.38 | 267.3 | 88.7 | |
| rc_AA401091_at | AA401091 | 826 | EST | #N/A | #N/A | 31.88 | 32.59 | 43.51 | | 30.55 | 19.82 | 28.68 | |
| rc_AA401562_s_at | AA401562 | 830 | EST | 50.45 | 0.00301 | 155.46 | 63.87 | 317.6 | | 3745.71 | 3628.4 | 1635.98 | |
| rc_AA401825_at | AA401825 | 831 | EST | #N/A | #N/A | 24.3 | 26.82 | 18.04 | | 65.22 | 57.51 | 46.54 | |
| growth arrest and DNA-damage-inducible, gamma | | | | | | | | | | | | | |
| rc_AA402224_at | AA402224 | 836 | KIAA0548 protein | 14.41 | 0.00012 | 37.55 | 48.88 | 48.58 | | 749.36 | 812.2 | 443.66 | |
| rc_AA402610_at | AA402610 | 839 | EST | #N/A | #N/A | 3.02 | 6.69 | 13.83 | | 27.54 | 23.2 | 17.78 | |
| rc_AA402656_at | AA402656 | 841 | EST | 12.05 | 0.00001 | -2.56 | 18.8 | 40.57 | | 342.11 | 315.47 | 205.61 | |
| AA404214_at | AA404214 | 846 | EST | #N/A | #N/A | 35.28 | 48.54 | 23.52 | | 70.66 | 66.71 | 55.97 | |
| rc_AA404248_at | AA404248 | 847 | EST | #N/A | #N/A | 11.96 | 11.18 | 10.84 | | 40.92 | 35.06 | 17.49 | |
| rc_AA404352_at | AA404352 | 850 | EST | 7 | 0.00059 | 26.7 | 20.02 | 33.28 | | 213.01 | 172.11 | 108 | |
| rc_AA405494_at | AA405494 | 858 | EST | #N/A | #N/A | 10.03 | 9.53 | 7.62 | | 59.95 | 44.88 | 50.8 | |
| rc_AA405495_at | AA405495 | 859 | EST | #N/A | #N/A | 26.12 | 22.63 | 43.42 | | 79 | 82.8 | 30.16 | |
| rc_AA405744_at | AA405744 | 863 | EST | #N/A | #N/A | 61.18 | 28.74 | 58.71 | | 64.39 | 57.95 | 35.67 | |
| rc_AA406363_at | AA406363 | 874 | EST | #N/A | #N/A | 6.85 | 5.69 | 15.69 | | 35.62 | 35.06 | 13.69 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | metastati metastati | | | normal | normal | |
|---|----------|--------|--|-------------|---------|-----------|--------|------------|---------------------|--------|---------|--------|-------------|---------------|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | Mean | Median | Std Dev | | set 2: Mean | set 2: Median |
| rc_AA406546_at | AA406546 | 879 | EST | #N/A | #N/A | -1.45 | -7.89 | 15.19 | 46.62 | 50.65 | 26.97 | | | |
| rc_AA406610_at | AA406610 | 880 | EST | #N/A | #N/A | 5.99 | 6.04 | 4.63 | 35.94 | 34.84 | 11.57 | | | |
| rc_AA410255_at | AA410255 | 882 | EST | 7.56 | 0.00043 | 0.82 | 4.15 | 11.49 | 195.75 | 236.93 | 110.49 | | | |
| rc_AA411795_at | AA411795 | 892 | EST | #N/A | #N/A | 72.18 | 53.17 | 44.28 | 130.27 | 131.65 | 23.71 | | | |
| rc_AA412063_at | AA412063 | 895 | EST | 8.26 | 0.00001 | 11.36 | 14.03 | 19.55 | 220.12 | 187.85 | 149.43 | | | |
| rc_AA412068_at | AA412068 | 896 | EST | #N/A | #N/A | 30.52 | 29.79 | 13.4 | 81.26 | 74.52 | 35.68 | | | |
| rc_AA412149_at | AA412149 | 897 | KIAA0480 gene product | #N/A | #N/A | 14.07 | 10.08 | 14.16 | 37.43 | 32.4 | 15.56 | | | |
| rc_AA412520_at | AA412520 | 903 | EST | #N/A | #N/A | 18.84 | 14.4 | 14.11 | 80.29 | 103.19 | 41.98 | | | |
| rc_AA412700_at | AA412700 | 904 | ubiquitin-conjugating enzyme E2L 6 | #N/A | #N/A | 139.65 | 95.44 | 135.61 | 275.39 | 273.98 | 112.87 | | | |
| 5-methyltetrahydrofolate-homocysteine | | | | | | | | | | | | | | |
| rc_AA416936_at | AA416936 | 910 | methylenetetrahydrofolate reductase | 4.98 | 0.00632 | 82.04 | 85.81 | 69.18 | 427.41 | 366.53 | 235.63 | | | |
| rc_AA417078_at | AA417078 | 916 | EST | 4.1 | 0.00414 | 36.75 | 35.35 | 15.12 | 189.88 | 171.1 | 150.02 | | | |
| rc_AA418398_at | AA418398 | 921 | EST | #N/A | #N/A | 0.1 | -6.02 | 17.92 | 30.41 | 32 | 20.72 | | | |
| rc_AA419608_at | AA419608 | 925 | EST | 9.19 | 0.00005 | 51.89 | 51.37 | 25.93 | 524.34 | 571.05 | 296.46 | | | |
| rc_AA419622_at | AA419622 | 926 | EST | 4.62 | 0.00386 | 24.88 | 17.15 | 26 | 158.88 | 162.5 | 112.57 | | | |
| rc_AA421051_at | AA421051 | 928 | serum-inducible kinase | #N/A | #N/A | 42.94 | 7.14 | 87.89 | 51.27 | 45.65 | 28 | | | |
| branched chain alpha-ketoacid dehydrogenase | | | | | | | | | | | | | | |
| rc_AA421052_at | AA421052 | 929 | kinase | 3.52 | 0.00869 | 77.76 | 94.75 | 43.63 | 251.45 | 221.35 | 109.93 | | | |
| rc_AA421561_at | AA421561 | 933 | insulin-like growth factor 2 (somatomedin A) | 9.98 | 0.00007 | 79.46 | 77.34 | 41.63 | 921.91 | 703.16 | 679.72 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | metastati metastati | | | normal | | |
|------------------|----------|--------|---|-------------|----------|---------|-----------|--------|------------|---------------------|--------|---------|--------|--------|---------|
| | | | | in metas | in metas | | c: Mean | Median | c: Std Dev | Mean | Median | Std Dev | Mean | Median | Std Dev |
| AA424307_at | AA424307 | 944 | EST | 5.73 | 0.0074 | 44.98 | 21.05 | 54.01 | 202.82 | 194.92 | 68.07 | | | | |
| rc_AA424798_at | AA424798 | 947 | EST | 17.45 | 0.00352 | 48.63 | 15.48 | 171.26 | 879.91 | 873.25 | 489.59 | | | | |
| rc_AA425214_at | AA425214 | 950 | EST | #N/A | #N/A | 2.71 | 2.07 | 4.88 | 21.4 | 20.31 | 10.15 | | | | |
| rc_AA426643_at | AA426643 | 970 | EST | #N/A | #N/A | 9.96 | 0.97 | 18.11 | 48.26 | 47.37 | 23.47 | | | | |
| rc_AA427537_at | AA427537 | 974 | DKFZP566J153 protein regulator of G-protein signalling 14 | #N/A | #N/A | 183.26 | 156.56 | 68.58 | 259.57 | 242.97 | 79.81 | | | | |
| rc_AA427579_at | AA427579 | 975 | signalling 14 | #N/A | #N/A | 13.35 | 13.28 | 16.49 | 34.79 | 25.25 | 25.11 | | | | |
| rc_AA427819_at | AA427819 | 980 | midline 2 | 3.44 | 0.00063 | 25.98 | 17.06 | 14.91 | 97.03 | 93.49 | 31.39 | | | | |
| rc_AA428150_at | AA428150 | 985 | EST | 5.24 | 0.00167 | 41.92 | 35.06 | 30.53 | 213.96 | 217.27 | 76.08 | | | | |
| rc_AA428325_at | AA428325 | 988 | EST | 8.36 | 0.00002 | -0.52 | 3.28 | 16.92 | 194.02 | 167.37 | 111.11 | | | | |
| rc_AA428900_at | AA428900 | 992 | EST | 7.01 | 0.00037 | 66.25 | 66.77 | 15.35 | 615.96 | 619.42 | 441.72 | | | | |
| rc_AA429038_at | AA429038 | 995 | EST | 3.29 | 0.00927 | 13.39 | 1.93 | 28.01 | 108.66 | 87.59 | 86.11 | | | | |
| rc_AA429478_at | AA429478 | 998 | EST | 3.41 | 0.02599 | 55.86 | 65.19 | 47.48 | 192.7 | 196 | 89.2 | | | | |
| rc_AA429651_at | AA429651 | 1002 | KIAA0871 protein | #N/A | #N/A | 15.52 | 13.25 | 17.03 | 44.75 | 41.91 | 28.67 | | | | |
| rc_AA432166_f_at | AA432166 | 1030 | succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD | #N/A | #N/A | 10.94 | 14.1 | 42.99 | 33.86 | 42.75 | 27.46 | | | | |
| rc_AA434225_at | AA434225 | 1035 | serum constituent protein | #N/A | #N/A | 1010.84 | 876.42 | 674.94 | 1022.5 | 746.49 | 681.49 | | | | |
| rc_AA435591_at | AA435591 | 1038 | kinesin family member 3B | 3.5 | 0.0001 | 3.57 | 3.68 | 10.34 | 75.9 | 81.12 | 29.32 | | | | |
| rc_AA435753_at | AA435753 | 1045 | EST | 4.71 | 0.00078 | 198.97 | 193.33 | 110.58 | 970.79 | 830.39 | 567.79 | | | | |
| rc_AA436156_s_at | AA436156 | 1051 | EST | #N/A | #N/A | 22.66 | 7.78 | 34.68 | 54.98 | 48.35 | 38.09 | | | | |
| rc_AA436548_at | AA436548 | 1054 | EST | #N/A | #N/A | 5.08 | 5.93 | 5.2 | 40.27 | 38.99 | 22.22 | | | | |
| rc_AA436880_at | AA436880 | 1058 | EST | 3.22 | 0.00699 | 4.71 | 9.21 | 13.85 | 86.89 | 68.41 | 66.5 | | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | change In metas | p value | metastati | | | normal | | |
|------------------|----------|--------|--|-------|---------|--------------------|---------|----------------------|------------------------|-------------------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | | | metastati c: Mean | metastati c: Median | metastati c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| rc_AA437295_at | AA437295 | 1062 | ribosomal protein L7a | 4.35 | 0.00347 | 19.67 | 20.38 | 43.07 | 139.16 | 140.38 | 70.9 | | |
| rc_AA443658_at | AA443658 | 1079 | transmembrane 7 superfamily member 2 | 9.06 | 0.00048 | 4.48 | 17.91 | 24.51 | 276.02 | 194.73 | 227.48 | | |
| rc_AA443934_at | AA443934 | 1083 | GTP-binding protein Rho7 | 3.09 | 0.00214 | 30.32 | 35.97 | 13.76 | 115.87 | 113.7 | 66.78 | | |
| rc_AA446342_at | AA446342 | 1088 | seven in absentia (Drosophila) homolog 1 | 4.84 | 0.00015 | 9.92 | 9.12 | 4.58 | 110.73 | 115.89 | 53.13 | | |
| rc_AA447802_at | AA447802 | 1108 | EST | #N/A | #N/A | 15.64 | 17.7 | 13.81 | 21.51 | 21.34 | 7.37 | | |
| rc_AA447876_at | AA447876 | 1109 | EST | #N/A | #N/A | 13.05 | 6.78 | 34.07 | 27.08 | 22.86 | 22.46 | | |
| rc_AA448300_at | AA448300 | 1116 | FXRD domain-containing ion transport regulator 1 (phospholemman) | 24.97 | 0.00001 | 118.64 | 81.63 | 70.34 | 2849.54 | 2905.51 | 994.41 | | |
| rc_AA449108_at | AA449108 | 1118 | EST | #N/A | #N/A | 10.9 | 18.13 | 15.28 | 52.58 | 57.3 | 23.76 | | |
| rc_AA449297_at | AA449297 | 1121 | EST | 3.78 | 0.00039 | 3.76 | 0.63 | 19.01 | 91.67 | 81.15 | 55.17 | | |
| rc_AA452158_at | AA452158 | 1141 | ras homolog gene family, member B | 28.96 | 0.00064 | -103.87 | -106.99 | 71.68 | 1071.9 | 1164.8 | 789.64 | | |
| rc_AA453770_s_at | AA453770 | 1157 | EST | 6.04 | 0.00524 | 46.33 | 25.95 | 53.45 | 217.46 | 212.4 | 70.02 | | |
| rc_AA454177_l_at | AA454177 | 1164 | EST | 10.3 | 0.0008 | 9.16 | 14.72 | 11.39 | 324.16 | 253.23 | 258.82 | | |
| rc_AA454667_at | AA454667 | 1167 | EST | #N/A | #N/A | 21.25 | 12.77 | 23.4 | 83.02 | 75.81 | 56.63 | | |
| rc_AA455111_at | AA455111 | 1173 | heterogeneous nuclear ribonucleoprotein C (C1/C2) | #N/A | #N/A | -31.71 | -40.39 | 38.45 | 38.96 | 36.83 | 26.21 | | |
| rc_AA455261_at | AA455261 | 1175 | chromobox homolog 7 | #N/A | #N/A | 32.5 | 45.54 | 26.51 | 66.78 | 66.08 | 30.15 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| | | | | fold change | | metastati | | | | normal | | | |
|------------------|----------|--------|---|---------------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|--------|-------|
| Affy ID | Genbank | Seq ID | Known Gene Name | in metas | p value | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | | |
| rc_AA455865_at | AA455865 | 1180 | phosphatidylinositol glycan, class B | 5.41 | 0.00004 | 11.68 | 8.67 | 10.65 | 133.15 | 134.74 | 63.3 | | |
| rc_AA455896_s_at | AA455896 | 1181 | | glypican 1 | 3.46 | 0.00887 | 16.1 | 4.35 | 40.39 | 120.52 | 137.84 | 66.93 | |
| rc_AA455987_at | AA455987 | 1183 | | EST | 5.36 | 0.00029 | 20.54 | 17.51 | 15.24 | 128.55 | 130.64 | 17.07 | |
| rc_AA455988_at | AA455988 | 1184 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) | 15.54 | 0.00001 | 10.13 | 11.88 | 8.38 | 354.42 | 375.91 | 141.08 | | |
| rc_AA456075_at | AA456075 | 1186 | | RAD23 (S. cerevisiae) homolog A | #N/A | #N/A | 33.34 | 38.35 | 32.93 | 90.47 | 66.92 | 66.03 | |
| rc_AA456080_at | AA456080 | 1187 | | | EST | #N/A | #N/A | 32.35 | 17.59 | 33.21 | 27.76 | 26.18 | 12.38 |
| rc_AA456147_at | AA456147 | 1188 | general transcription factor | 4.23 | 0.00088 | 4.61 | 0.17 | 9.08 | 102.1 | 89.95 | 63.84 | | |
| rc_AA456289_at | AA456289 | 1189 | | IIIA | 15.31 | 0.00004 | 18.07 | 17.84 | 39.22 | 512.64 | 542.52 | 303.15 | |
| rc_AA456326_at | AA456326 | 1191 | | EST | 3.35 | 0.00489 | 17.08 | 2.74 | 30.38 | 111.5 | 102.17 | 68.09 | |
| rc_AA456612_at | AA456612 | 1195 | | EST | #N/A | #N/A | 164.11 | 136.36 | 117.01 | 254.26 | 266.45 | 84.11 | |
| AA456687_at | AA456687 | 1197 | | EST | 3.08 | 0.01189 | 17.88 | 37.03 | 53.32 | 130.65 | 118.55 | 65.44 | |
| rc_AA456845_at | AA456845 | 1198 | KIAA0680 gene product | #N/A | #N/A | 23.95 | 17.11 | 17.99 | 67.15 | 63.46 | 49.27 | | |
| rc_AA458652_at | AA458652 | 1202 | | EST | 8.26 | 0.00001 | 19.3 | 18.21 | 17.18 | 203.23 | 218.67 | 53.52 | |
| rc_AA459005_at | AA459005 | 1210 | | EST | #N/A | #N/A | -3.57 | 12.22 | 40.05 | 49.76 | 42.58 | 28.85 | |
| rc_AA459256_at | AA459256 | 1212 | lectin, mannose-binding, 1 | 3.01 | 0.00094 | 3.83 | 8.1 | 8.32 | 65.91 | 63.36 | 39.92 | | |
| rc_AA460661_at | AA460661 | 1229 | | EST | 7.02 | 0.00053 | -1.52 | -6.03 | 15.81 | 184.62 | 198.21 | 108.17 | |
| rc_AA461448_at | AA461448 | 1240 | | EST | #N/A | #N/A | 1.74 | -4.19 | 22.52 | 58.65 | 56.06 | 32.42 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | metastati | | normal | | normal | |
|---|----------|--------|-----------------|-------------|----------|---------|-----------|-----------|-----------|--------|--------|-------------|---------------|----------------|
| | | | | in metas | in metas | | c: Mean | c: Median | c: Std | Mean | Median | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA463729_at | AA463729 | 1250 | EST | 4.07 | 0.00676 | 19.31 | 19.05 | 13.37 | 150.62 | 116.86 | 156.67 | | | |
| rc_AA463876_at | AA463876 | 1252 | EST | 3.31 | 0.00109 | 9.81 | 11.89 | 10.39 | 73.95 | 73.76 | 46.64 | | | |
| rc_AA464606_at | AA464606 | 1261 | MRS1 protein | #N/A | #N/A | 24.35 | 19.03 | 39.62 | 59.55 | 36.75 | 57.76 | | | |
| rc_AA465381_at | AA465381 | 1272 | EST | #N/A | #N/A | 88.83 | 36.24 | 130.22 | 102.73 | 113.07 | 52.43 | | | |
| rc_AA465720_at | AA465720 | 1274 | EST | #N/A | #N/A | 11.5 | 21.33 | 37.22 | 93.06 | 108.97 | 43.26 | | | |
| solute carrier family 21 (organic anion transporter), member 9 | | | | | | | | | | | | | | |
| rc_AA470153_at | AA470153 | 1275 | | 13.26 | 0.00315 | 47.49 | 48.57 | 116.54 | 726.75 | 713.23 | 297.62 | | | |
| homolog of mouse quaking QKI (KH domain RNA binding protein) | | | | | | | | | | | | | | |
| rc_AA478104_at | AA478104 | 1296 | | #N/A | #N/A | -7.07 | -11.44 | 23.2 | 62.06 | 47.17 | 56.07 | | | |
| rc_AA478441_at | AA478441 | 1302 | cathepsin F | 5.07 | 0.00752 | 53.85 | 67.48 | 43.52 | 243.44 | 243.61 | 69.17 | | | |
| rc_AA479148_at | AA479148 | 1311 | EST | 38.05 | 0 | 6.2 | 1.32 | 14.38 | 895.91 | 847.72 | 362.53 | | | |
| AA479266_at | AA479266 | 1312 | EST | #N/A | #N/A | 18.04 | 21.7 | 25.73 | 42.53 | 38.32 | 18.46 | | | |
| S-adenosylhomocysteine hydrolase-like 1 | | | | | | | | | | | | | | |
| rc_AA479488_at | AA479488 | 1313 | | 4 | 0.0269 | 75.18 | 60.93 | 59.8 | 241.1 | 222.96 | 112.87 | | | |
| rc_AA479961_at | AA479961 | 1320 | EST | #N/A | #N/A | 33.49 | 28.45 | 10.58 | 88.13 | 89.35 | 36.9 | | | |
| rc_AA479968_s_at | AA479968 | 1321 | arylsulfatase A | 9.01 | 0.00224 | 37.97 | 20.36 | 45.8 | 331.32 | 312.63 | 97.49 | | | |
| rc_AA480991_s_at | AA480991 | 1323 | EST | 8.59 | 0.00156 | 48.08 | 25.74 | 51.03 | 444.29 | 309.38 | 367.89 | | | |
| MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) | | | | | | | | | | | | | | |
| rc_AA480997_i_at | AA480997 | 1324 | | #N/A | #N/A | 16 | 20.58 | 9.93 | 68.53 | 55.62 | 63.6 | | | |
| rc_AA481057_f_at | AA481057 | 1325 | EST | #N/A | #N/A | 16.3 | 18.55 | 8.1 | 33.83 | 37.89 | 23.22 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | metastati metastati | | | normal | | |
|------------------|----------|--------|---|----------------------------|---------|-----------|--------|--------|---------------------|--------|--------|----------------|------------------|-------------------|
| | | | | | | c: Mean | Median | Dev | c: Mean | Median | Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_AA486407_at | AA486407 | 1347 | EST | #N/A | #N/A | 33.22 | 47.88 | 28.61 | 81.72 | 97.02 | 55.07 | | | |
| rc_AA486567_at | AA486567 | 1350 | EST | 5 | 0.00002 | 4.65 | 2.5 | 21.62 | 131.53 | 98.76 | 95.59 | | | |
| rc_AA486794_at | AA486794 | 1351 | EST | #N/A | #N/A | 49.57 | 52.25 | 18.73 | 78.8 | 72.55 | 31.84 | | | |
| rc_AA487195_at | AA487195 | 1354 | EST | #N/A | #N/A | 8.73 | 7.94 | 9.21 | 21.04 | 14.67 | 16.52 | | | |
| rc_AA487503_at | AA487503 | 1356 | EST | 8.85 | 0.00012 | 13.8 | 17.99 | 8.76 | 220.45 | 255.47 | 119.11 | | | |
| rc_AA487576_at | AA487576 | 1357 | EST | #N/A | #N/A | -12.17 | -14.87 | 17.17 | 26.05 | 25.27 | 11.13 | | | |
| rc_AA489009_at | AA489009 | 1366 | EST | #N/A | #N/A | 15.19 | 18.01 | 8.67 | 59.19 | 45.15 | 41.42 | | | |
| rc_AA490882_s_at | AA490882 | 1381 | EST | 3.29 | 0.00319 | 20.67 | 13.84 | 27.06 | 100.67 | 98.47 | 54.46 | | | |
| rc_AA490890_at | AA490890 | 1382 | EST | 3.02 | 0.00007 | 20.26 | 21.34 | 9.23 | 75.61 | 65.02 | 33.37 | | | |
| rc_AA490947_at | AA490947 | 1383 | EST | #N/A | #N/A | 34.15 | 35 | 21.49 | 56.24 | 38.75 | 49.85 | | | |
| rc_AA490964_at | AA490964 | 1384 | EST | #N/A | #N/A | 20.3 | 17.53 | 11.39 | 47.7 | 41.84 | 25.18 | | | |
| rc_AA495803_at | AA495803 | 1392 | EST | #N/A | #N/A | 95.29 | 83.46 | 90.72 | 94.07 | 93.85 | 37.65 | | | |
| rc_AA495924_at | AA495924 | 1395 | kinesin family member 3B | #N/A | #N/A | 4.16 | 3.28 | 2.95 | 35.69 | 34.43 | 19.93 | | | |
| rc_AA496053_at | AA496053 | 1396 | EST | 3.28 | 0.00095 | 5.36 | 2.22 | 17.58 | 81.79 | 94.01 | 42.77 | | | |
| rc_AA496927_at | AA496927 | 1402 | EST | #N/A | #N/A | 24.89 | 26.85 | 9.47 | 58.2 | 58.42 | 17.68 | | | |
| rc_AA496936_at | AA496936 | 1403 | EST | #N/A | #N/A | 17.71 | 9.86 | 20.19 | 30.24 | 34.4 | 14.77 | | | |
| rc_AA504324_at | AA504324 | 1412 | EST | #N/A | #N/A | 45.99 | 38.81 | 31.27 | 74.31 | 72.05 | 31.59 | | | |
| rc_AA521290_at | AA521290 | 1421 | EST | 4.53 | 0.0148 | 46.54 | 22.84 | 63.63 | 166.84 | 174.65 | 58.28 | | | |
| rc_AA598412_at | AA598412 | 1425 | EST | #N/A | #N/A | -2.4 | -5.93 | 29.83 | 59 | 52.53 | 29.41 | | | |
| rc_AA598453_s_at | AA598453 | 1429 | EST | #N/A | #N/A | 7.27 | 7.06 | 9.67 | 67.15 | 54.25 | 41.65 | | | |
| rc_AA598685_at | AA598685 | 1435 | lectin, galactoside-binding, soluble, 8 (galectin 8) | #N/A | #N/A | 16.45 | 11.35 | 11.87 | 55.9 | 55.08 | 42.18 | | | |
| rc_AA599107_at | AA599107 | 1443 | EST | #N/A | #N/A | 53.34 | 10 | 88.85 | 77.28 | 58.08 | 40.75 | | | |
| rc_AA599199_at | AA599199 | 1444 | endothelin converting enzyme 1 | #N/A | #N/A | 187.77 | 108.97 | 225.55 | 695.29 | 680.26 | 375.12 | | | |
| rc_AA599214_at | AA599214 | 1446 | EST | #N/A | #N/A | 10.94 | 7.36 | 12.27 | 34.58 | 36 | 14.54 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | metastati | | normal | | normal | |
|---|----------|--------|-----------------------------|-------------|--------------|---------|-----------|------------|-----------|------------|-------------|---------------|----------------|----------------|
| | | | | in metas | in metastati | | c: Mean | c: Std Dev | c: Mean | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Std Dev |
| rc_AA599365_at | AA599365 | 1449 | decorin | #N/A | #N/A | #N/A | 36.41 | 21.53 | 34.43 | 21.53 | 83.84 | 84.81 | 43.41 | 43.41 |
| rc_AA600248_at | AA600248 | 1461 | EST | #N/A | #N/A | #N/A | 59.11 | 32.47 | 59.91 | 32.47 | 80.55 | 71.14 | 61.42 | 61.42 |
| rc_AA608546_at | AA608546 | 1463 | EST | 12.52 | 0.00003 | #N/A | -19.59 | 29.39 | -29.07 | 29.39 | 310.07 | 300.44 | 189.6 | 189.6 |
| rc_AA608723_at | AA608723 | 1467 | EST | #N/A | #N/A | #N/A | 17.44 | 13.31 | 15.29 | 13.31 | 66.54 | 70.38 | 20.94 | 20.94 |
| rc_AA609316_at | AA609316 | 1481 | EGF-like-domain, multiple 5 | 7.97 | 0.00011 | #N/A | 22.6 | 25.56 | 21.61 | 25.56 | 236.54 | 226.79 | 65.9 | 65.9 |
| rc_AA609519_at | AA609519 | 1482 | EST | 8.13 | 0.00009 | #N/A | 29.3 | 22.59 | 22.08 | 22.59 | 261.82 | 243.76 | 105.33 | 105.33 |
| rc_AA609715_at | AA609715 | 1488 | EST | #N/A | #N/A | #N/A | -1.49 | 10.63 | -3.92 | 10.63 | 29.09 | 33.14 | 17.26 | 17.26 |
| NOT3 (negative regulator of transcription 3, yeast) | | | | | | | | | | | | | | |
| rc_AA620965_at | AA620965 | 1511 | homolog | #N/A | #N/A | #N/A | 4.34 | 16.51 | 8.96 | 16.51 | 48.05 | 40.77 | 32.06 | 32.06 |
| similar to Caenorhabditis elegans protein C42C1.9 | | | | | | | | | | | | | | |
| rc_AA621209_at | AA621209 | 1516 | EST | 6.34 | 0.00144 | #N/A | 22.77 | 46.78 | 19.95 | 46.78 | 214.61 | 167.05 | 138.24 | 138.24 |
| rc_AA621235_at | AA621235 | 1517 | EST | 3.44 | 0.0021 | #N/A | 26.29 | 23.17 | 24.68 | 23.17 | 114.75 | 113.36 | 65.35 | 65.35 |
| catenin (cadherin-associated protein), alpha- | | | | | | | | | | | | | | |
| rc_AA621315_at | AA621315 | 1521 | like 1 | #N/A | #N/A | #N/A | 191.28 | 182.69 | 141.04 | 182.69 | 313.23 | 281.93 | 134.57 | 134.57 |
| rc_AA621796_at | AA621796 | 1531 | kinesin family member 3B | 4.44 | 0.00032 | #N/A | 21.81 | 8.64 | 23.64 | 8.64 | 128.01 | 124.81 | 70.04 | 70.04 |
| AB000114_at | AB000114 | 1532 | osteomodulin | #N/A | #N/A | #N/A | -2.62 | 29.14 | -0.81 | 29.14 | 31.94 | 25.4 | 20.87 | 20.87 |
| homogenitase 1,2-dioxygenase (homogenitase oxidase) | | | | | | | | | | | | | | |
| AF000573_rna1_at | AF000573 | 1543 | oxidase | 13.76 | 0.00002 | #N/A | 9.05 | 17.33 | 13.23 | 17.33 | 380.3 | 348.9 | 256.4 | 256.4 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|--|--|--------|--|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| AF007216_at C02532_at C15871_at C16420_s_at | AF007216 C02532 C15871 C16420 | 1550 | solute carrier family 4, sodium bicarbonate cotransporter, member 4 | 5.79 | 0.00005 | 14.85 | 9.84 | 13.93 | 157.72 | 162.44 | 99.26 |
| | | 1563 | EST | #N/A | #N/A | 10.12 | 16.41 | 16.79 | 32.27 | 34.25 | 11.02 |
| | | 1575 | EST | 3.26 | 0.00046 | 13.83 | 18.19 | 16.99 | 79.77 | 83.41 | 40.17 |
| | | 1576 | EST | 5.95 | 0.00119 | 26.92 | 20.84 | 24.82 | 205.53 | 234.17 | 120.92 |
| C18029_at rc_C20653_at | C18029 C20653 | 1577 | tumor susceptibility gene 101 | #N/A | #N/A | 27.46 | 26.72 | 26.09 | 94.81 | 95.79 | 33.89 |
| | | 1578 | EST | 10.59 | 0.00001 | 7.99 | 2.12 | 11.85 | 251.82 | 299.09 | 106.09 |
| rc_C20982_at rc_C21130_at rc_D11802_at | C20982 C21130 D11802 | 1582 | aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) | #N/A | #N/A | 68.8 | 85.38 | 28.73 | 104.44 | 88.12 | 66.28 |
| | | 1583 | EST | 8.79 | 0.00008 | 17.56 | 8.6 | 19.19 | 277.18 | 238.8 | 188.55 |
| | | 1597 | angiotensinogen | 5.65 | 0.00009 | 55.88 | 52.43 | 25.14 | 319.73 | 291.02 | 132.07 |
| | | | | | | | | | | | |
| rc_D11835_at | D11835 | 1598 | low density lipoprotein receptor (familial hypercholesterolemia) | 21.76 | 0.00307 | 76.38 | 23.21 | 131.25 | 895.7 | 910.39 | 322.98 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|-------------|---------|--------|--|----------------------------|---------|-----------|-----------|---------------|----------------|------------------|-------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| D12485_at | D12485 | 1600 | phosphodiesterase I/nucleotide pyrophosphatase 1 (homologous to mouse Ly- 41 antigen) | 4.57 | 0.00008 | -2.69 | -0.53 | 9.86 | 101.7 | 90.07 | 46.62 |
| D12620_s_at | D12620 | 1601 | cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) | 35.09 | 0.00015 | 41.08 | 36.71 | 10.11 | 604.7 | 631.98 | 249.32 |
| D13243_s_at | D13243 | 1602 | pyruvate kinase, liver and RBC | 20.22 | 0 | -35.85 | -34.85 | 51.7 | 579.28 | 445.53 | 502 |
| D13814_s_at | D13814 | 1611 | angiotensin receptor | 3.12 | 0.00101 | 13.86 | 10.01 | 12.82 | 79.69 | 75.71 | 45.03 |
| D14012_s_at | D14012 | 1612 | 1, angiotensin receptor 1B HGF activator | 12.75 | 0.0035 | 160.15 | 216.05 | 107.03 | 1705.96 | 1963.23 | 794.42 |
| D14664_at | D14664 | 1616 | KIAA0022 gene product | 8.98 | 0.00011 | 14.15 | 13.51 | 9.07 | 233.08 | 248.97 | 111.44 |
| D14686_at | D14686 | 1617 | aminomethyltransferase (glycine cleavage system protein T) | #N/A | #N/A | 76.93 | 90.12 | 29.68 | 171.07 | 190.08 | 34.32 |
| D14695_at | D14695 | 1618 | KIAA0025 gene product; MMS-inducible gene | 6.48 | 0 | 28.53 | 28.21 | 12 | 196.04 | 197.12 | 77.25 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|----------------|---------|--------|---|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| D16350_at | D16350 | 1620 | SA (rat hypertension-associated) homolog | 3.83 | 0.00117 | 27.34 | 29.05 | 12.27 | 128.95 | 133.42 | 74.27 |
| D16626_at | D16626 | 1622 | histidine ammonia-lyase | 22.66 | 0 | 11.74 | 8.13 | 16.04 | 538.78 | 535.2 | 166.14 |
| D16626_at | D16626 | 1622 | histidine ammonia-lyase | 22.66 | 0 | 12.06 | 22.91 | 55.95 | 289.6 | 256.22 | 113.59 |
| D31716_at | D31716 | 1647 | basic transcription element binding protein 1 | 5.35 | 0.00086 | 16.08 | 23.65 | 17.64 | 166.06 | 203.79 | 87.22 |
| D31815_at | D31815 | 1648 | regucalcin (senescence marker protein-30) | 10.55 | 0.00037 | 11.48 | 10.25 | 7 | 298.48 | 281.03 | 183.56 |
| D45288_at | D45288 | 1661 | EST | #N/A | #N/A | -19.35 | -33.07 | 27.77 | 31.63 | 32.56 | 42.02 |
| rc_D45529_at | D45529 | 1662 | EST | 3.82 | 0.00193 | 12.24 | -3.36 | 29.18 | 126.63 | 109.06 | 70.64 |
| rc_D45714_at | D45714 | 1664 | EST | 5.64 | 0.00384 | 34.3 | 29.86 | 13.09 | 301.07 | 218.14 | 282.7 |
| D49742_at | D49742 | 1668 | hyaluronan-binding protein 2 | 18.13 | 0.00012 | 11.38 | -0.72 | 41.45 | 509.66 | 531.78 | 127.5 |
| D50312_at | D50312 | 1669 | potassium inwardly-rectifying channel, subfamily J, member 8 | #N/A | #N/A | -2.39 | 3.94 | 24.71 | 76.55 | 72.56 | 48.96 |
| D50582_at | D50582 | 1670 | potassium inwardly-rectifying channel, subfamily J, member 11 | #N/A | #N/A | 61.44 | 65.47 | 28.34 | 70.38 | 76.35 | 25.4 |
| rc_D56989_f_at | D56989 | 1687 | EST | #N/A | #N/A | 8.83 | 6.61 | 9.79 | 77.62 | 55.56 | 72.14 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | metastati metastati | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|--|---------|--------|-----------------------|-------------------------|---------|-----------|-----------|---------------------|-----------|-----------------------|-------------------------|--------------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | c: Median | | | |
| | | | | | | | | | | | | |
| Sec23 (S. cerevisiae) | | | | | | | | | | | | |
| D57823_at | D57823 | 1690 | homolog A | 4.43 | 0 | 13.37 | 13.08 | 8.38 | 94.25 | 87.66 | 30.56 | |
| D57916_s_at | D57916 | 1691 | EST | #N/A | #N/A | 67.05 | 42.08 | 79.49 | 126.25 | 103.85 | 69.38 | |
| rc_D59294_at | D59294 | 1693 | EST | #N/A | #N/A | 1.31 | 0.89 | 6.58 | 22.83 | 20.84 | 14.1 | |
| rc_D59554_f_at | D59554 | 1698 | EST | 6.7 | 0 | 6.09 | 9.79 | 34.83 | 184.48 | 158.33 | 79.55 | |
| rc_D60769_s_at | D60769 | 1703 | KIAA0096 protein | 4.31 | 0.00142 | 13.44 | 13.91 | 10.95 | 119.96 | 107.2 | 86.36 | |
| D61991_at | D61991 | 1706 | EST | 4.84 | 0.00005 | 22.03 | 21.01 | 10.8 | 131.66 | 150.48 | 60.06 | |
| D62103_s_at | D62103 | 1707 | EST | 4.11 | 0.0263 | 96.52 | 111.02 | 79.07 | 349.4 | 258.95 | 229.11 | |
| ficolin (collagen/fibrinogen domain-containing lectin) 2 | | | | | | | | | | | | |
| D63160_at | D63160 | 1709 | (hucolin) | 4.01 | 0.00391 | 51.13 | 46.11 | 30.07 | 219.26 | 228.53 | 125.06 | |
| Zic family member 1 (odd-paired Drosophila homolog) | | | | | | | | | | | | |
| D76435_at | D76435 | 1716 | paired | #N/A | #N/A | 7.52 | 9.44 | 7.51 | 28.48 | 22.05 | 16.54 | |
| D78011_at | D78011 | 1717 | dihydropyrimidinase | 21.37 | 0.00003 | 22.34 | 11.34 | 31.83 | 640.3 | 680.03 | 206.48 | |
| sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)-like | | | | | | | | | | | | |
| D85181_at | D85181 | 1750 | like | 9.56 | 0.00005 | 31.54 | 25.11 | 23.09 | 350.04 | 388.34 | 151.37 | |
| D85433_at | D85433 | 1751 | EST | #N/A | #N/A | 45.14 | 48.1 | 33.75 | 45.46 | 44.56 | 22.01 | |
| D86983_at | D86983 | 1758 | p53-responsive gene 2 | #N/A | #N/A | 44.18 | 43.24 | 14.93 | 56.19 | 53 | 16.12 | |
| solute carrier family 23 (nucleobase transporters), member 1 | | | | | | | | | | | | |
| D87075_at | D87075 | 1760 | member 1 | 4.15 | 0.00067 | 5.77 | -0.83 | 26.24 | 119.77 | 104.75 | 72.62 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | metastati | | normal | | normal | |
|----------------|---------|--------|---|-------------|---------|-----------|--------|------------|---------|-------------|---------------|----------------|--|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | Mean | set 2: Mean | set 2: Median | set 2: Std Dev | |
| D90042_at | D90042 | 1767 | N-acetyltransferase 2 (arylamine N-acetyltransferase) | 7.06 | 0 | 5.13 | 18.92 | 32.5 | 167.38 | 176.16 | 66.7 | | |
| D90282_at | D90282 | 1769 | carbamoyl-phosphate synthetase 1, mitochondrial | 27.29 | 0.00002 | 8.24 | 12.24 | 8.02 | 712.98 | 819.32 | 415.69 | | |
| rc_F04611_at | F04611 | 1792 | EST | 23.96 | 0.00018 | 42.65 | 18.88 | 62.74 | 1011.12 | 1040.46 | 589.37 | | |
| rc_F04677_at | F04677 | 1794 | EST | #N/A | #N/A | 138.06 | 123.28 | 34.39 | 355.75 | 310.97 | 168.21 | | |
| rc_F04944_s_at | F04944 | 1795 | acyl-Coenzyme A oxidase | 4.01 | 0.00242 | 40.92 | 33.99 | 28.07 | 191.04 | 192.25 | 99.98 | | |
| rc_F09350_at | F09350 | 1801 | EST | 4.79 | 0.00088 | 13.91 | -6.46 | 33.97 | 147.64 | 130.28 | 79.24 | | |
| rc_f09687_s_at | F09687 | 1806 | EST | #N/A | #N/A | 12.72 | 8.26 | 28.12 | 58.85 | 57.03 | 31.82 | | |
| rc_F09729_at | F09729 | 1807 | EST | #N/A | #N/A | 9.35 | 20.58 | 23.17 | 55.49 | 55.78 | 27.37 | | |
| rc_F09979_at | F09979 | 1809 | EST | 4.36 | 0.02555 | 6.98 | 6.51 | 20.72 | 226.47 | 116.41 | 288.21 | | |
| rc_F10149_at | F10149 | 1810 | EST | #N/A | #N/A | 111.86 | 108.46 | 60.06 | 257.05 | 276.87 | 165.09 | | |
| rc_F10276_s_at | F10276 | 1814 | dual specificity phosphatase 6 | 8.13 | 0.0001 | 19.64 | 13.06 | 12.33 | 240.65 | 275.65 | 138.17 | | |
| rc_F10380_at | F10380 | 1816 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) | #N/A | #N/A | 36.92 | 34.01 | 13.56 | 106.49 | 93.71 | 83.35 | | |
| rc_F10381_s_at | F10381 | 1817 | KIAA0541 protein | #N/A | #N/A | 22.16 | 25.03 | 8.75 | 64.94 | 71.82 | 26.24 | | |
| rc_F10418_at | F10418 | 1818 | EST | #N/A | #N/A | 44.91 | 44.45 | 22.72 | 64.3 | 52.54 | 31.96 | | |
| rc_F10874_f_at | F10874 | 1823 | EST | 4.19 | 0.00025 | 233.85 | 209.96 | 107.99 | 1016.95 | 990.04 | 477.31 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|----------------|---------|--------|--|----------------------------|---------|-----------|-----------|------------|--------|-------------|--------|---------------|--------|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal | set 2: Mean | normal | set 2: Median | normal |
| rc_F13624_at | F13624 | 1825 | breast cancer anti-estrogen resistance 3 | #N/A | #N/A | 27.76 | 19.2 | 32.49 | 90.8 | 73.79 | 59.27 | | |
| rc_F13782_s_at | F13782 | 1827 | LIM binding domain 2 | 4.17 | 0.00109 | -0.64 | 5.61 | 22.4 | 100.8 | 119.01 | 55.07 | | |
| rc_H01059_l_at | H01059 | 1830 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | #N/A | #N/A | 9.13 | 9.22 | 13.53 | 32.73 | 34.27 | 21.05 | | |
| rc_H02855_at | H02855 | 1832 | EST | 5.96 | 0.00458 | 5.06 | 1.15 | 14.13 | 261.57 | 93.25 | 407.93 | | |
| rc_H03348_at | H03348 | 1833 | claudin 1 | 5.77 | 0.0001 | 1.48 | 7.75 | 17.79 | 135.1 | 134.05 | 75.43 | | |
| rc_H05970_at | H05970 | 1849 | EST | #N/A | #N/A | 9.16 | 12.81 | 14.19 | 68.16 | 65.08 | 40.19 | | |
| rc_H09331_f_at | H09331 | 1865 | EST | #N/A | #N/A | 313.2 | 309.79 | 122.67 | 512.04 | 486.42 | 149.27 | | |
| rc_H09353_at | H09353 | 1866 | EST | 23.06 | 0.00094 | 45.11 | 18.95 | 65.29 | 782.6 | 824.74 | 226.28 | | |
| rc_H10661_at | H10661 | 1871 | EST | 4.54 | 0.00276 | 31.29 | 18.75 | 28.5 | 132.09 | 124.86 | 64.37 | | |
| rc_H11739_s_at | H11739 | 1876 | glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P) | 10.33 | 0.00023 | -21.2 | -37.69 | 28.32 | 290.05 | 210.37 | 244.67 | | |
| rc_H12593_at | H12593 | 1880 | zinc-finger protein 265 | 10.72 | 0.0056 | 39.96 | -9.15 | 111.74 | 515.58 | 506.07 | 224.5 | | |
| rc_H16098_at | H16098 | 1885 | EST | #N/A | #N/A | 45.29 | 37.73 | 26.92 | 87.28 | 94.49 | 38.15 | | |
| rc_H17472_s_at | H17472 | 1888 | EST | #N/A | #N/A | 12.2 | 9.54 | 8.57 | 31.08 | 31.66 | 13.28 | | |
| rc_H19089_at | H19089 | 1894 | EST | #N/A | #N/A | 76.83 | 44.82 | 89.14 | 76.54 | 74.4 | 40.21 | | |
| rc_H19504_f_at | H19504 | 1895 | EST | 3.13 | 0.04948 | 77.07 | 49.48 | 64.05 | 227.6 | 221.91 | 125.23 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|--|---------|--------|------------------------------|----------------------------|---------|-----------|--------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_H20543_at | H20543 | 1897 | DKFZP586B1621 protein | 31.03 | 0.00074 | 62.11 | 36.98 | 80.24 | 1684.92 | 1680.81 | 731.79 |
| H20627_at | H20627 | 1898 | EST | #N/A | #N/A | 30.59 | 30.04 | 23.84 | 79.8 | 87.46 | 43.37 |
| rc_H24081_at | H24081 | 1901 | KIAA1035 protein | #N/A | #N/A | 19.72 | 18.46 | 5.69 | 24.15 | 27.08 | 9.52 |
| rc_H25124_at | H25124 | 1903 | EST | 3.65 | 0.00004 | 20.47 | 14.4 | 12.59 | 95.09 | 85.36 | 34.91 |
| rc_H29568_at | H29568 | 1914 | EST | 11.45 | 0.00058 | 232.54 | 140.09 | 218.85 | 2206.49 | 1884.76 | 783.84 |
| rc_H30270_at | H30270 | 1915 | EST | 17.09 | 0.00001 | 61.64 | 60.29 | 25.01 | 1224.59 | 1332.66 | 695.76 |
| H39627_at | H39627 | 1920 | EST | #N/A | #N/A | 73.92 | 101.48 | 54.09 | 155.43 | 158.44 | 39.98 |
| cytochrome P450, subfamily | | | | | | | | | | | |
| H46990_at | H46990 | 1933 | IIE (ethanol-inducible) | 3.2 | 0.00095 | -0.27 | -6.33 | 16.23 | 72.1 | 71.1 | 37.01 |
| rc_H47838_at | H47838 | 1936 | carboxypeptidase B2 (plasma) | 16.74 | 0.00002 | -26.99 | -41.82 | 25.87 | 401.55 | 412.78 | 188.81 |
| ATP-binding cassette, sub-family C (CFTR/MRP), member 6 | | | | | | | | | | | |
| rc_H49417_s_at | H49417 | 1939 | member 6 | #N/A | #N/A | 16.93 | 17.31 | 8.56 | 62.68 | 54.75 | 48.37 |
| rc_H52251_at | H52251 | 1942 | EST | #N/A | #N/A | 25.41 | 22.3 | 15.29 | 33.86 | 34.48 | 19.95 |
| rc_H53829_at | H53829 | 1946 | EST | #N/A | #N/A | 44.31 | 40.52 | 36.62 | 99.9 | 98.22 | 46.1 |
| 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like 1 | | | | | | | | | | | |
| rc_H56584_at | H56584 | 1951 | SNAP25-like 1 | 9.5 | 0 | 1.95 | 10.13 | 31.43 | 223.03 | 233.37 | 105.28 |
| rc_H56965_at | H56965 | 1952 | EST | #N/A | #N/A | 0.18 | 0.68 | 12.9 | 61.03 | 73.89 | 30.12 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|----------------|---------|--------|--|----------------------------|---------|-----------|-----------|------------|--------------------|----------------------|-----------------------|--------------------|-----------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | normal set 2: Mean | normal set 2: Std Dev |
| rc_H57850_at | H57850 | 1958 | protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform | 3.02 | 0.00123 | 41.36 | 36.05 | 15.14 | 131.12 | 130.36 | 53.67 | | |
| rc_h58692_s_at | H58692 | 1960 | formyltetrahydrofolate dehydrogenase | 81.41 | 0 | -2.66 | 5.46 | 16.1 | 1886.69 | 1520.43 | 1129.35 | | |
| rc_H60317_at | H60317 | 1965 | EST | #N/A | #N/A | 18.86 | 22.34 | 11.81 | 38.92 | 39.1 | 18.67 | | |
| H61002_at | H61002 | 1967 | EST | #N/A | #N/A | 68.96 | 23.38 | 102.25 | 88.87 | 93.79 | 36.34 | | |
| H66367_at | H66367 | 1977 | EST | 6.68 | 0.0001 | -5.44 | -2.13 | 18.66 | 155.38 | 149.31 | 70.77 | | |
| rc_H68239_f_at | H68239 | 1983 | EST | #N/A | #N/A | 26.96 | 17.94 | 15.81 | 66.76 | 66.18 | 51.67 | | |
| rc_H69138_at | H69138 | 1986 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog | 6.76 | 0.00142 | 42.88 | 30.87 | 38.35 | 328.51 | 313.13 | 218.8 | | |
| rc_H69565_at | H69565 | 1987 | EST | 4.11 | 0.00002 | 15.45 | 16.92 | 9.4 | 95.6 | 94.91 | 42.92 | | |
| rc_H70485_at | H70485 | 1988 | EST | #N/A | #N/A | 113.44 | 81.62 | 63.73 | 232.9 | 256.86 | 107.1 | | |
| rc_H70554_at | H70554 | 1989 | EST | 10.99 | 0 | -11.73 | -19.98 | 33.09 | 292.66 | 288.78 | 153.17 | | |
| rc_H70627_s_at | H70627 | 1990 | EST | #N/A | #N/A | 17.89 | 17.62 | 8.85 | 42.72 | 41.34 | 11.7 | | |
| H72650_at | H72650 | 1994 | EST | #N/A | #N/A | 81.21 | 98.79 | 41.38 | 122 | 125 | 42.24 | | |
| rc_H73535_s_at | H73535 | 1996 | EST | 6.89 | 0.00202 | 154.24 | 97.36 | 149.45 | 912.39 | 956.58 | 383.35 | | |
| rc_H77494_at | H77494 | 1999 | EST | #N/A | #N/A | 9.65 | 6.64 | 15.53 | 42.67 | 47.73 | 27.54 | | |
| rc_H79820_at | H79820 | 2004 | EST | 3.25 | 0.01466 | 10.64 | 2 | 22.28 | 113.3 | 113.19 | 95.96 | | |
| rc_H81070_f_at | H81070 | 2006 | RNA helicase-related protein | 25.74 | 0.00126 | 93.43 | 62.01 | 121.29 | 2044.42 | 2051.11 | 615.84 | | |
| rc_H81964_s_at | H81964 | 2008 | SEC14 (S. cerevisiae)-like 1 | #N/A | #N/A | 9.95 | 15.7 | 12.54 | 29.9 | 21.14 | 20.56 | | |
| rc_H82424_at | H82424 | 2009 | EST | #N/A | #N/A | 41.99 | 48.17 | 21.1 | 65.11 | 69.41 | 36.73 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | metastati | | | normal | | |
|----------------|---------|--------|---|-------------|----------|---------|-----------|--------|--------|-----------|--------|--------|-------------|---------------|----------------|
| | | | | In metas | in metas | | c: Mean | Median | Dev | c: Std | Mean | Median | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_H82735_s_at | H82735 | 2010 | NOT3 (negative regulator of transcription 3, yeast) homolog | #N/A | #N/A | #N/A | -1.13 | 6.14 | 29.78 | 58.77 | 54.86 | 35.76 | | | |
| rc_H82966_s_at | H82966 | 2011 | apolipoprotein B (including Ag(x) antigen) | 3.42 | 0.00769 | 0.2 | 1 | 15.26 | 100.93 | 77.36 | 96.78 | | | | |
| rc_H83109_f_at | H83109 | 2012 | EST | 16.55 | 0.00001 | 2.74 | 4.43 | 21.21 | 417.46 | 421.97 | 224.35 | | | | |
| rc_H87765_at | H87765 | 2017 | KIAA0626 gene product | 3.86 | 0.00131 | 5.2 | 7.91 | 19.6 | 94.26 | 93.78 | 60.64 | | | | |
| rc_H89980_at | H89980 | 2026 | protein phosphatase 1, regulatory (inhibitor) subunit 5 | 31.13 | 0.00006 | 12.16 | 13.82 | 12.3 | 990.48 | 1005.21 | 755.6 | | | | |
| rc_H90417_s_at | H90417 | 2028 | EST | 4.17 | 0.015 | 14.23 | -10.79 | 70.02 | 191.04 | 154.37 | 125.5 | | | | |
| rc_H93381_at | H93381 | 2036 | EST | 24.23 | 0 | 6.08 | -0.69 | 28.81 | 621.48 | 640.77 | 214.25 | | | | |
| rc_H93562_at | H93562 | 2038 | proline synthetase co-transcribed (bacterial homolog) | 3.17 | 0.00113 | 20.83 | 14.13 | 20.46 | 89.3 | 84.36 | 37.72 | | | | |
| rc_H93745_s_at | H93745 | 2040 | GS2 gene | #N/A | #N/A | 4.52 | 8.01 | 8.31 | 47.92 | 46.53 | 28.87 | | | | |
| rc_H95079_at | H95079 | 2046 | EST | #N/A | #N/A | 7.05 | 11.03 | 7.33 | 39.79 | 33.3 | 29.08 | | | | |
| rc_H95089_at | H95089 | 2047 | EST | #N/A | #N/A | 13.05 | 13.54 | 4.03 | 31.99 | 31.89 | 13.19 | | | | |
| rc_H95358_at | H95358 | 2049 | EST | 3.17 | 0.00182 | -5.85 | -5.95 | 11.57 | 74.74 | 72.66 | 42.36 | | | | |
| rc_H95978_at | H95978 | 2052 | EST | 8.55 | 0.00046 | 12.28 | 14.38 | 10.71 | 240.91 | 246.43 | 147.67 | | | | |
| rc_H96392_at | H96392 | 2053 | EST | #N/A | #N/A | 12.6 | 9.93 | 33.15 | 35.98 | 53.46 | 42.74 | | | | |
| rc_H96897_at | H96897 | 2056 | KIAA0336 gene product | #N/A | #N/A | 35.22 | 19.98 | 42.05 | 48.46 | 50.39 | 33.36 | | | | |
| rc_H97587_s_at | H97587 | 2060 | endothelin receptor type B | #N/A | #N/A | -5.07 | -3.35 | 14.02 | 39.65 | 36.54 | 21.7 | | | | |
| rc_H97670_at | H97670 | 2061 | EST | #N/A | #N/A | 23.31 | 29.71 | 31.35 | 101.35 | 128.08 | 56.78 | | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastatic | | | normal | | |
|------------------|---------|--------|---|--------|----------|---------|------------|--------|---------|---------|---------|---------|
| | | | | change | in metas | | Mean | Median | Std Dev | Mean | Median | Std Dev |
| rc_H98083_at | H98083 | 2067 | EST | | 5.09 | 0.00025 | 11.73 | 11.11 | 3.97 | 121.51 | 104.88 | 70.52 |
| rc_H99393_s_at | H99393 | 2076 | endothelin receptor type 2 | | 3.43 | 0.00093 | 4.63 | 9.33 | 11.96 | 79.18 | 70.67 | 42.71 |
| | | | | | | | | | | | | |
| J00098_cds1_s_at | J00098 | 2086 | apolipoprotein A-1, apolipoprotein C-III | | #N/A | #N/A | 96.71 | 29.74 | 269.46 | 9836.26 | 8356.89 | 8217.05 |
| J02943_at | J02943 | 2090 | corticosteroid binding globulin | | 18.98 | 0.00087 | 57.44 | 39.79 | 44.72 | 880.54 | 924.99 | 144.24 |
| J03242_s_at | J03242 | 2092 | insulin-like growth factor 2 (somatomedin A) | | 4.01 | 0.00042 | 40.37 | 45.32 | 15.53 | 179.86 | 172.23 | 104.64 |
| | | | solute carrier family 2 (facilitated glucose transporter), member 2 | | 21.99 | 0.00004 | 21.12 | 16.81 | 24.34 | 571.66 | 593.24 | 118.08 |
| J03810_at | J03810 | 2104 | carbonyl reductase 1 | | 5.19 | 0.00001 | 9.77 | 22.83 | 29.45 | 145.33 | 139.19 | 73.11 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|-------------|---------|--------|---|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| J04093_s_at | J04093 | 2106 | UDP glycosyltransferase 1 | 18.92 | 0 | 8.62 | 8.7 | 12.9 | 462.51 | 511 | 215.46 |
| J05037_at | J05037 | 2116 | serine dehydratase | 16.24 | 0.00015 | 12.71 | 32.78 | 67.98 | 626.47 | 497.97 | 306.18 |
| J05158_at | J05158 | 2117 | carboxypeptidase N, polypeptide 2, 83kD | 8.52 | 0 | 2.27 | -7.78 | 21.43 | 209.63 | 218.19 | 81.01 |
| K02100_at | K02100 | 2123 | ornithine carbamoyltransferase | 10.24 | 0.00009 | 6.1 | 3.97 | 11.14 | 253.26 | 300.99 | 126.18 |
| K02402_at | K02402 | 2125 | coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) | 28.81 | 0.00001 | 10.4 | 2.94 | 28.08 | 742.92 | 734.01 | 215.88 |
| K02766_at | K02766 | 2126 | complement component 9 | 21.24 | 0 | 23.15 | 14.02 | 21.18 | 652.66 | 656.14 | 320.1 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 69.92 | 0 | 3.07 | 9.83 | 30.14 | 1767.25 | 1790.36 | 741.7 |
| K03192_f_at | K03192 | 2127 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 69.92 | 0 | -1.32 | -6.49 | 12.52 | 1087.08 | 1034.79 | 451.92 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|-------------|---------|--------|---|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| L00389_f_at | L00389 | 2132 | cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2 | #N/A | #N/A | 69.38 | 86.39 | 64.81 | 222.59 | 184.81 | 121.16 |
| L00972_at | L00972 | 2133 | cystathionine-beta-synthase | 7.19 | 0.00008 | 30.44 | 29.08 | 21.44 | 268.9 | 253.33 | 153.24 |
| L04751_at | L04751 | 2138 | cytochrome P450, subfamily IVA, polypeptide 11 | 36.79 | 0.00004 | 32.39 | 23.29 | 32.64 | 1164.28 | 1183.4 | 334.08 |
| L07956_at | L07956 | 2148 | glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) | 5.6 | 0.00029 | 19.13 | 18.57 | 16.75 | 166.17 | 184.57 | 75.67 |
| L09717_at | L09717 | 2153 | lysosomal-associated membrane protein 2 | 4.06 | 0.00034 | 16.78 | 9.78 | 21.83 | 115.12 | 111.26 | 57.66 |
| L11244_s_at | L11244 | 2155 | complement component 4-binding protein, beta | 43.33 | 0 | 0.49 | -8.84 | 36.95 | 1147.16 | 1114.71 | 441.14 |
| L11244_s_at | L11244 | 2155 | complement component 4-binding protein, beta serine | 43.33 | 0 | -13.27 | -16.78 | 12.92 | 292.9 | 341.12 | 114.93 |
| L11931_at | L11931 | 2159 | hydroxymethyltransferase 1 (soluble) | 7.27 | 0.00041 | -18.81 | -31.65 | 26.43 | 188.25 | 181.11 | 114.89 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|-----------|---------|--------|---|----------------------------|---------|-----------|-----------|---------------|----------------|------------------|-------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| L13689_at | L13689 | 2164 | murine leukemia viral (bmi-1) oncogene homolog activating transcription factor | #N/A | #N/A | 32.33 | 34.76 | 18.57 | 63.42 | 77.84 | 36.39 |
| L19871_at | L19871 | 2172 | 3 | #N/A | #N/A | 72.2 | 31 | 78.72 | 98.22 | 85.66 | 61.41 |
| L26336_at | L26336 | 2185 | heat shock 70kD protein 2 | #N/A | #N/A | 15.67 | 14.08 | 10.72 | 31.12 | 33.86 | 10.1 |
| L27050_at | L27050 | 2186 | apolipoprotein F | 10.26 | 0.00026 | -23.8 | -20.7 | 14.43 | 258.1 | 252.65 | 124.08 |
| L27841_at | L27841 | 2187 | pericentriolar material 1 | #N/A | #N/A | 58.75 | 58.95 | 40.61 | 90.06 | 82.71 | 28.43 |
| L32140_at | L32140 | 2192 | afamin | 17.31 | 0.00003 | 9.44 | 16 | 10.75 | 426.89 | 464.97 | 221.11 |
| L32179_at | L32179 | 2193 | arylamide deacetylase (esterase) | 23.83 | 0 | 22.94 | 24.96 | 16.06 | 688.97 | 675.71 | 305.75 |
| L32961_at | L32961 | 2194 | 4-aminobutyrate aminotransferase | #N/A | #N/A | 15.64 | 7.44 | 15.63 | 76.44 | 79.62 | 26.55 |
| L33799_at | L33799 | 2196 | procollagen C-endopeptidase enhancer | #N/A | #N/A | 87.45 | 73.5 | 89.14 | 230.54 | 248.1 | 130.08 |
| L34081_at | L34081 | 2199 | bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase) | 11.96 | 0.00008 | 6.09 | 4.41 | 14.12 | 314.27 | 330.42 | 174.43 |
| L41067_at | L41067 | 2213 | nuclear factor of activated T-cells, cytoplasmic 3 | 4.96 | 0.00473 | 57.54 | 60.41 | 36.65 | 261.77 | 228.95 | 119.65 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | metastati | | | normal | | |
|-------------------------------------|----------------------------|----------------------|--|-------------|----------|---------|-----------|-----------|------------|-----------|--------|--------|-------------|---------------|----------------|
| | | | | in metas | in metas | | c: Mean | c: Median | c: Std Dev | normal | normal | normal | set 2: Mean | set 2: Median | set 2: Std Dev |
| L41067_at L44424_at L48516_at | L41067 L44424 L48516 | 2213 2216 2220 | nuclear factor of activated T-cells, cytoplasmic 3 UMP-CMP Kinase paraoxonase 3 | 4.96 | #N/A | 0.00473 | 30.25 | 13.66 | 32.44 | 73.87 | 77.38 | 52.02 | 73.87 | 77.38 | 52.02 |
| | | | | #N/A | #N/A | #N/A | 23.79 | 18.2 | 26.85 | 57.57 | 43.3 | 36.92 | 57.57 | 43.3 | 36.92 |
| | | | | 22.21 | 0.00004 | 0.00004 | 36.05 | 28.85 | 37.25 | 896.92 | 896.69 | 337.05 | 896.92 | 896.69 | 337.05 |
| M10058_at | M10058 | 2230 | asialoglycoprotein receptor 1 | 23.96 | 0 | -47.64 | -42.75 | 75.52 | 591.6 | 603.68 | 188.25 | | | | |
| M10943_at M11437_cds1_at | M10943 M11437 | 2234 2238 | metallothionein 1F (functional) kininogen | 3.88 | 0 | 53.15 | 52.73 | 8.81 | 217.65 | 186.71 | 86.73 | | | | |
| | | | | 18.38 | 0.00006 | 20.84 | 10.7 | 36.84 | 535.53 | 539.53 | 186.97 | | | | |
| | | | | | | | | | | | | | | | |
| M11567_ma1_at | M11567 | 2239 | angiotensin, ribonuclease, RNase A family, 5 | 32.25 | 0.0001 | 2.5 | -18.19 | 58.03 | 1019.17 | 968.25 | 273.9 | | | | |
| M12625_at | M12625 | 2245 | lecithin-cholesterol acyltransferase protein C (inactivator of coagulation factors Va and VIIIa) EST | 4.55 | 0.01584 | 110.15 | 128.06 | 73.94 | 447.22 | 425.61 | 138.52 | | | | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | |
| M12712_s_at M12759_at | M12712 M12759 | 2246 2247 | kallikrein B plasma, (Fletcher factor) 1 | 7.37 | 0.01866 | 107.12 | 177.74 | 113.63 | 646.94 | 628.19 | 326.15 | | | | |
| | | | | #N/A | #N/A | 27.23 | 21.91 | 28.99 | 97.65 | 103.06 | 53.91 | | | | |
| | | | | | | | | | | | | | | | |
| M13143_at | M13143 | 2249 | coagulation factor VII | 10.39 | 0.00019 | 38.55 | 37.19 | 32.81 | 402.05 | 441.15 | 122.27 | | | | |
| M13232_s_at | M13232 | 2251 | coagulation factor VII (serum prothrombin conversion accelerator) | 5.9 | 0.00014 | 43.46 | 42.59 | 18.46 | 248.65 | 275.82 | 70.94 | | | | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | |
| M13699_at | M13699 | 2253 | ceruloplasmin (ferroxidase) | 15.85 | 0.00012 | 36.21 | 37.43 | 44.51 | 688.89 | 638.74 | 329.28 | | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastati | | | normal | | |
|-------------|---------|--------|--|--------|----------|---------|-----------|--------|------------|-------------|---------------|----------------|
| | | | | change | in metas | | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| M14091_at | M14091 | 2257 | thyroxin-binding globulin | 10.66 | 0.00024 | 1.76 | 2.84 | 9.9 | 269.26 | 284.66 | 119.28 | |
| M14777_s_at | M14777 | 2263 | glutathione S-transferase A2, glutathione S-transferase A3 | #N/A | #N/A | -24.81 | -27.52 | 27.54 | 2842.35 | 2790.19 | 1048.69 | |
| M15465_s_at | M15465 | 2266 | pyruvate kinase, liver and RBC | 6.1 | 0.00069 | 3.06 | 3.32 | 11.38 | 158.56 | 132.57 | 102.11 | |
| M15656_at | M15656 | 2268 | aldolase B, fructose-bisphosphate | 96.66 | 0 | -44.61 | -66.97 | 59.8 | 2911.78 | 2539.75 | 1883.04 | |
| M16594_at | M16594 | 2272 | glutathione S-transferase A2 | 73.21 | 0 | -3.62 | -9.74 | 18.15 | 1602.11 | 1787.28 | 655.41 | |
| M16967_at | M16967 | 2275 | coagulation factor V (proaccelerin, labile factor) | 5.56 | 0.00047 | 22.71 | 26.49 | 30.11 | 204.85 | 248.05 | 88.92 | |
| M16973_at | M16973 | 2276 | complement component 8, beta polypeptide | 22.75 | 0.00001 | 20.03 | 23.43 | 31.9 | 686.99 | 714.82 | 203.16 | |
| M16974_s_at | M16974 | 2277 | complement component 8, alpha polypeptide | 49.47 | 0.00046 | 28.24 | -6.62 | 84.02 | 1843.82 | 1920.94 | 524.62 | |
| M17466_at | M17466 | 2279 | coagulation factor XII (Hageman factor) | 9.76 | 0.00285 | 94.21 | 63.47 | 93.18 | 706.11 | 724.27 | 261.46 | |
| M20218_at | M20218 | 2288 | coagulation factor XI (plasma thromboplastin antecedent) | 6.4 | 0.00004 | 38.74 | 45.83 | 14.62 | 247.85 | 259.47 | 69.46 | |
| M20786_at | M20786 | 2290 | alpha-2-plasmin inhibitor | 16.95 | 0.00709 | 58.96 | -14.12 | 171 | 1074.45 | 1132.06 | 620.06 | |

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | metastati | | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|--------------------------|------------------|--------------|---|----------------------|--------------------|----------------|----------------|----------------|--------------------|----------------------|-----------------------|--------------------|----------------------|-----------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | | |
| M22324_at | M22324 | 2295 | alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) | #N/A | #N/A | 224.68 | 25.21 | 471.53 | 365.81 | 363.02 | 134.32 | | | |
| M23234_s_at | M23234 | 2299 | ATP-binding cassette, sub-family B (MDR/TAP), member 4 | 10.05 | 0 | -4.37 | -11.49 | 29.05 | 255.03 | 242.93 | 112.08 | | | |
| M24283_at | M24283 | 2303 | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain | 3.19 | 0.04985 | 77.88 | 34.05 | 69.45 | 207.07 | 183.74 | 121.4 | | | |
| M26393_s_at M29194_at | M26393 M29194 | 2309 2315 | lipase, hepatic | 16.27 12.18 | 0.00007 0.00012 | 16.81 18.97 | 12.39 11.91 | 48.16 30.61 | 677.3 352.8 | 775.54 332.28 | 358.47 87.49 | | | |
| M30185_at | M30185 | 2321 | cholesteryl ester transfer protein, plasma | 3.83 | 0.0013 | -37.15 | -29.18 | 28.09 | 93.07 | 86.04 | 61.35 | | | |
| M30257_s_at M30269_at | M30257 M30269 | 2322 2323 | vascular cell adhesion molecule 1 nidogen (enactin) | 3.11 3.4 | 0.00064 0.00026 | 17.33 19.81 | 13.46 26.36 | 10.06 14.57 | 78.1 96.8 | 82.04 94.16 | 35.74 42.52 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change In metas | p value | metastati | | metastati | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|----------------|---------|--------|---|----------------------------|---------|-----------|--------|-----------|---------|--------------------------|----------------------------|-----------------------------|
| | | | | | | c: Mean | Median | c: Mean | Median | | | |
| M33317_f_at | M33317 | 2338 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 | 32.63 | 0 | 44.53 | 35.06 | 29.77 | 1613.89 | 1437.34 | 1086.43 | |
| M61853_at | M61853 | 2369 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18 | 7.82 | 0.00024 | 12.17 | 12.44 | 4.36 | 191.94 | 204.27 | 91.68 | |
| M61854_s_at | M61854 | 2370 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase) | 3.3 | 0.04185 | 52.7 | 55.56 | 44.01 | 321.6 | 166.36 | 430.71 | |
| M63967_at | M63967 | 2378 | aldehyde dehydrogenase 5 | 4.04 | 0.00058 | 34.59 | 36.64 | 5.46 | 164.38 | 178.74 | 87.39 | |
| M64174_at | M64174 | 2379 | Janus kinase 1 (a protein tyrosine kinase) | #N/A | #N/A | 10.42 | 10.81 | 15.82 | 59.51 | 59.38 | 27.77 | |
| M64554_rna1_at | M64554 | 2380 | coagulation factor XIII, B polypeptide | 5.87 | 0.00011 | -4.73 | -4.91 | 7.92 | 137.26 | 136.8 | 72.05 | |
| M64590_at | M64590 | 2381 | glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P) | 6.41 | 0.00002 | 14.28 | 17.87 | 8.65 | 152.26 | 127.72 | 82.96 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | metastati | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|---------------|---------|--------|---|----------------------------|---------|-----------|-----------|---------------|---------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | c: Std Dev | | | |
| M64929_at | M64929 | 2383 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | #N/A | #N/A | 64.63 | 38.82 | 95.31 | 106.38 | 88.13 | 67.95 | |
| M65134_s_at | M65134 | 2385 | complement component 5 protein C inhibitor | 12.01 | 0.00012 | 2.31 | 3.66 | 7.43 | 303.27 | 337.95 | 151.33 | |
| M68516_ma1_at | M68516 | 2387 | plasminogen activator (inhibitor III) | 20.54 | 0 | -1.34 | -11.78 | 20.54 | 466.81 | 481.06 | 119.75 | |
| M68840_at | M68840 | 2388 | monoamine oxidase A | 3.96 | 0.01396 | 42.09 | 28.9 | 45.52 | 182 | 201.64 | 94.09 | |
| M69177_at | M69177 | 2392 | monoamine oxidase B | 11.64 | 0.00001 | 21.97 | 20.41 | 20.83 | 322.15 | 340.27 | 94 | |
| M74719_at | M74719 | 2396 | transcription factor 4 carboxypeptidase B2 | #N/A | #N/A | 8.97 | 15.15 | 10.62 | 46.89 | 44.78 | 12.66 | |
| M75106_at | M75106 | 2397 | (plasma) | 40.63 | 0 | 19.77 | 30.19 | 22.24 | 1170.81 | 1124.59 | 329.77 | |
| M76665_at | M76665 | 2398 | hydroxysteroid (11-beta) | 19.22 | 0.00004 | 33.41 | 17.51 | 23.86 | 628.97 | 670.88 | 196.22 | |
| M83216_s_at | M83216 | 2407 | dehydrogenase 1 caldesmon 1 flavin containing | 4.27 | 0.00037 | 7.89 | 2.98 | 12.17 | 105.21 | 109.38 | 55.62 | |
| M83772_at | M83772 | 2409 | monooxygenase 3 | 19.54 | 0 | 6.88 | -0.95 | 15.39 | 504.14 | 595.51 | 245.03 | |
| M86873_s_at | M86873 | 2414 | plasminogen,plasminogen- like | 17.54 | 0 | -3.92 | -8.08 | 6.71 | 410.11 | 403.69 | 218.51 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | normal | | |
|---|---------|--------|--|-------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | in metas | p value | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 | | | | | | | | | | | |
| M88163_at | M88163 | 2416 | | 3.37 | 0.00098 | 17.39 | 17.52 | 7.25 | 84.41 | 91.86 | 41.42 |
| M88338_at | M88338 | 2417 | serum constituent protein mevalonate kinase | #N/A | #N/A | 134.22 | 128.76 | 53.79 | 155.51 | 140.27 | 70.28 |
| M88468_at | M88468 | 2418 | (mevalonic aciduria) methylmalonate-semialdehyde | #N/A | #N/A | 89.85 | 108.13 | 54.23 | 214.81 | 260.33 | 86.76 |
| M93405_at | M93405 | 2424 | dehydrogenase | 23.06 | 0 | 16.51 | 27.77 | 20.66 | 679.66 | 734.58 | 307.25 |
| M94065_at | M94065 | 2425 | dihydroorotate dehydrogenase | 6.47 | 0.00013 | 30.26 | 20.14 | 17.64 | 202.13 | 183.44 | 86.43 |
| M95767_at | M95767 | 2432 | chitobiase, di-N-acetyl- | 4.94 | 0.00004 | 26.01 | 37.13 | 21.53 | 173.07 | 153.03 | 95 |
| CD36 antigen (collagen type I receptor, thrombospondin receptor) | | | | | | | | | | | |
| M98399_s_at | M98399 | 2437 | | #N/A | #N/A | 4.71 | 4.58 | 5.51 | 47.65 | 38.28 | 35.2 |
| rc_N21626_at | N21626 | 2445 | EST | #N/A | #N/A | 29.77 | 24.63 | 25.09 | 59.18 | 46.15 | 33.56 |
| rc_N22404_at | N22404 | 2450 | EST | 3.99 | 0.01152 | 30.59 | 23.97 | 55.32 | 193.63 | 130.09 | 162.83 |
| rc_N22434_at | N22434 | 2451 | EST | 4.37 | 0.01725 | 100.96 | 66.55 | 110.62 | 334.51 | 328.98 | 150.7 |
| rc_N22938_s_at | N22938 | 2453 | serum amyloid A4, constitutive | 35.39 | 0.00128 | 163.4 | 145.31 | 160.24 | 4244.44 | 3330.35 | 2358.25 |
| rc_N24879_at | N24879 | 2460 | EST | 9.44 | 0.00008 | 6.2 | 5.49 | 23.52 | 280.93 | 337.77 | 165.77 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | metastati | | | normal | | |
|---|---------|--------|----------------------------|-------------|----------|---------|-----------|--------|--------|-----------|--------|--------|-------------|---------------|----------------|
| | | | | in metas | in metas | | c: Mean | Median | Dev | c: Std | Mean | Median | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_N24973_at | N24973 | 2462 | EST | #N/A | #N/A | #N/A | 30.46 | 28.45 | 11.29 | | 56.57 | 59.09 | | | 22.87 |
| rc_N25262_at | N25262 | 2465 | EST | #N/A | #N/A | #N/A | 31.16 | 28.04 | 9.03 | | 64.13 | 64.97 | | | 18.29 |
| rc_N27524_at | N27524 | 2472 | EST | 3.13 | 0.00216 | 0.00216 | 14.18 | 22.08 | 20.51 | | 87.67 | 98.26 | | | 42.62 |
| progesterone membrane binding protein | | | | | | | | | | | | | | | |
| N27670_at | N27670 | 2474 | binding protein | 6.15 | 0.00321 | 0.00321 | 38.66 | 15.48 | 47.19 | | 252.94 | 292.34 | | | 133.48 |
| kynurenine 3-monooxygenase | | | | | | | | | | | | | | | |
| rc_N29353_at | N29353 | 2477 | (kynurenine 3-hydroxylase) | 4.78 | 0.00019 | 0.00019 | -4.7 | -5.88 | 13.94 | | 109.79 | 101.27 | | | 53.38 |
| rc_N29543_at | N29543 | 2479 | EST | #N/A | #N/A | #N/A | 11.66 | 9.07 | 5.04 | | 59.21 | 51.22 | | | 30.43 |
| rc_N29740_at | N29740 | 2480 | EST | #N/A | #N/A | #N/A | 48.71 | 27.45 | 46.9 | | 80.01 | 77.9 | | | 37.18 |
| rc_N31952_at | N31952 | 2490 | EST | 3.13 | 0.01481 | 0.01481 | 36.21 | 27.5 | 25.04 | | 133.49 | 147.66 | | | 83.03 |
| rc_N32071_at | N32071 | 2491 | EST | 8.75 | 0.00006 | 0.00006 | 40.89 | 43.12 | 15.37 | | 421.21 | 488.49 | | | 238.4 |
| rc_N34804_at | N34804 | 2497 | DKFZP434J214 protein | 8.08 | 0.00028 | 0.00028 | 6.99 | 5.94 | 33.73 | | 344.08 | 176.4 | | | 532.11 |
| rc_N34919_at | N34919 | 2499 | EST | #N/A | #N/A | #N/A | 7.39 | 8 | 6.82 | | 52.96 | 44.23 | | | 24.23 |
| rc_N35247_at | N35247 | 2500 | EST | #N/A | #N/A | #N/A | 39.9 | 33.56 | 15.03 | | 117.08 | 116.14 | | | 57.05 |
| rc_N36085_at | N36085 | 2505 | EST | #N/A | #N/A | #N/A | 20.98 | 19.21 | 13.89 | | 58.28 | 58 | | | 22.95 |
| rc_N40320_at | N40320 | 2514 | EST | 7.56 | 0.01584 | 0.01584 | 99.72 | 83.43 | 128.45 | | 558.37 | 595.16 | | | 250.67 |
| rc_N45320_at | N45320 | 2519 | EST | #N/A | #N/A | #N/A | 11.39 | 11.26 | 7.06 | | 50.75 | 36 | | | 39.19 |
| rc_N45998_at | N45998 | 2520 | EST | 3.14 | 0.00337 | 0.00337 | 28.42 | 22.62 | 13.52 | | 99.42 | 110.53 | | | 49.55 |
| rc_N47469_at | N47469 | 2522 | EST | 3.34 | 0.00329 | 0.00329 | 20.35 | 13.91 | 20.65 | | 104.74 | 99.87 | | | 61.84 |
| rc_N48155_at | N48155 | 2525 | EST | #N/A | #N/A | #N/A | 17.08 | 16.77 | 14.66 | | 97.37 | 54.69 | | | 99.7 |
| adaptor-related protein complex 2, mu 1 subunit | | | | | | | | | | | | | | | |
| rc_N48315_at | N48315 | 2527 | complex 2, mu 1 subunit | 5.3 | 0.0149 | 0.0149 | 62.03 | 30.66 | 52.29 | | 368.37 | 331.28 | | | 260.93 |
| rc_N48674_at | N48674 | 2530 | EST | 4.06 | 0.00028 | 0.00028 | 2.7 | 4.57 | 10.52 | | 94.61 | 72.82 | | | 54.62 |
| rc_N50038_at | N50038 | 2541 | EST | #N/A | #N/A | #N/A | 0.25 | 5.19 | 45.95 | | 47.04 | 41.45 | | | 16.56 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|----------------|---------|--------|--|----------------------------|---------|-----------|--------|---------------|----------------|---------|---------|----------------|---------|
| | | | | | | Mean | Median | c: Std Dev | set 2: Mean | Median | Std Dev | set 2: Mean | Std Dev |
| rc_N51117_at | N51117 | 2544 | EST | 9.68 | 0.00081 | 8.23 | 4.5 | 11.88 | 327.53 | 296.4 | 266.42 | 327.53 | 266.42 |
| rc_N52845_at | N52845 | 2554 | EST | 5.53 | 0.00088 | 28.56 | 30.14 | 14.95 | 219.38 | 230.31 | 149.67 | 219.38 | 149.67 |
| rc_N53757_at | N53757 | 2560 | EST | 3.97 | 0.00255 | 99.49 | 80.7 | 56.09 | 365.45 | 324.21 | 118.42 | 365.45 | 118.42 |
| rc_N54053_at | N54053 | 2561 | secreted phosphoprotein 2, 24kD | 60.39 | 0.00087 | 44.3 | -18.16 | 166.47 | 2749.73 | 2790.77 | 1230.33 | 2749.73 | 1230.33 |
| rc_N54311_at | N54311 | 2564 | EST | 4.82 | 0.00183 | 9.77 | 9.36 | 25.17 | 160.29 | 130.17 | 124.7 | 160.29 | 124.7 |
| rc_N54604_at | N54604 | 2570 | EST | 3.72 | 0.00741 | 2.36 | 2.08 | 35.23 | 133.06 | 119.1 | 109.95 | 133.06 | 109.95 |
| rc_N54792_at | N54792 | 2571 | cytidine monophosphate-N- acetylneuraminic acid | 3.23 | 0.00099 | 28.36 | 27.42 | 6.39 | 110.19 | 77.69 | 87.32 | 110.19 | 87.32 |
| rc_N55272_at | N55272 | 2574 | hydroxylase (CMP-N- acetylneuraminase) | #N/A | #N/A | 22.71 | 13.6 | 24.4 | 45.08 | 47.45 | 14.77 | 45.08 | 14.77 |
| N57464_at | N57464 | 2576 | CCAAT/enhancer binding protein (C/EBP), delta | 14.69 | 0.00018 | 22.28 | 11.43 | 38.78 | 429.29 | 442.58 | 169.83 | 429.29 | 169.83 |
| rc_N57934_s_at | N57934 | 2577 | forminotransferase | 13.81 | 0.00171 | 806.55 | 477.9 | 939.39 | 9051.2 | 6373.16 | 8542.52 | 9051.2 | 8542.52 |
| rc_N59089_at | N59089 | 2581 | cyclodeaminase | 4.74 | 0.00055 | 38.4 | 36.58 | 24.6 | 215.54 | 167.6 | 133.64 | 215.54 | 133.64 |
| rc_N59532_s_at | N59532 | 2585 | aminomethyltransferase (glycine cleavage system protein T) | 6.73 | 0.00005 | 12.43 | 2.55 | 17.66 | 196.37 | 155.84 | 122.13 | 196.37 | 122.13 |
| rc_N59543_at | N59543 | 2587 | PDZ domain containing 1 | 9.96 | 0.00052 | 1.2 | -2.89 | 17.29 | 303.49 | 259.23 | 225.96 | 303.49 | 225.96 |
| rc_N59550_at | N59550 | 2588 | EST | 25.56 | 0.00024 | 19.9 | 2.53 | 65.91 | 855.88 | 774.72 | 358.3 | 855.88 | 358.3 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | normal | | |
|----------------|---------|--------|--|-------------|-----------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | in metas | metastati | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_N62523_at | N62523 | 2592 | hepatic leukemia factor | 5.02 | 0.00087 | 9.04 | 6.67 | 16.46 | 144.8 | 148.62 | 85.03 | |
| rc_N62922_at | N62922 | 2596 | EST | #N/A | #N/A | 14.92 | 14.15 | 2.75 | 54.94 | 52.4 | 18.93 | |
| rc_N63047_at | N63047 | 2597 | EST | #N/A | #N/A | 4.13 | 0.93 | 9.72 | 14.78 | 15.63 | 8.24 | |
| rc_N63172_at | N63172 | 2599 | cell division cycle 42 (GTP-binding protein, 25kD) | #N/A | #N/A | 26.88 | 33.1 | 24.75 | 60.99 | 57.64 | 40.01 | |
| rc_N63698_at | N63698 | 2604 | EST | 7.92 | 0.00001 | 19.14 | 18.14 | 12.14 | 221.25 | 212.4 | 122.32 | |
| rc_N64017_at | N64017 | 2606 | EST | 5.27 | 0.00022 | 5.45 | 8.71 | 8.71 | 122.34 | 135.27 | 55.58 | |
| rc_N64436_at | N64436 | 2609 | EST | 3.51 | 0.00441 | 24.46 | 20.38 | 21.08 | 119.24 | 133.44 | 70.66 | |
| rc_N65959_at | N65959 | 2612 | EST | 5.43 | 0.00044 | 3.51 | 3.25 | 22.24 | 142.87 | 149.26 | 79.26 | |
| rc_N66130_at | N66130 | 2614 | progesterone membrane binding protein | 3.98 | 0.0106 | 29.02 | 21.05 | 33.88 | 172.14 | 181.78 | 114.84 | |
| rc_N66613_at | N66613 | 2617 | EST | #N/A | #N/A | 25.61 | 22.34 | 26.39 | 62.58 | 50.13 | 51.99 | |
| rc_N67009_s_at | N67009 | 2622 | prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) | 3.55 | 0.00956 | 25.95 | 11.35 | 38.17 | 122.85 | 124.39 | 65.69 | |
| rc_N67105_at | N67105 | 2624 | EST | 5.01 | 0.00176 | -0.75 | 0.21 | 16.38 | 143.36 | 102.9 | 121.4 | |
| rc_N67876_s_at | N67876 | 2628 | insulin-like growth factor 1 (somatomedin C) | 8.89 | 0.00042 | 11.81 | 15.88 | 8.82 | 267.41 | 145.79 | 238.35 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | metastati metastati | | | normal | | |
|---------------------------------|---------|--------|---|-------------|---------|-----------|--------|------------|---------------------|----------------------|-----------------------|---------|---------|--|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | | |
| activating transcription factor | | | | | | | | | | | | | | |
| rc_N67974_at | N67974 | 2630 | 4 (tax-responsive enhancer element B67) | #N/A | #N/A | 5.67 | -0.08 | 15.97 | 82.1 | 74.13 | 59.47 | 82.1 | 59.47 | |
| rc_N68133_at | N68133 | 2633 | EST | #N/A | #N/A | 2.35 | -5.53 | 16.59 | 58.69 | 37.21 | 57.82 | 58.69 | 57.82 | |
| betaine-homocysteine | | | | | | | | | | | | | | |
| rc_N68596_s_at | N68596 | 2636 | methytransferase | 40.99 | 0 | -6.75 | -13.81 | 19.15 | 1061.81 | 1013.27 | 574.42 | 1061.81 | 574.42 | |
| rc_N68871_at | N68871 | 2638 | EST | #N/A | #N/A | 4.3 | 4.02 | 8.66 | 34.08 | 36.71 | 14.33 | 34.08 | 14.33 | |
| rc_N70305_at | N70305 | 2655 | EST | 4.41 | 0.00078 | -13.99 | -13.48 | 10.76 | 105.8 | 97.72 | 72.15 | 105.8 | 72.15 | |
| rc_N70358_s_at | N70358 | 2657 | growth hormone receptor | 34.35 | 0 | 20.93 | 29.26 | 36.06 | 1449.57 | 1157.97 | 1115.22 | 1449.57 | 1115.22 | |
| rc_N71542_at | N71542 | 2665 | kidney- and liver-specific gene | 21.05 | 0 | -14.76 | -18.28 | 14.3 | 471.65 | 486.43 | 226.63 | 471.65 | 226.63 | |
| rc_n71935_s_at | N71935 | 2667 | multiple PDZ domain protein | 16.28 | 0 | 12.84 | 19.17 | 14.1 | 410.92 | 422.1 | 218.42 | 410.92 | 218.42 | |
| rc_N72200_at | N72200 | 2669 | EST | #N/A | #N/A | 12.93 | 14.15 | 14.26 | 57.8 | 56.14 | 30.12 | 57.8 | 30.12 | |
| rc_N73561_at | N73561 | 2676 | EST | 12.96 | 0.00011 | 17.04 | 4.48 | 25.06 | 516.79 | 458.57 | 393.69 | 516.79 | 393.69 | |
| rc_N73883_at | N73883 | 2682 | EST | 9.35 | 0 | 18.47 | 23.48 | 17.67 | 256.78 | 276.41 | 95.34 | 256.78 | 95.34 | |
| deiodinase, iodothyronine, | | | | | | | | | | | | | | |
| rc_N74025_at | N74025 | 2685 | type I | 22.79 | 0 | -7.64 | 2.14 | 15.95 | 527.67 | 515.68 | 256.99 | 527.67 | 256.99 | |
| rc_N74422_at | N74422 | 2686 | EST | 30.32 | 0 | 23.57 | 28.41 | 36.93 | 1063.07 | 1094.48 | 371.26 | 1063.07 | 371.26 | |
| collectin sub-family member | | | | | | | | | | | | | | |
| rc_N74624_at | N74624 | 2688 | 10 (C-type lectin) | #N/A | #N/A | 33.8 | 34.24 | 5.13 | 71.81 | 62.09 | 43.57 | 71.81 | 43.57 | |
| rc_N75072_at | N75072 | 2689 | EST | 3.73 | 0.00379 | 5.14 | 6.21 | 15.5 | 104.12 | 104.99 | 81.79 | 104.12 | 81.79 | |
| N75120_at | N75120 | 2690 | EST | #N/A | #N/A | 20.59 | 23.42 | 10.65 | 61.42 | 58.88 | 13.84 | 61.42 | 13.84 | |
| rc_N76086_r_at | N76086 | 2695 | EST | #N/A | #N/A | 8.23 | 7.19 | 6.54 | 55.55 | 55.02 | 35.47 | 55.55 | 35.47 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | metastati | | normal | | normal | |
|--|---------|--------|----------------------------|-------------|---------|-----------|--------|------------|-------------|---------------|----------------|---------------|----------------|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Median | set 2: Std Dev |
| rc_N80129_i_at | N80129 | 2703 | metallothionein 1L | 66.48 | 0.00415 | 179.8 | 104.5 | 643.06 | 10421.47 | 6358.88 | 9618.98 | 6358.88 | 9618.98 |
| N87590_at | N87590 | 2707 | EST | #N/A | #N/A | 1.04 | -3.72 | 9.99 | 64.67 | 59.2 | 35.53 | 59.2 | 35.53 |
| rc_N91882_at | N91882 | 2720 | alpha2,3-sialyltransferase | 14.52 | 0.00024 | -0.18 | 0.18 | 34.36 | 512.3 | 550.51 | 320.62 | 550.51 | 320.62 |
| rc_N93191_at | N93191 | 2730 | EST | 3.25 | 0.00232 | 174.54 | 168.53 | 56.36 | 659.95 | 565.08 | 409.15 | 565.08 | 409.15 |
| rc_N93403_at | N93403 | 2734 | EST | #N/A | #N/A | 4.44 | 7.63 | 11.8 | 48.84 | 38.39 | 30.93 | 38.39 | 30.93 |
| rc_N93470_at | N93470 | 2736 | EST | #N/A | #N/A | 14.01 | 8.69 | 17.09 | 77.86 | 66.84 | 70.45 | 66.84 | 70.45 |
| rc_N93764_at | N93764 | 2737 | EST | 5.92 | 0.0109 | 113.46 | 68.13 | 96.98 | 771.74 | 792.59 | 504.88 | 792.59 | 504.88 |
| N94146_at | N94146 | 2739 | EST | 8.05 | 0 | 28.92 | 34.7 | 14.14 | 258.82 | 265.55 | 101.53 | 265.55 | 101.53 |
| N99542_at | N99542 | 2747 | orosomucoid 1 | 8.41 | 0.00001 | 6.74 | 10.14 | 21.89 | 226.06 | 187.68 | 146.11 | 187.68 | 146.11 |
| glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) * | | | | | | | | | | | | | |
| rc_R02365_f_at | R02365 | 2755 | disease | 17.17 | 0.00124 | 0.92 | -5.3 | 9.39 | 768.72 | 444.03 | 841.02 | 444.03 | 841.02 |
| rc_R05309_f_at | R05309 | 2759 | EST | 3.72 | 0.0008 | 21.94 | 13.92 | 18.75 | 96.81 | 100.54 | 31.73 | 100.54 | 31.73 |
| SEC24 (S. cerevisiae) related gene family, member | | | | | | | | | | | | | |
| rc_R05490_at | R05490 | 2761 | B | 3.03 | 0.00317 | 5.87 | 3.49 | 12.23 | 75.28 | 78.17 | 48.59 | 78.17 | 48.59 |
| rc_R06002_s_at | R06002 | 2763 | EST | 10.15 | 0.00003 | 10.52 | 8.26 | 20.8 | 292.89 | 264.17 | 160.28 | 264.17 | 160.28 |
| rc_R06271_s_at | R06271 | 2766 | EST | 6.14 | 0.00063 | 23.1 | 18.95 | 21.07 | 208.75 | 221.65 | 107.72 | 221.65 | 107.72 |
| rc_R06273_f_at | R06273 | 2767 | EST | #N/A | #N/A | 138 | 103.77 | 75.66 | 235.98 | 183.78 | 122.56 | 183.78 | 122.56 |
| rc_R06543_at | R06543 | 2769 | EST | #N/A | #N/A | 61.75 | 61.42 | 88.77 | 163.57 | 144.04 | 96.98 | 144.04 | 96.98 |
| rc_R06746_at | R06746 | 2771 | EST | 15.77 | 0.00009 | 13.37 | -0.9 | 39.24 | 455.48 | 410.16 | 191.35 | 410.16 | 191.35 |
| rc_R06860_at | R06860 | 2773 | EST | #N/A | #N/A | 84.61 | 75.89 | 71.35 | 104.51 | 116.59 | 44.71 | 116.59 | 44.71 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | metastati metastati | | | normal | | |
|--------------------------------------|---------|--------|---------------------------------------|-------------|---------|-----------|--------|--------|---------------------|---------|---------|-------------|---------|---------|
| | | | | In metas | p value | c: Mean | Median | Dev | set 2: Mean | Median | Std Dev | set 2: Mean | Median | Std Dev |
| glucokinase (hexokinase 4) | | | | | | | | | | | | | | |
| rc_R06977_f_at | R06977 | 2775 | regulatory protein | 6.1 | 0.00049 | -47.7 | -38.97 | 37.79 | 152.22 | 150.69 | 87.15 | 152.22 | 150.69 | 87.15 |
| rc_R08564_at | R08564 | 2780 | plasminogen-like | 60.18 | 0.00091 | 69.78 | 24 | 105.91 | 2485.63 | 2384.62 | 531.43 | 2485.63 | 2384.62 | 531.43 |
| rc_R09053_at | R09053 | 2783 | EST | 5.9 | 0.0002 | 6.45 | 17.17 | 35.01 | 186.87 | 204.61 | 113.19 | 186.87 | 204.61 | 113.19 |
| rc_R10287_at | R10287 | 2785 | EST | 11.2 | 0.0003 | 7.46 | 4.94 | 35.03 | 376.82 | 434.91 | 198.74 | 376.82 | 434.91 | 198.74 |
| rc_R10684_at | R10684 | 2788 | EST | 5.51 | 0.00741 | 28.67 | 1.31 | 62.39 | 217.05 | 221.32 | 122.94 | 217.05 | 221.32 | 122.94 |
| rc_R12472_at | R12472 | 2789 | EST | 55.18 | 0.00011 | 32.21 | 3.13 | 76.26 | 2002.79 | 1930.03 | 1097.37 | 2002.79 | 1930.03 | 1097.37 |
| rc_R12579_at | R12579 | 2790 | EST | 3.5 | 0.00137 | 54.49 | 37.84 | 26.65 | 198.7 | 194.59 | 92.03 | 198.7 | 194.59 | 92.03 |
| R19808_at | R19808 | 2796 | EST | #N/A | #N/A | 9.95 | 12.2 | 25.55 | 27.53 | 25.43 | 10.61 | 27.53 | 25.43 | 10.61 |
| rc_R31104_f_at | R31104 | 2811 | EST | #N/A | #N/A | -6.45 | 0.74 | 37.65 | 32.27 | 26.77 | 13.57 | 32.27 | 26.77 | 13.57 |
| R31641_at | R31641 | 2814 | EST | 9.96 | 0.00011 | 29.02 | 21.83 | 31.18 | 350.89 | 330.68 | 166.29 | 350.89 | 330.68 | 166.29 |
| rc_R33146_at | R33146 | 2819 | EST | 7 | 0.00043 | 3.32 | 2.1 | 10.76 | 179.67 | 195.02 | 107 | 179.67 | 195.02 | 107 |
| KIAA0327 gene product | | | | | | | | | | | | | | |
| rc_R34362_at | R34362 | 2822 | synaptotagmin 1 | 5.4 | 0.04615 | 621.7 | 353.73 | 689.66 | 2107.55 | 2121.04 | 1000.75 | 2107.55 | 2121.04 | 1000.75 |
| rc_R39238_at | R39238 | 2836 | lecithin-cholesterol | #N/A | #N/A | 16.06 | 16.03 | 9.94 | 26.8 | 23.84 | 16.46 | 26.8 | 23.84 | 16.46 |
| rc_R40395_s_at | R40395 | 2841 | acyltransferase | 37.33 | 0.00032 | 0.98 | -46.23 | 77.82 | 1192.03 | 1230.66 | 281.28 | 1192.03 | 1230.66 | 281.28 |
| rc_R40556_s_at | R40556 | 2843 | EST | 3.57 | 0.00184 | 8.98 | 8.28 | 11.75 | 91.55 | 95.59 | 58.66 | 91.55 | 95.59 | 58.66 |
| crystallin, zeta (quinone reductase) | | | | | | | | | | | | | | |
| rc_R40946_f_at | R40946 | 2845 | paraoxonase 1 | 6.14 | 0.00156 | 18.65 | 19.52 | 14.3 | 205.48 | 220.3 | 137.27 | 205.48 | 220.3 | 137.27 |
| rc_R43174_s_at | R43174 | 2848 | downregulated in renal cell carcinoma | 74.04 | 0.00038 | 47.94 | -8.83 | 119.68 | 2926.85 | 3104.07 | 1318.41 | 2926.85 | 3104.07 | 1318.41 |
| carcinoma | | | | | | | | | | | | | | |
| rc_R43347_at | R43347 | 2849 | EST | #N/A | #N/A | 36.93 | 32.68 | 30.41 | 105.66 | 100.62 | 28.62 | 105.66 | 100.62 | 28.62 |
| rc_R43365_at | R43365 | 2850 | EST | 5.37 | 0.00103 | 5.57 | 6.67 | 12.18 | 150.58 | 112.8 | 122.96 | 150.58 | 112.8 | 122.96 |
| rc_R43910_at | R43910 | 2852 | EST | 5.71 | 0 | 23.41 | 24.6 | 11.1 | 156.7 | 166.34 | 52.21 | 156.7 | 166.34 | 52.21 |
| rc_R45480_i_at | R45480 | 2863 | cyclin K | #N/A | #N/A | 27.21 | 17.36 | 21.39 | 71.04 | 79.77 | 50.88 | 71.04 | 79.77 | 50.88 |
| rc_R49602_at | R49602 | 2885 | EST | 36.5 | 0.00001 | 19.25 | 9.65 | 26.41 | 970.39 | 905.54 | 322.69 | 970.39 | 905.54 | 322.69 |
| rc_R51831_at | R51831 | 2891 | EST | 5.03 | 0.00761 | 5.89 | 2.5 | 44.67 | 221.54 | 195.97 | 179.99 | 221.54 | 195.97 | 179.99 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | normal | | |
|--|---------|--------|----------------------------|-------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | in metas | p value | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_R52822_i_at | R52822 | 2896 | EST | 12.79 | 0.00001 | 10.78 | 0.35 | 28.51 | 380.07 | 441.17 | 180.12 |
| rc_R53044_at | R53044 | 2898 | KIAA0981 protein | #N/A | #N/A | 17.84 | 25.74 | 11.45 | 48.77 | 44.34 | 18.43 |
| rc_R53891_at | R53891 | 2900 | EST | #N/A | #N/A | 9.88 | 5.59 | 10.68 | 66.28 | 52.16 | 49.21 |
| rc_R59312_at | R59312 | 2913 | EST | #N/A | #N/A | 34.37 | 35.83 | 22.13 | 94.44 | 91.55 | 36.35 |
| rc_R59722_at | R59722 | 2916 | EST | 19.74 | 0.00016 | 18.78 | -4.94 | 51.34 | 628.69 | 642.78 | 316.88 |
| rc_R60959_at | R60959 | 2919 | EST | #N/A | #N/A | 31.21 | 23.86 | 17.79 | 72.94 | 69.87 | 45.25 |
| rc_R62519_f_at | R62519 | 2926 | EST | 10.83 | 0.00243 | 73.01 | 104.54 | 56.5 | 707.38 | 751.42 | 357.22 |
| R63545_at | R63545 | 2927 | EST | 5.4 | 0.00202 | 2.58 | 9.54 | 17.4 | 157.98 | 128.33 | 139.55 |
| fatty-acid-Coenzyme A | | | | | | | | | | | |
| rc_R63734_at | R63734 | 2928 | ligase, long-chain 3 | #N/A | #N/A | 13.28 | 17.42 | 12.17 | 42.74 | 39.66 | 18.51 |
| R64534_at | R64534 | 2934 | EST | #N/A | #N/A | 12.11 | 14.54 | 5.77 | 40.32 | 40.98 | 17.27 |
| kynurenine 3-monooxygenase | | | | | | | | | | | |
| rc_R65593_s_at | R65593 | 2935 | (kynurenine 3-hydroxylase) | 21.27 | 0.00007 | 28.84 | 18.5 | 43.46 | 704.58 | 812.38 | 352.86 |
| gamma-glutamyl carboxylase | | | | | | | | | | | |
| rc_R67970_s_at | R67970 | 2940 | carboxylase | 9.45 | 0.00212 | 85.44 | 59.33 | 76.67 | 655.11 | 692.66 | 267.95 |
| rc_R70319_at | R70319 | 2946 | EST | #N/A | #N/A | 5.34 | 2.91 | 8.92 | 29.23 | 29.18 | 10.78 |
| rc_R70791_at | R70791 | 2949 | EST | #N/A | #N/A | 127.11 | 110.15 | 41.83 | 73.19 | 57.2 | 56.17 |
| differentially expressed in adenocarcinoma of the lung | | | | | | | | | | | |
| R71459_at | R71459 | 2953 | adenocarcinoma of the lung | #N/A | #N/A | 16.9 | 11.46 | 16.47 | 37.42 | 30.98 | 20.83 |
| rc_R73468_at | R73468 | 2957 | EST | #N/A | #N/A | 9.97 | 10.43 | 9.69 | 38.29 | 44.82 | 17.14 |
| rc_R73816_at | R73816 | 2961 | EST | 11.53 | 0.00259 | -26.88 | -30.68 | 10.09 | 462.31 | 374.67 | 450.91 |
| R77539_at | R77539 | 2965 | EST | #N/A | #N/A | 5.91 | 14.55 | 25.48 | 70.5 | 59.8 | 31.72 |
| rc_R78713_s_at | R78713 | 2968 | EST | #N/A | #N/A | 0.27 | -1.59 | 8.92 | 70.57 | 57.33 | 56.37 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastati | | metastati | | normal | | normal | | |
|-----------------------------|---------|--------|--------------------------------|--------|----------|---------|-----------|--------|------------|---------|---------|---------|--------|--|--|
| | | | | change | in metas | | c: Mean | Median | c: Std Dev | Mean | Median | Std Dev | | | |
| | | | | | | | | | | | | | | | |
| phosphatidylserine | | | | | | | | | | | | | | | |
| R82229_at | R82229 | 2975 | decarboxylase | 3.08 | 0.03455 | 84.63 | 80.61 | 67.01 | 228.19 | 232.06 | 58.38 | | | | |
| rc_R91060_at | R91060 | 2981 | EST | #N/A | #N/A | 59.14 | 37.15 | 56.04 | 85.88 | 61.99 | 68.99 | | | | |
| rc_R93507_at | R93507 | 2991 | EST | #N/A | #N/A | 19.53 | 20.08 | 11 | 67.62 | 67.56 | 44.22 | | | | |
| rc_R93714_at | R93714 | 2992 | fetuin B | 10.42 | 0.00043 | -60.74 | -65.14 | 57.99 | 280.62 | 301.36 | 203.86 | | | | |
| rc_R93908_at | R93908 | 2994 | EST | 5.8 | 0.02699 | 66.75 | 29.54 | 129.46 | 348.58 | 301.29 | 173.81 | | | | |
| rc_R94674_s_at | R94674 | 2996 | EST | 10.76 | 0.00008 | 0.91 | 4.15 | 14.66 | 269.49 | 288.56 | 148.06 | | | | |
| rc_R96822_at | R96822 | 3000 | EST | 8.25 | 0.00008 | 16.45 | 17.01 | 30.67 | 250.81 | 257.18 | 131.85 | | | | |
| cytochrome P450, subfamily | | | | | | | | | | | | | | | |
| VIIIB (sterol 12-alpha- | | | | | | | | | | | | | | | |
| rc_R97419_at | R97419 | 3004 | hydroxylase), polypeptide 1 | 65.07 | 0.0039 | 152.16 | -3.42 | 302.56 | 4114.39 | 3837.4 | 1458.43 | | | | |
| rc_R97804_at | R97804 | 3008 | EST | #N/A | #N/A | 144.46 | 187.67 | 95.8 | 193.05 | 201.89 | 61.84 | | | | |
| R98073_at | R98073 | 3009 | EST | 46.87 | 0 | -4.33 | -9.52 | 11.43 | 1161.51 | 1291.95 | 564.26 | | | | |
| rc_R98105_at | R98105 | 3011 | EST | #N/A | #N/A | 132.16 | 97.16 | 141.15 | 373.83 | 342.91 | 215.89 | | | | |
| rc_R98413_at | R98413 | 3012 | EST | 9.71 | 0.00007 | 38.74 | 28.05 | 21.96 | 402.49 | 443.47 | 212.95 | | | | |
| rc_R98624_at | R98624 | 3013 | EST | 21.32 | 0 | 15.01 | 4.48 | 22.97 | 686.81 | 542.22 | 466.97 | | | | |
| rc_R99014_at | R99014 | 3015 | EST | #N/A | #N/A | 26.99 | 17.82 | 29.49 | 49.82 | 52.35 | 18 | | | | |
| CD5 antigen-like (scavenger | | | | | | | | | | | | | | | |
| rc_R99591_at | R99591 | 3016 | receptor cysteine rich family) | 9.52 | 0.00006 | 87.08 | 72.59 | 28.25 | 1035.39 | 904.92 | 691.83 | | | | |
| S62539_s_at | S62539 | 3022 | insulin receptor substrate 1 | 3.7 | 0.01307 | 28.26 | 13.05 | 40.92 | 132.59 | 97.52 | 103.35 | | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|----------------|---------|--------|--|----------------------------|---------|-----------|-----------|---------------|--------------------------|----------------------------|-----------------------------|--------------------------|-----------------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | normal set 2: Mean | normal set 2: Std Dev |
| S68287_at | S68287 | 3025 | aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4) | 24.11 | 0 | 6.23 | 6.37 | 9.75 | 510.59 | 569.32 | 165.14 | | |
| S69232_at | S69232 | 3027 | electron-transferring- flavoprotein dehydrogenase | 4.9 | 0.00017 | 2.73 | 4.9 | 4.29 | 113.33 | 103.27 | 60.93 | | |
| S70004_at | S70004 | 3029 | glycogen synthase 2 (liver) | 9.96 | 0.00001 | -0.03 | -4.28 | 11.42 | 225.1 | 212.32 | 102.76 | | |
| S72370_at | S72370 | 3030 | pyruvate carboxylase | 5.31 | 0.00075 | 3.83 | 5.81 | 23.1 | 113.03 | 118.49 | 50.19 | | |
| S77410_at | S77410 | 3035 | angiotensin receptor 1 ras homolog gene family, | 10.4 | 0 | 18.77 | 17.34 | 10.85 | 266.59 | 284.37 | 98.14 | | |
| S82240_at | S82240 | 3039 | member E | #N/A | #N/A | 19.9 | 6.78 | 30.8 | 75.14 | 74.07 | 40.43 | | |
| T08879_at | T08879 | 3049 | cathepsin F | 5.29 | 0.0008 | 17.98 | 14.06 | 12.92 | 156.33 | 180.88 | 79.67 | | |
| rc_T16306_at | T16306 | 3068 | EST | #N/A | #N/A | 24.23 | 23.64 | 24.91 | 58.82 | 63.62 | 22.35 | | |
| | | | protein tyrosine phosphatase type IVA, | | | | | | | | | | |
| rc_T40895_at | T40895 | 3117 | member 1 | #N/A | #N/A | 1575.59 | 2039.82 | 1098.29 | 4148.86 | 2440.28 | 4169.52 | | |
| rc_T46901_at | T46901 | 3123 | EST | 77.28 | 0.0006 | 11.33 | -31.1 | 121.66 | 2608.54 | 2853.98 | 691.43 | | |
| rc_T48075_f_at | T48075 | 3130 | hemoglobin, alpha 1 | 32.56 | 0.00172 | 246.19 | 164.89 | 271.65 | 7193.85 | 5199.28 | 6317.01 | | |
| rc_T50773_s_at | T50773 | 3136 | apolipoprotein C-IV | #N/A | #N/A | 94.77 | 43.61 | 169.6 | 8473.97 | 6484.47 | 7036.85 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | metastati | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|--|---------|--------|-----------------|----------------------------|---------|-----------|-----------|---------------|---------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | c: Std Dev | | | |
| solute carrier family 22 (extraneuronal monoamine transporter), member 3 | | | | | | | | | | | | |
| rc_T51617_at | T51617 | 3138 | EST | 17.67 | 0.00018 | 29.08 | 19.44 | 56.17 | 669.34 | 725.25 | 402.58 | |
| rc_T51930_at | T51930 | 3139 | EST | 9.99 | 0.00066 | 8.27 | 9.41 | 5.97 | 325.48 | 218.59 | 298.12 | |
| RNA helicase-related protein paraoxonase 3 | | | | | | | | | | | | |
| rc_T56281_f_at | T56281 | 3151 | EST | 32.34 | 0.00002 | 71.16 | 62.87 | 44.81 | 2132.07 | 2146.52 | 824.76 | |
| T57140_s_at | T57140 | 3152 | EST | 28.8 | 0 | -1.37 | -7.55 | 22.26 | 825.16 | 979.66 | 487.32 | |
| rc_T58756_at | T58756 | 3156 | EST | 13.39 | 0.00013 | 7.38 | -19.91 | 46.26 | 390.04 | 386.76 | 164.41 | |
| small inducible cytokine subfamily A (Cys-Cys), member 16 | | | | | | | | | | | | |
| rc_T58775_at | T58775 | 3157 | EST | 21.18 | 0.00006 | 11.93 | -0.59 | 34.83 | 577.14 | 540.96 | 205.27 | |
| carbamoyl-phosphate synthetase 1, mitochondrial ketohexokinase | | | | | | | | | | | | |
| rc_T59148_s_at | T59148 | 3158 | EST | 88.89 | 0 | 17.1 | 2.26 | 49.29 | 3384.09 | 3845.28 | 2295.81 | |
| rc_T61256_s_at | T61256 | 3162 | EST | 13.59 | 0.00425 | 55.8 | 29.78 | 120.62 | 752.99 | 846.1 | 315.74 | |
| rc_T61654_f_at | T61654 | 3166 | EST | #N/A | #N/A | 66.98 | -33.89 | 208.52 | 9388.4 | 4297.02 | 12058.3 | |
| rc_T64933_r_at | T64933 | 3174 | EST | #N/A | #N/A | 1.58 | 10.35 | 17.94 | 52.88 | 40.46 | 54.68 | |
| rc_T65443_s_at | T65443 | 3175 | EST | #N/A | #N/A | 10.45 | 9.99 | 13.16 | 70.03 | 75.01 | 29 | |
| glutaryl-Coenzyme A dehydrogenase | | | | | | | | | | | | |
| rc_T66189_s_at | T66189 | 3178 | EST | 8.61 | 0.00003 | 17.08 | 20.49 | 23.82 | 269.19 | 301.13 | 136.96 | |
| rc_T67520_at | T67520 | 3182 | EST | #N/A | #N/A | 52.46 | 49.25 | 28.02 | 105.56 | 113.95 | 38.23 | |
| rc_T67705_s_at | T67705 | 3183 | EST | 31.6 | 0.00705 | 168.64 | 37.91 | 284.26 | 2403.76 | 2437.4 | 683.22 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|--|---------|--------|--|-----------------------------|---------|-----------|-----------|---------------|----------------|------------------|-------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| rc_T67931_at | T67931 | 3184 | fibrinogen, B beta polypeptide | 49.55 | 0 | -22.74 | -22.4 | 23.54 | 1187.95 | 1000.67 | 692.18 |
| T68083_at T68510_at rc_T68711_at rc_T68855_at rc_T69020_s_at rc_T69164_at | T68083 | 3185 | short-chain dehydrogenase/reductase 1 | 4.03 | 0.01593 | 65.11 | 47.59 | 67.87 | 263.22 | 280.22 | 136.48 |
| | T68510 | 3187 | EST | 3.87 | 0.00617 | 0.88 | -1.97 | 11.33 | 113.31 | 94.26 | 103.92 |
| | T68711 | 3188 | EST | 37.65 | 0.00036 | 19.73 | -26.69 | 95.05 | 1388.67 | 1074.67 | 890.91 |
| | T68855 | 3189 | EST | 34.04 | 0 | 8.38 | 6.98 | 9 | 800.27 | 911.26 | 406.27 |
| | T69020 | 3193 | EST | 5.39 | 0.00383 | 32.69 | 17.15 | 46.31 | 202.05 | 208.64 | 90.02 |
| | T69164 | 3195 | EST | 4.38 | 0.00548 | 34.31 | 17.81 | 30.85 | 173.2 | 167.2 | 85.34 |
| rc_T69284_s_at rc_T69305_at T69384_at rc_T71978_at | | | mannose-binding lectin (protein C) 2, soluble (opsonic defect) | 36.53 | 0 | 9.82 | 0.32 | 17.14 | 1147.2 | 618.07 | 972.57 |
| | T69284 | 3196 | EST | #N/A | #N/A | -107.09 | -119.3 | 45.51 | 4052.6 | 4262.37 | 3025.26 |
| | T69305 | 3197 | EST | | | | | | | | |
| | T69384 | 3198 | 1 | period (Drosophila) homolog | 5.88 | 0.01219 | 37.94 | 19.8 | 90.03 | 232.84 | 205.78 |
| | T71978 | 3205 | EST | 4.39 | 0.0017 | 41.46 | 58.86 | 43.93 | 218.38 | 208.73 | 89.39 |
| rc_T72171_s_at rc_T72502_at rc_T72906_at rc_T73442_at | T72171 | 3206 | thyroxin-binding globulin | 10.41 | 0.00163 | 5.48 | -20.52 | 54.58 | 492.89 | 371.71 | 454.89 |
| | T72502 | 3208 | EST | 8.87 | 0.00009 | 24.11 | 24.41 | 28.19 | 308.87 | 271.27 | 179.15 |
| | T72906 | 3210 | EST | 7.56 | 0.00062 | 4.88 | 3.04 | 14.04 | 233.73 | 199.26 | 211.99 |
| | T73442 | 3213 | EST | 94.41 | 0 | 28.55 | 25.96 | 25.95 | 3170.29 | 3275.73 | 1073.74 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|--|--|--|--|---|---|---|---|--|--|--|--|
| | | | | | | metastati c: Mean | metastati c: Median | metastati c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| rc_T73739_s_at | T73739 | 3214 | alanine-glyoxylate amino transferase (oxalosis l; hyperoxaluria l; glycolic aciduria; serine- pyruvate aminotransferase) | 16.18 | 0.00277 | 1891.22 | 896.45 | 2229.6 | 26094.38 | 15281.08 | 25947.4 |
| rc_T74542_s_at | T74542 | 3215 | UDP glycosyltransferase 2 family, polypeptide B10 | 32.36 | 0.00004 | 27.96 | 25.04 | 64.23 | 1374.78 | 1445.94 | 869.3 |
| rc_T74608_at | T74608 | 3216 | hydroxyacid oxidase (glycolate oxidase) 1 | 14.03 | 0 | -3.14 | -1.78 | 23.12 | 360.97 | 328.7 | 194.85 |
| rc_T82323_at | T82323 | 3231 | immunoglobulin superfamily, member 4 | 10.14 | 0 | 14.47 | 5.07 | 19.91 | 264.33 | 229.92 | 135.46 |
| T83397_at rc_T84084_at | T83397 T84084 | 3233 3234 | phytanoyl-CoA hydroxylase (Refsum disease) EST | 63.6 #N/A | 0 #N/A | -17.97 21.47 | -4.64 21.35 | 35.51 9.96 | 1404.6 68.96 | 1421.69 66.69 | 605.99 27.4 |
| rc_T84491_at rc_T86482_at rc_T87224_at rc_T90037_at rc_T90520_at rc_T91161_at | T84491 T86482 T87224 T90037 T90520 T91161 | 3235 3238 3241 3246 3249 3253 | CUG triplet repeat, RNA- binding protein 2 transferrin EST EST EST EST | #N/A 11.15 #N/A 3.99 8.67 3.48 | #N/A 0.00006 #N/A 0.0016 0.00072 0.00002 | 32.84 7.6 584.24 23.17 9.05 9.95 | 34.93 9.41 451.54 25.82 -7.07 2.64 | 8.15 12.34 184.49 23.62 25.65 11.55 | 79.08 316.82 909.33 150.67 306.39 77.85 | 80.41 197.03 851.86 107.18 362.5 70.8 | 33.03 302.36 431.47 126.19 204.34 30.28 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | normal | | | normal | | |
|-------------|---------|--------|--|-------------|---------|-----------|--------|------------|-------------|---------------|----------------|-------------|---------------|----------------|
| | | | | In metas | p value | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| T95813_f_at | T95813 | 3262 | KIAA1051 protein | 38.38 | 0.00008 | 56.83 | 42.22 | 56.86 | 2271.29 | 1809.29 | 1537.82 | | | |
| U00115_at | U00115 | 3272 | B-cell CLL/lymphoma 6 (zinc finger protein 51) | 5.18 | 0.00045 | 16.17 | 10.31 | 26.94 | 132.13 | 133.88 | 32.06 | | | |
| U01120_at | U01120 | 3274 | glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) | 13.41 | 0.00147 | 83.05 | 45.5 | 91.8 | 878.33 | 693.43 | 495.6 | | | |
| U02388_at | U02388 | 3278 | cytochrome P450, subfamily IVF, polypeptide 2 | 9.38 | 0.00001 | -4.93 | -3.43 | 18.14 | 207.48 | 207.15 | 90.12 | | | |
| U03056_at | U03056 | 3280 | hyaluronoglucosaminidase 1 | 6.64 | 0 | 12.68 | 11.77 | 4.73 | 139.32 | 137.21 | 43.97 | | | |
| U05861_at | U05861 | 3285 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) | 23.22 | 0.00002 | 47.98 | 44.41 | 21.91 | 1070.69 | 962.74 | 359.01 | | | |
| U06641_s_at | U06641 | 3287 | UDP glycosyltransferase 2 family, polypeptide B15 | 24.32 | 0.00001 | 56.39 | 62.92 | 54.9 | 1762.46 | 1615.25 | 1206.06 | | | |
| U06863_at | U06863 | 3288 | folistatin-like 1 | 3.09 | 0.00091 | 43.48 | 45.73 | 14.83 | 141.97 | 149.4 | 59.45 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|---------------|---------|--------|--|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| U08006_s_at | U08006 | 3290 | complement component 8, alpha polypeptide | 16 | 0.00111 | 47.06 | 31.92 | 47.52 | 633.01 | 661.72 | 102.98 |
| U08198_ma1_at | U08198 | 3292 | complement component 8, gamma polypeptide | 19.71 | 0 | -29.27 | -38.32 | 47.54 | 544.28 | 630.51 | 234.87 |
| U08854_s_at | U08854 | 3293 | UDP glycosyltransferase 2 family, polypeptide B15 | 7.38 | 0.00005 | 10.72 | 6.45 | 10.71 | 181.08 | 184.97 | 91.81 |
| U11313_at | U11313 | 3297 | sterol carrier protein 2 | 5.44 | 0.00187 | 17.39 | 0.82 | 35.86 | 181.8 | 228.15 | 99.25 |
| U12778_at | U12778 | 3301 | acyl-Coenzyme A dehydrogenase, short/branched chain | 5.68 | 0.00116 | 5.23 | 6.16 | 7.33 | 147.06 | 158.14 | 91.5 |
| U13061_ma1_at | U13061 | 3302 | sulfotransferase family 2A, dehydroepiandrosterone (DHEA) -preferring, member 1 | 11.32 | 0.00048 | 9.86 | 7.49 | 19.46 | 369.12 | 431.45 | 213.83 |
| U15174_at | U15174 | 3310 | BCL2/adenovirus E1B 19kD- interacting protein 3 | #N/A | #N/A | 41.72 | 11.86 | 49.01 | 129.19 | 138.02 | 68.72 |
| U15932_at | U15932 | 3311 | dual specificity phosphatase 5 | #N/A | #N/A | 47.94 | 27.05 | 47.87 | 86.73 | 86.97 | 38.45 |
| U17989_at | U17989 | 3316 | nuclear autoantigen | #N/A | #N/A | 14.21 | 12.72 | 6.13 | 44.22 | 41.28 | 19.09 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|---------------|---------|--------|---|----------------------------|---------|-----------|-----------|------------|-------------|---------------|----------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev |
| U19495_s_at | U19495 | 3319 | stromal cell-derived factor 1 | 4.59 | 0.00011 | 7.17 | 5.76 | 5.65 | 103.81 | 114.61 | 50.36 |
| U19523_at | U19523 | 3320 | GTP cyclohydrolase 1 (dopa-responsive dystonia) | 5.25 | 0.00029 | 12.84 | 12.26 | 15.75 | 136.86 | 142.71 | 66.64 |
| U20530_at | U20530 | 3322 | secreted phosphoprotein 2, 24kD | 16.93 | 0 | 12.63 | 11.54 | 9.93 | 383.92 | 421.24 | 128.02 |
| U20938_at | U20938 | 3324 | dihydropyrimidine dehydrogenase | 3.92 | 0.00053 | 6.66 | 6.08 | 7.12 | 90.66 | 97.02 | 44.64 |
| U22029_f_at | U22029 | 3327 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 | 71.98 | 0 | 5.05 | 10.11 | 21.51 | 1968.7 | 1339.04 | 1937.45 |
| U22662_at | U22662 | 3329 | nuclear receptor subfamily 1, group H, member 3 | #N/A | #N/A | 5.71 | 14.46 | 20.18 | 63.21 | 58.72 | 37.5 |
| U31342_at | U31342 | 3344 | nucleobindin 1 | #N/A | #N/A | 77.59 | 66.2 | 40.03 | 183.59 | 197.29 | 58.86 |
| U32576_ma1_at | U32576 | 3347 | apolipoprotein C-IV | 18.59 | 0.00005 | 311.97 | 318.75 | 271.42 | 1299.4 | 1145.33 | 698.02 |
| U32576_ma1_at | U32576 | 3347 | apolipoprotein C-IV | 18.59 | 0.00005 | -7.01 | -23.2 | 62.7 | 606.88 | 608.66 | 224.72 |
| U32989_at | U32989 | 3348 | tryptophan 2,3-dioxygenase | 10.07 | 0.02825 | 166.12 | 22.7 | 333.99 | 527.61 | 473.11 | 268.8 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | p value | metastati | | | | normal | | | |
|------------------|---------|--------|---|-------------|----------|---------|-----------|-----------|------------|-------------|---------------|----------------|--------|--|
| | | | | in metas | in metas | | c: Mean | c: Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | | |
| U37055_rna1_s_at | U37055 | 3353 | macrophage stimulating 1 (hepatocyte growth factor-like),macrophage stimulating, pseudogene 9 | 18.28 | | 0 | -7.37 | -38.2 | 47.48 | 549.49 | 626.51 | | 217.69 | |
| U37143_at | U37143 | 3354 | cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 | #N/A | | #N/A | 33.79 | 28.24 | 31.46 | 116.06 | 131.46 | | 48.68 | |
| U37547_at | U37547 | 3355 | apoptosis inhibitor 1 | #N/A | | #N/A | 29.52 | 19.51 | 48.74 | 93.6 | 112.45 | | 52.27 | |
| U39226_at | U39226 | 3358 | myosin VIIA (Usher syndrome 1B (autosomal recessive, severe)) | #N/A | | #N/A | 33.54 | 31.07 | 8.59 | 53.24 | 50.47 | | 20.86 | |
| U46689_at | U46689 | 3366 | aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase) | 3.5 | 0.01292 | | 31.22 | 25.36 | 49.19 | 124.41 | 136.16 | | 53.23 | |
| U48707_at | U48707 | 3371 | protein phosphatase 1, regulatory (inhibitor) subunit 1A | 14.22 | 0 | | -1.33 | -1.45 | 20.92 | 319.97 | 310.24 | | 125.51 | |
| U49082_at | U49082 | 3373 | transporter protein | 9.17 | 0.00088 | | 71.87 | 46.71 | 56.13 | 563.34 | 515.31 | | 179.82 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | metastati | | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
|-------------|---------|--------|---|----------------------------|---------|-----------|-----------|---------------|----------------------|------------------------|----------------------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | c: Mean | c: Median | c: Std Dev | metastati c: Mean | metastati c: Median | metastati c: Std Dev | | | |
| U49248_at | U49248 | 3374 | ATP-binding cassette, sub- family C (CFTR/MRP), member 2 | 7.06 | 0.00067 | 30.01 | 26.03 | 36.14 | 231.96 | 249.25 | 91.2 | | | |
| U50929_at | U50929 | 3380 | betaine-homocysteine methyltransferase | 36.91 | 0 | 8.63 | 2.82 | 20.35 | 898.57 | 865.9 | 313.61 | | | |
| U51010_s_at | U51010 | 3381 | nicotinamide N- methyltransferase | 27.79 | 0.00366 | 105.25 | 43.72 | 204.23 | 1589.66 | 1590.62 | 536.04 | | | |
| U56814_at | U56814 | 3393 | deoxyribonuclease I-like 3 | 29.43 | 0.00003 | 5.04 | 11.75 | 22.3 | 853.78 | 1073.24 | 434.79 | | | |
| U57094_at | U57094 | 3394 | RAB27A, member RAS oncogene family | #N/A | #N/A | 30.85 | 31.58 | 23.86 | 93.06 | 93.79 | 50.75 | | | |
| U59111_at | U59111 | 3397 | dermatan sulphate proteoglycan 3 | #N/A | #N/A | 32.34 | 26.73 | 15.11 | 68.69 | 64.44 | 32.48 | | | |
| U59423_at | U59423 | 3399 | MAD (mothers against decapentaplegic, Drosophila) homolog 1 | #N/A | #N/A | 17.46 | 16.81 | 10.17 | 60.5 | 51.09 | 37.25 | | | |
| U60061_at | U60061 | 3400 | fasciculation and elongation protein zeta 2 (zygin II) | #N/A | #N/A | 61.44 | 29.18 | 68.3 | 55.02 | 66.29 | 38.2 | | | |
| U66672_at | U66672 | 3407 | ATP-binding cassette, sub- family A (ABC1), member 5 | #N/A | #N/A | 78.03 | 41.24 | 72.76 | 105.45 | 97.64 | 60.15 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | p value | metastati | | metastati | | normal | | normal | |
|---------------|---------|--------|---|--------|----------|---------|-----------|--------|------------|-------------|---------------|----------------|---------------|----------------|
| | | | | change | In metas | | c: Mean | Median | c: Std Dev | set 2: Mean | set 2: Median | set 2: Std Dev | set 2: Median | set 2: Std Dev |
| U68233_at | U68233 | 3412 | nuclear receptor subfamily 1, group H, member 4 | 6.76 | 0.00022 | 19.94 | 9.8 | 29.99 | 198.25 | 233.6 | 83.71 | | | |
| U69141_at | U69141 | 3414 | glutaryl-Coenzyme A dehydrogenase | 3.06 | 0.00053 | 35.13 | 27.91 | 13.89 | 108.36 | 119.26 | 34.82 | | | |
| U70732_ma1_at | U70732 | 3415 | glutamic-pyruvate transaminase (alanine aminotransferase) | 27.63 | 0 | -47.95 | -65.21 | 50.88 | 696.22 | 732.8 | 284.7 | | | |
| U70732_ma1_at | U70732 | 3415 | glutamic-pyruvate transaminase (alanine aminotransferase) | 27.63 | 0 | -1.44 | 3.98 | 66.42 | 201.88 | 218.68 | 136.17 | | | |
| U72515_at | U72515 | 3416 | putative protein similar to nesso (Drosophila) | #N/A | #N/A | 45.44 | 58.93 | 45.12 | 137.35 | 138.01 | 55.38 | | | |
| U73514_at | U73514 | 3419 | hydroxyacyl-Coenzyme A dehydrogenase, type II | 3.79 | 0.01392 | 9.85 | -22.7 | 56.91 | 159.74 | 161.9 | 127.8 | | | |
| U77396_at | U77396 | 3426 | LPS-induced TNF-alpha factor | 4.47 | 0.00108 | 30.53 | 33.74 | 31.54 | 169.83 | 141.36 | 87.43 | | | |
| U77594_at | U77594 | 3428 | retinoic acid receptor responder (tazarotene induced) 2 | 11.95 | 0.00527 | 94.59 | 122.86 | 71.01 | 838.98 | 864.02 | 313.87 | | | |
| U79716_at | U79716 | 3437 | reelin | 3.51 | 0.00053 | 14.44 | 9.15 | 15.58 | 90.6 | 101.49 | 36.51 | | | |
| U80226_s_at | U80226 | 3439 | 4-aminobutyrate aminotransferase | #N/A | #N/A | 39.69 | 51.46 | 20.33 | 86.94 | 91.76 | 24.15 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|--------------|---------|--------|--|----------------------------|---------|----------------------|------------------------|----------------------------|--------------------------|----------------------------|-----------------------------|--|--|
| | | | | | | metastati c: Mean | metastati c: Median | metastati c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | |
| U81607_at | U81607 | 3440 | A kinase (PRKA) anchor protein (gravin) 12 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2 | #N/A | #N/A | 18.75 | 8.46 | 50.91 | 82.7 | 78.31 | 62.79 | | |
| U82108_s_at | U82108 | 3441 | | 3.19 | 0.01545 | 58.61 | 78.15 | 43.49 | 130.34 | 122.39 | 73.74 | | |
| U83461_at | U83461 | 3444 | solute carrier family 31 (copper transporters), member 2 | #N/A | #N/A | 24.64 | 21.28 | 13.16 | 51.79 | 48.53 | 20.85 | | |
| U85193_at | U85193 | 3447 | nuclear factor I/B | #N/A | #N/A | 21.84 | 23.61 | 4.44 | 72.71 | 68.69 | 32.02 | | |
| U90544_at | U90544 | 3454 | solute carrier family 17 (sodium phosphate), member 2 | 6.42 | 0.00023 | -3.14 | -5.18 | 19.12 | 157.41 | 168.92 | 63.8 | | |
| U95090_at | U95090 | 3464 | nephrosis 1, congenital, Finnish type (nephtrin) | 14.01 | 0.00018 | 40.49 | 30.15 | 38.71 | 554.93 | 539.41 | 183.55 | | |
| U95090_at | U95090 | 3464 | nephrosis 1, congenital, Finnish type (nephtrin) | 14.01 | 0.00018 | 4.97 | 5.87 | 18.32 | 188.83 | 201.08 | 88.01 | | |
| W02027_s_at | W02027 | 3465 | EST | #N/A | #N/A | 7.28 | 2.64 | 14.09 | 30.56 | 28.52 | 12.47 | | |
| W03796_at | W03796 | 3468 | EST | 8.3 | 0.0032 | 8.13 | -19.16 | 75.11 | 336.51 | 383.56 | 190.14 | | |
| rc_W15417_at | W15417 | 3473 | KIAA0699 protein | #N/A | #N/A | 30.82 | 20.85 | 38.03 | 83.24 | 81.29 | 49.83 | | |
| W16686_at | W16686 | 3476 | basic helix-loop-helix domain containing, class B, 2 | #N/A | #N/A | 46.29 | -6.45 | 123.94 | 100.9 | 83.13 | 79.01 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | metastati | | | | normal | | | |
|--|---------|--------|---------------------------|--------|---------|-----------|--------|--------|--------|---------|---------|---------|--------|
| | | | | change | p value | metastati | c: | Median | Dev | Mean | Median | Std Dev | normal |
| W27503_at | W27503 | 3486 | KIAA0679 protein | #N/A | #N/A | 17.31 | 17.31 | 21.95 | 21.95 | 27.71 | 27.51 | 5.28 | |
| W28235_at | W28235 | 3487 | EST | #N/A | #N/A | 95.97 | 150.37 | 81.4 | 81.4 | 271.36 | 307.26 | 108.42 | |
| W28824_at | W28824 | 3493 | EST | 15.8 | 0.00006 | -1.99 | -5.59 | 17.64 | 17.64 | 441.67 | 509.29 | 251 | |
| Kreiser (mouse) maf-related | | | | | | | | | | | | | |
| W36290_s_at | W36290 | 3501 | leucine zipper homolog | 3.94 | 0.02718 | 48.52 | 10.45 | 73.21 | 73.21 | 157.7 | 156.24 | 65.15 | |
| W38778_s_at | W38778 | 3507 | EST | #N/A | #N/A | -55.97 | -63.87 | 44.35 | 44.35 | 78.01 | 37.07 | 137.01 | |
| rc_W42429_at | W42429 | 3509 | EST | #N/A | #N/A | 98.32 | 80.07 | 52.23 | 52.23 | 252.63 | 300.68 | 162.35 | |
| rc_W45560_at | W45560 | 3525 | EST | 5.06 | 0.00996 | 86.81 | 62.95 | 81.92 | 81.92 | 369.61 | 354.89 | 158.02 | |
| rc_W48860_at | W48860 | 3537 | EST | #N/A | #N/A | 36.89 | 39 | 14.08 | 14.08 | 52.69 | 41.31 | 21.1 | |
| CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein | | | | | | | | | | | | | |
| W52581_at | W52581 | 3543 | II) | 3.08 | 0.00091 | 10.92 | 8.89 | 10.63 | 10.63 | 71.35 | 58.02 | 37.28 | |
| W58520_at | W58520 | 3552 | nucleoporin 88kD | #N/A | #N/A | 24.77 | 26.75 | 16.56 | 16.56 | 81.88 | 87.47 | 37.77 | |
| rc_W58756_at | W58756 | 3554 | EST | 12.17 | 0.00087 | 93.37 | 88.97 | 71.48 | 71.48 | 1363.71 | 1064.26 | 1032.27 | |
| rc_W60186_at | W60186 | 3557 | EST | 3.24 | 0.00228 | 19.15 | 26.5 | 27.35 | 27.35 | 101.92 | 109.68 | 47.85 | |
| rc_W63741_at | W63741 | 3566 | EST | #N/A | #N/A | -11.85 | -13.73 | 14.25 | 14.25 | 28.54 | 17.1 | 44.58 | |
| rc_W67147_at | W67147 | 3568 | deleted in liver cancer 1 | 9.74 | 0.00002 | 16.09 | 9.11 | 24.66 | 24.66 | 282.59 | 235.29 | 169.33 | |
| rc_W67199_at | W67199 | 3569 | EST | 3.09 | 0.01528 | 30.05 | 35 | 12.16 | 12.16 | 123.27 | 117.99 | 90.47 | |
| rc_W70131_at | W70131 | 3577 | EST | #N/A | #N/A | 108.21 | 30.68 | 183.05 | 183.05 | 118.49 | 100.66 | 53.4 | |
| rc_W72044_at | W72044 | 3580 | insulin induced gene 1 | 24.58 | 0.00001 | 41.6 | 36.28 | 36.46 | 36.46 | 1133.09 | 940.16 | 723.6 | |
| rc_W72079_at | W72079 | 3581 | EST | 6.36 | 0.00641 | 46.78 | 17.94 | 66.71 | 66.71 | 261.7 | 214.62 | 175.87 | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change | | metastati | | | metastati metastati | | | normal | | |
|---|---------|--------|---------------------|-------------|---------|-----------|--------|------------|---------------------|----------------------|-----------------------|--------|--|--|
| | | | | in metas | p value | c: Mean | Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | | |
| oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase | | | | | | | | | | | | | | |
| rc_W72382_at | W72382 | 3584 | dehydrogenase | #N/A | #N/A | 37.21 | 6.21 | 66.91 | 3403.46 | 3255.54 | 1538.23 | | | |
| rc_W72471_at | W72471 | 3585 | EST | #N/A | #N/A | 17.93 | 13.32 | 10.61 | 71.51 | 76.9 | 29.33 | | | |
| rc_W72972_at | W72972 | 3587 | EST | 5.61 | 0.00939 | 44.7 | 26.44 | 80.59 | 277.4 | 270.63 | 183.07 | | | |
| rc_W73382_at | W73382 | 3591 | EST | #N/A | #N/A | 62.97 | 39.05 | 67.26 | 87.32 | 89.49 | 28.17 | | | |
| rc_W79422_s_at | W79422 | 3604 | fumarylacetoacetate | 14.94 | 0.00059 | -18.4 | -19.27 | 33.52 | 467.37 | 554.19 | 306.71 | | | |
| rc_W81053_at | W81053 | 3610 | EST | 4.91 | 0.00164 | -21.38 | -13.04 | 24.17 | 135.84 | 109.34 | 113.36 | | | |
| rc_W85765_at | W85765 | 3618 | EST | 3.83 | 0.00379 | 3.6 | 1.46 | 7.87 | 108.99 | 77.01 | 109.58 | | | |
| rc_W85847_at | W85847 | 3619 | EST | 7.28 | 0.00024 | 4.15 | 5.29 | 9.26 | 187.31 | 160.02 | 130.73 | | | |
| rc_W85886_at | W85886 | 3621 | EST | 3.46 | 0.00814 | -6.09 | -2.4 | 11.46 | 99.92 | 68.44 | 97.4 | | | |
| protein C inhibitor (plasminogen activator inhibitor III) | | | | | | | | | | | | | | |
| rc_W86431_s_at | W86431 | 3627 | inhibitor III) | 14.94 | 0.00152 | 3.16 | 5.55 | 12.03 | 606.44 | 395.34 | 590.7 | | | |
| rc_W86600_at | W86600 | 3628 | EST | 32.14 | 0 | 12.67 | 7.49 | 15.61 | 792.37 | 807.74 | 313.83 | | | |
| homogentisate 1,2-dioxygenase (homogentisate oxidase) | | | | | | | | | | | | | | |
| rc_W87454_at | W87454 | 3632 | oxidase) | 7.93 | 0.00149 | 11.36 | 5.83 | 39.02 | 336.07 | 275.03 | 315.24 | | | |
| STAT induced STAT inhibitor-2 | | | | | | | | | | | | | | |
| rc_W87480_at | W87480 | 3633 | Inhibitor-2 | 3.24 | 0.01063 | 31.91 | 26.07 | 30.44 | 129.06 | 119.73 | 80.94 | | | |
| protein Z, vitamin K-dependent plasma glycoprotein | | | | | | | | | | | | | | |
| rc_W87606_s_at | W87606 | 3635 | glycoprotein | 9.23 | 0.00085 | 2.53 | -1.74 | 9.98 | 268.59 | 280.44 | 184.7 | | | |
| putative glycine-N-acyltransferase | | | | | | | | | | | | | | |
| rc_W88946_at | W88946 | 3639 | acyltransferase | 58.26 | 0 | 2.16 | -22.13 | 39.9 | 1717.54 | 1821.77 | 502.55 | | | |
| rc_W90018_f_at | W90018 | 3642 | EST | #N/A | #N/A | -2.1 | 4.12 | 13.16 | 59.32 | 53.19 | 41.68 | | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold | | metastati | | | | normal | | | |
|----------------|---------|--------|--|--------|---------|-----------|-------|--------|---------|---------|---------|---------|--------|
| | | | | change | p value | metastati | c: | Median | Dev | Mean | Median | Std Dev | normal |
| rc_W90396_at | W90396 | 3645 | EST | #N/A | #N/A | 16.1 | 15.26 | 11.11 | 23.65 | 3697.54 | 22.93 | 10.28 | |
| rc_W92148_s_at | W92148 | 3650 | kininogen | 51.09 | 0.00376 | 220.31 | 42.96 | 427.59 | 11.11 | 3697.54 | 4015.04 | 1444.99 | |
| rc_W94942_i_at | W94942 | 3661 | dual specificity phosphatase 10 | 7.23 | 0.00137 | 19.36 | 16.05 | 11.9 | 250.16 | 281.49 | 160.43 | | |
| rc_W95041_at | W95041 | 3662 | EST | 12.79 | 0.00001 | 6.66 | 5.17 | 3.55 | 291.2 | 298.05 | 115.81 | | |
| X02160_at | X02160 | 3671 | insulin receptor | 5.29 | 0.0001 | 10.06 | 8.21 | 10.89 | 77.32 | 65.71 | 45.53 | | |
| X02176_s_at | X02176 | 3672 | complement component 9 protein C (inactivator of coagulation factors Va and VIIIa) | 9.61 | 0.00004 | 47.28 | 46.34 | 28.54 | 507.56 | 507.21 | 261.45 | | |
| X02750_at | X02750 | 3673 | VIIIa | 7.04 | 0.00079 | 55.79 | 52.95 | 30.08 | 373.11 | 367.46 | 95.74 | | |
| X06562_at | X06562 | 3686 | growth hormone receptor | 10.87 | 0.00001 | 10.46 | 6.89 | 15.53 | 291.31 | 314.9 | 160.29 | | |
| X07618_s_at | X07618 | 3691 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a (pseudogene) | 35.79 | 0.00065 | 59.61 | 12.32 | 101.97 | 1429.98 | 1631.04 | 671.55 | | |
| X07618_s_at | X07618 | 3691 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a (pseudogene) | 35.79 | 0.00065 | 40.81 | 38.21 | 14.35 | 609.22 | 605.91 | 330.02 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|----------------|---------|--------|--|----------------------------|---------|-----------|--------|---------------|---------|---------|---------|
| | | | | | | c: Mean | Median | c: Std Dev | Mean | Median | Std Dev |
| X07619_s_at | X07619 | 3692 | cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a (pseudogene) | 4.96 | 0.00004 | 32.26 | 33.56 | 10.88 | 177.56 | 206.15 | 77.69 |
| X07732_at | X07732 | 3693 | hepsin (transmembrane protease, serine 1) | 28.21 | 0 | -8.34 | -12 | 39.24 | 678.15 | 672.42 | 183.61 |
| X07767_at | X07767 | 3694 | protein kinase, cAMP- dependent, catalytic, alpha | 5.94 | 0.00028 | 16.15 | 19.43 | 11.48 | 152.58 | 160.88 | 73.73 |
| X12662_rna1_at | X12662 | 3697 | arginase, liver | 20.59 | 0 | 11.33 | 10.15 | 12.81 | 486.71 | 479.11 | 199.71 |
| X13227_at | X13227 | 3698 | D-amino-acid oxidase | 4.81 | 0.0002 | 25.1 | 33.95 | 26.2 | 166.22 | 147.21 | 77.49 |
| X13930_f_at | X13930 | 3700 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 | 38.52 | 0 | 52.66 | 64.02 | 31.42 | 2408.66 | 1948.18 | 1843.46 |
| X14787_at | X14787 | 3704 | thrombospondin 1 | 3.69 | 0.01115 | 21.81 | 22.87 | 7.7 | 143.24 | 86.81 | 166.32 |
| X14813_at | X14813 | 3705 | acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl- Coenzyme A thiolase) | 11.61 | 0.0002 | 59.4 | 71.51 | 42.45 | 712.58 | 704.45 | 258.91 |
| X15393_rna1_at | X15393 | 3707 | motilin | #N/A | #N/A | 70.16 | 55.83 | 27.07 | 113.93 | 117.96 | 26.14 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | normal | | |
|-------------|---------|--------|--|----------------------------|---------|----------------------|------------------------|----------------------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | metastati c: Mean | metastati c: Median | metastati c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| X15422_at | X15422 | 3708 | mannose-binding lectin (protein C) 2, soluble (opsonic defect) | 8.29 | 0.00015 | 2.28 | 2.69 | 7.25 | 208.25 | 221.14 | 123.22 |
| X16260_s_at | X16260 | 3710 | inter-alpha (globulin) inhibitor, H1 polypeptide hepatocyte growth factor (hepapoietin A; scatter factor) | 44.65 | 0.00933 | 40.4 | 36.54 | 67 | 1261.99 | 1133 | 523.31 |
| X16323_at | X16323 | 3711 | hematopoietic cell-specific Lyn substrate 1 | #N/A | #N/A | 10.65 | 6.56 | 6.59 | 32.58 | 30.52 | 9.66 |
| X16663_at | X16663 | 3714 | paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein) | #N/A | #N/A | 48.32 | 28.69 | 56.44 | 81.51 | 83.53 | 33.75 |
| X17094_at | X17094 | 3717 | alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine- pyruvate aminotransferase) | 8.5 | 0 | -1.85 | 7.01 | 25.41 | 190.11 | 216.35 | 74.11 |
| X53414_at | X53414 | 3728 | pregnancy-zone protein | 13.87 | 0.00003 | 138.92 | 110.29 | 90.59 | 1856.57 | 1888.79 | 846.06 |
| X54380_at | X54380 | 3730 | | 8.44 | 0.00059 | 4.93 | 3.19 | 19.26 | 274.41 | 255.4 | 203.47 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|------------------|---------|--------|---|----------------------------|---------|----------------------|------------------------|----------------------------|-----------------------------|-------------------------------|--------------------------|----------------------------|-----------------------------|
| | | | | | | metastati c: Mean | metastati c: Median | metastati c: Std Dev | metastati set 2: Mean | metastati set 2: Median | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev |
| X56411_ma1_at | X56411 | 3737 | alcohol dehydrogenase 4 (class II), pi polypeptide | 25.14 | 0.00144 | 55.53 | 11.29 | 102.45 | 991.98 | 943.64 | 991.98 | 943.64 | 448.31 |
| X57025_at | X57025 | 3742 | insulin-like growth factor 1 (somatomedin C) | 4.72 | 0.00087 | 5.88 | 10.95 | 10.22 | 120.82 | 100.54 | 120.82 | 100.54 | 85.16 |
| X60673_s_at | X60673 | 3752 | adenylate kinase 3 | 8.3 | 0.00016 | 23.02 | 32.17 | 44.24 | 331.58 | 324.75 | 331.58 | 324.75 | 164.03 |
| X63359_at | X63359 | 3759 | UDP glycosyltransferase 2 family, polypeptide B10 | 13.66 | 0.00051 | 55.28 | 48.57 | 41.25 | 669.93 | 732.6 | 669.93 | 732.6 | 161.42 |
| X63417_at | X63417 | 3760 | c-myc promoter-binding protein | #N/A | #N/A | 28.85 | 27.75 | 24.56 | 68.08 | 56.34 | 68.08 | 56.34 | 33.18 |
| X64877_at | X64877 | 3766 | H factor (complement)-like 3 | 14.6 | 0 | 14.6 | 7.51 | 21.01 | 387.8 | 402.95 | 387.8 | 402.95 | 151.23 |
| X64877_s_at | X64877 | 3766 | H factor (complement)-like 3 | 12.33 | 0 | 6.14 | 8.26 | 14.25 | 262.65 | 268.29 | 262.65 | 268.29 | 84.84 |
| X65727_cds2_s_at | X65727 | 3768 | glutathione S-transferase A2, glutathione S-transferase A3 | 73.64 | 0 | 21.03 | 17.39 | 15.18 | 2162.22 | 2183.18 | 2162.22 | 2183.18 | 1435.52 |
| X65962_s_at | X65962 | 3769 | cytochrome P450, subfamily IIC (mephenytoin 4- hydroxylase) | 5.47 | 0.00014 | 36.73 | 31.48 | 11.66 | 247.79 | 149.39 | 247.79 | 149.39 | 208.59 |
| X76105_at | X76105 | 3794 | death-associated protein | 3.02 | 0.00944 | 30.12 | 33.72 | 31.36 | 108.68 | 118.36 | 108.68 | 118.36 | 56.75 |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|------------------|---------|--------|--|----------------------------|---------|-----------|-----------|------------|--------------------|----------------------|-----------------------|--|--|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | | |
| X78992_at | X78992 | 3802 | butyrate response factor 2 (EGF-response factor 2) | 4.69 | 0.01995 | 64.86 | 31.76 | 66.31 | 318.26 | 336.95 | 207.43 | | |
| X79981_at | X79981 | 3806 | cadherin 5, VE-cadherin (vascular epithelium) | #N/A | #N/A | 45.01 | 41.07 | 11.65 | 80.92 | 80.1 | 8.57 | | |
| X86401_s_at | X86401 | 3815 | glycine amidinotransferase (L-arginine:glycine amidinotransferase) | 22.7 | 0 | 19.17 | 9.16 | 19.13 | 646 | 721.34 | 274.64 | | |
| X90999_at | X90999 | 3820 | hydroxyacyl glutathione hydrolase; glyoxalase 2 | 5.27 | 0.00047 | 16.15 | 26.83 | 26.47 | 170.37 | 179.54 | 76.98 | | |
| X91148_at | X91148 | 3821 | microsomal triglyceride transfer protein (large polypeptide, 88kD) | 5.91 | 0.00045 | 15.37 | 3.85 | 31.49 | 173.77 | 189.11 | 83.82 | | |
| X92396_at | X92396 | 3823 | synaptobrevin-like 1 | #N/A | #N/A | 40.87 | 17.73 | 57.17 | 67.49 | 61.23 | 31.24 | | |
| X92475_at | X92475 | 3824 | TBA1 gene | #N/A | #N/A | 56.74 | 63.84 | 25.6 | 66.2 | 63.72 | 20.36 | | |
| X94563_xp12_r_at | X94563 | 3831 | EST | 3.52 | 0.00928 | 76.79 | 66.4 | 52.64 | 274.91 | 244.92 | 177.63 | | |
| X95190_at | X95190 | 3832 | acyl-Coenzyme A oxidase 2, branched chain | 12.81 | 0 | -80.53 | -76.73 | 37.81 | 285.88 | 349.39 | 119.31 | | |
| X97160_rna1_at | X97160 | 3838 | transcription factor binding to IGHM enhancer 3 | #N/A | #N/A | 61.31 | 49.54 | 30.41 | 75.26 | 66.36 | 29.46 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | | normal | | | |
|----------------------------|---------|--------|---|----------------------------|---------|-----------|-----------|------------|---------|-------------|---------------|----------------|--------|
| | | | | | | c: Mean | c: Median | c: Std Dev | normal | set 2: Mean | set 2: Median | set 2: Std Dev | normal |
| X98337_s_at Y00097_s_at | X98337 | 3840 | complement factor H related 3, complement factor H- related 4 | 13.5 | 0.00001 | 18.76 | 22.2 | 33.33 | 411.51 | 375.08 | 169.37 | | |
| | Y00097 | 3844 | | 3.4 | 0.00233 | 19.43 | 16.39 | 33.67 | 105.39 | 104.75 | 39.99 | | |
| Y00317_at | Y00317 | 3845 | UDP glycosyltransferase 2 family, polypeptide B4 | 18.34 | 0.00001 | -9.82 | -11.91 | 20.96 | 456.09 | 477.28 | 257.07 | | |
| | Y00317 | 3845 | | 18.34 | 0.00001 | 11.31 | 14.85 | 7.33 | 231.32 | 282.35 | 122.76 | | |
| Y00339_s_at Y10659_at | Y00339 | 3847 | carbonic anhydrase II interleukin 13 receptor, alpha 1 | 6.89 | 0 | 6.23 | -1.39 | 18.22 | 168.76 | 178.44 | 69.52 | | |
| | Y10659 | 3859 | | 4.22 | 0.00061 | 18.27 | 12.85 | 25.15 | 123.23 | 134.47 | 49.24 | | |
| Y10659_at Y12711_at | Y10659 | 3859 | interleukin 13 receptor, alpha 1 | 4.22 | 0.00061 | 15.82 | 16.3 | 16.79 | 81.75 | 89.09 | 37.01 | | |
| | Y12711 | 3861 | | 14.83 | 0.00285 | 26.37 | 16.12 | 99.79 | 1061.83 | 935.43 | 829.85 | | |
| Z28339_at Z29481_at | Z28339 | 3875 | aldo-keto reductase family 1, member D1 (delta 4-3- ketosteroid-5-beta- reductase) | 24.66 | 0 | 3.67 | 3.48 | 5.1 | 527.72 | 552.17 | 156.66 | | |
| | Z29481 | 3877 | | 6.39 | 0.00029 | 546.48 | 440.33 | 293.12 | 2012.12 | 1797.38 | 944.18 | | |

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

| Affy ID | Genbank | Seq ID | Known Gene Name | fold change in metas | p value | metastati | | | metastati | | | normal set 2: Mean | normal set 2: Median | normal set 2: Std Dev | |
|----------------|---------|--------|---|-------------------------|---------|-----------|-----------|------------|----------------------|------------------------|-------------------------|--------------------------|----------------------------|-----------------------------|--|
| | | | | | | c: Mean | c: Median | c: Std Dev | metastati c: Mean | metastati c: Median | metastati c: Std Dev | | | | |
| Z30425_at | Z30425 | 3878 | nuclear receptor subfamily 1, group 1, member 3 | 26.64 | 0 | 5.66 | 7.49 | 8.02 | 181.6 | 192.48 | 76.65 | | | | |
| rc_Z38161_at | Z38161 | 3884 | | EST | 4.38 | 0.0011 | 11.84 | 12.14 | 6.32 | 111.16 | 107.62 | 80.11 | | | |
| rc_Z38192_s_at | Z38192 | 3885 | | EST | 3.35 | 0.00184 | -0.28 | -4.75 | 17.86 | 87.12 | 87.23 | 52.58 | | | |
| rc_Z38910_at | Z38910 | 3898 | | EST | #N/A | #N/A | 0.68 | 2.75 | 12.7 | 35.49 | 32.21 | 23.55 | | | |
| rc_Z39394_at | Z39394 | 3904 | | EST | #N/A | #N/A | 10.11 | 10.43 | 11.1 | 24.06 | 22.96 | 11.11 | | | |
| rc_Z39622_s_at | Z39622 | 3910 | | EST | 4.4 | 0.00001 | 19.65 | 21.87 | 11.97 | 110.87 | 115.21 | 36.19 | | | |
| rc_Z39833_at | Z39833 | 3913 | | GTP-binding protein | 16.89 | 0.00034 | 35.79 | 41.07 | 84.59 | 957.61 | 1080.1 | 674.72 | | | |
| rc_Z39976_at | Z39976 | 3915 | | EST | 5.76 | 0.00012 | 13.09 | 7.15 | 18.64 | 165.45 | 151.05 | 98.9 | | | |
| rc_Z40259_s_at | Z40259 | 3919 | | EST | 8.18 | 0.00002 | 14.39 | 8.61 | 11.98 | 218.4 | 223.24 | 122.06 | | | |
| | | | | ariadne, Drosophila, | | | | | | | | | | | |
| rc_z41271_s_at | Z41271 | 3930 | homolog of | #N/A | #N/A | 51.96 | 64.49 | 36.28 | 145.09 | 126.18 | 57.57 | | | | |
| rc_Z41356_at | Z41356 | 3932 | EST | #N/A | #N/A | 4.46 | 15.94 | 28.44 | 82.7 | 48.14 | 71.73 | | | | |
| rc_Z41634_at | Z41634 | 3934 | EST | #N/A | #N/A | 16.4 | 16.07 | 3 | 51.19 | 48.49 | 33 | | | | |
| | | | flavin containing | | | | | | | | | | | | |
| Z47553_at | Z47553 | 3939 | monooxygenase 5 | 6.17 | 0.00011 | 4.86 | 1.26 | 8.96 | 141.98 | 165.57 | 59.33 | | | | |
| Z48054_at | Z48054 | 3941 | peroxisome receptor 1 | #N/A | #N/A | 46.89 | 51.87 | 23.55 | 78.16 | 80.88 | 26.87 | | | | |
| | | | glucokinase (hexokinase 4) | | | | | | | | | | | | |
| Z48475_at | Z48475 | 3943 | regulatory protein | 13.84 | 0 | -42.61 | -53.52 | 23.46 | 305.23 | 239.52 | 155.98 | | | | |
| Z48633_at | Z48633 | 3944 | EST | #N/A | #N/A | -5.51 | -6.39 | 13.15 | 36.84 | 40.63 | 26.33 | | | | |
| | | | small inducible cytokine | | | | | | | | | | | | |
| Z49269_at | Z49269 | 3945 | subfamily A (Cys-Cys), member 14 | 18.46 | 0.00001 | 1.88 | -25.63 | 41.94 | 526.13 | 532.29 | 166.67 | | | | |
| | | | guanidinoacetate N- | | | | | | | | | | | | |
| Z49878_at | Z49878 | 3946 | methyltransferase | 13.96 | 0.00021 | 44.63 | 45.34 | 41.76 | 615.57 | 659.09 | 196.31 | | | | |

What is claimed is:

1. A method of diagnosing liver cancer in a patient, comprising:
 - (a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of
5 liver cancer.
2. A method of detecting the progression of liver cancer in a patient, comprising:
 - (a) detecting the level of expression in a tissue sample of two or more genes
10 from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression.
3. A method of monitoring the treatment of a patient with liver cancer, comprising:
 - 15 (a) administering a pharmaceutical composition to the patient;
 - (b) preparing a gene expression profile from a cell or tissue sample from the patient; and
 - (c) comparing the patient gene expression profile to a gene expression from a cell population selected from the group consisting of normal liver cells,
20 hepatocellular carcinoma and metastatic liver carcinoma.
4. A method of treating a patient with liver cancer, comprising:
 - (a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;
 - 25 (b) preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells; and
 - (c) comparing the patient expression profile to a gene expression profile selected from the group consisting of normal liver cells, hepatocellular carcinoma and metastatic liver carcinoma
30
5. A method of diagnosing hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma.

5 6. A method of detecting the progression of hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

10

7. A method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising:

(a) administering a pharmaceutical composition to the patient;
(b) preparing a gene expression profile from a cell or tissue sample from the
15 patient; and

(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both.

20 8. A method of treating a patient with hepatocellular carcinoma, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;

(b) preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells; and

25 (c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising hepatocellular cells.

9. A method of diagnosing a metastatic liver tumor in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer.

5

10. A method of detecting the progression of a metastatic liver cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver cancer progression.

10

11 A method of monitoring the treatment of a patient with a metastatic liver cancer, comprising:

(a) administering a pharmaceutical composition to the patient;

15 (b) preparing a gene expression profile from a cell or tissue sample from the patient; and

(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both.

20

12. A method of treating a patient with a metastatic liver tumor, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;

25 (b) preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells; and

(c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells.

13. A method of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, comprising:

30

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

5 14. A method of screening for an agent capable of modulating the onset or progression of liver cancer, comprising:

 (a) preparing a first gene expression profile of a cell population comprising liver cancer cells, wherein the expression profile determines the expression level of one or more genes from Tables 3-9 ;

10 (b) exposing the cell population to the agent;

 (c) preparing second gene expression profile of the agent-exposed cell population; and

 (d) comparing the first and second gene expression profiles.

15 15. The method of claim 14, wherein the liver cancer is a hepatocellular carcinoma.

 16. The method of claim 14, wherein the liver cancer is a metastatic liver cancer.

20 17. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 .

 18. A composition according to claim 17, wherein the composition comprises at least 3 oligonucleotides.

25 19. A composition according to claim 17, wherein the composition comprises at least 5 oligonucleotides.

 20. A composition according to claim 17, wherein the composition comprises at
30 least 7 oligonucleotides.

21. A composition according to claim 17, wherein the composition comprises at least 10 oligonucleotides.

22. A composition according to any one of claims 17-21, wherein the
5 oligonucleotides are attached to a solid support.

23. A composition according to claim 22, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.
10

24. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9.

25. A solid support according to claim 24, wherein the oligonucleotides are
15 covalently attached to the solid support.

26. A solid support according to claim 24, wherein the oligonucleotides are non-covalently attached to the solid support.

20 27. A solid support according to claim 24, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.

28. A solid support according to claim 24, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.
25

29. A solid support according to claim 24, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

30. A solid support according to claim 24, wherein the support comprises at least
30 about 10,000 different oligonucleotides in discrete locations per square centimeter.

31. A computer system comprising:

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(a) a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9 ; and

(b) a user interface to view the information.

5 32. A computer system of claim 31, wherein the database further comprises sequence information for the genes.

 33. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the set of genes in normal liver tissue.

10

 34. A computer system of claim 31, wherein the database further comprises information identifying the expression level of the set of genes in liver cancer tissue.

 35. A computer system of claim 34, wherein the liver cancer tissue comprises
15 hepatocellular carcinoma cells.

 36. A computer system of claim 34, wherein the liver cancer tissue comprises metastatic liver cancer cells.

20 37. A computer system of any of claims 31-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

 38. A computer system of claim 37, wherein the external database is GenBank.

25

 39. A method of using a computer system of any one of claims 31-36 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising:

 (a) comparing the expression level of at least one gene in Tables 3, 4, 5, 6, 8 or 3-9
30 in the tissue or cell to the level of expression of the gene in the database.

40. A method of claim 39, wherein the expression level of at least two genes are compared.

41. A method of claim 39, wherein the expression level of at least five genes are
5 compared.

42. A method of claim 39, wherein the expression level of at least ten genes are compared.

10 43. A method of claim 39, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in liver cancer.

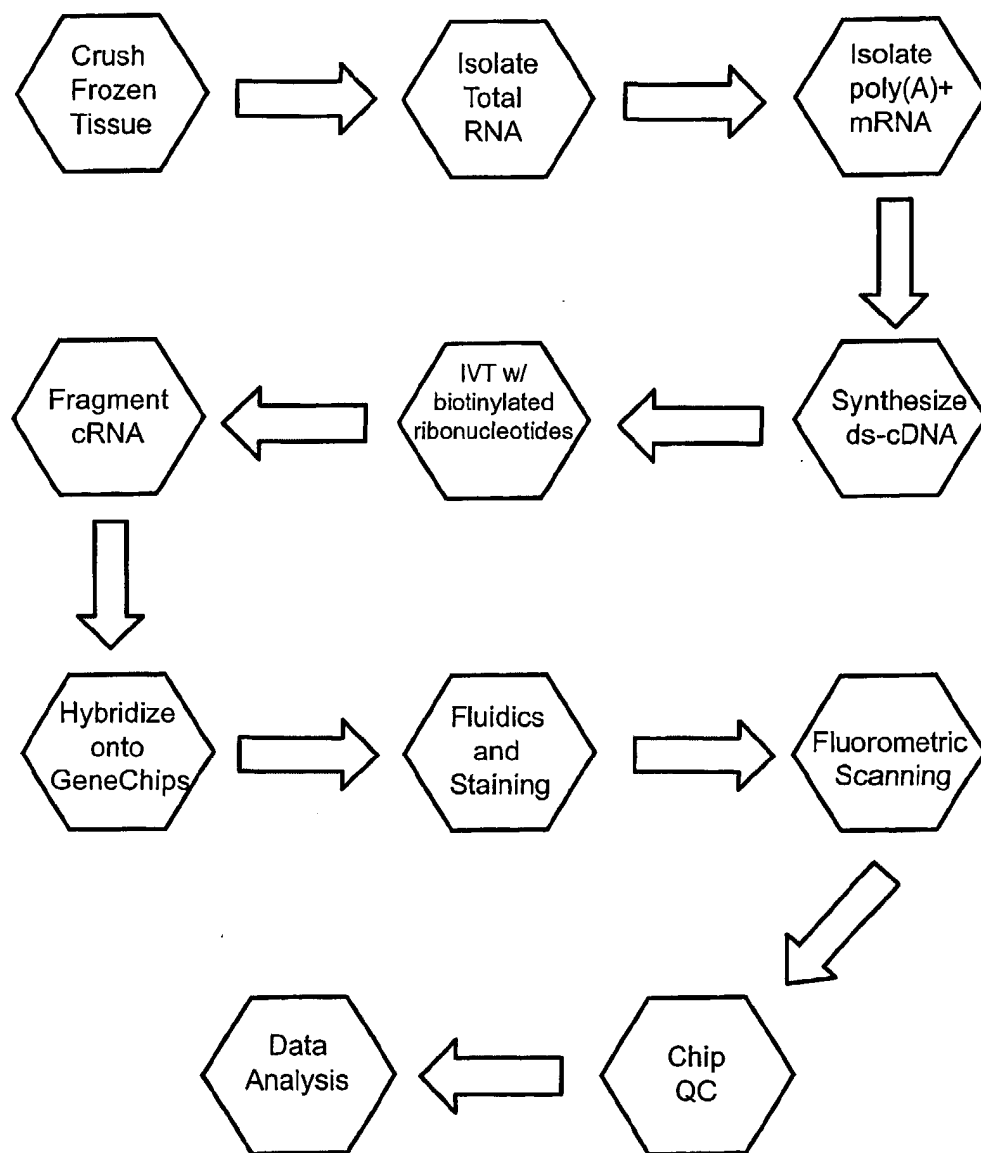
FIGURE 1

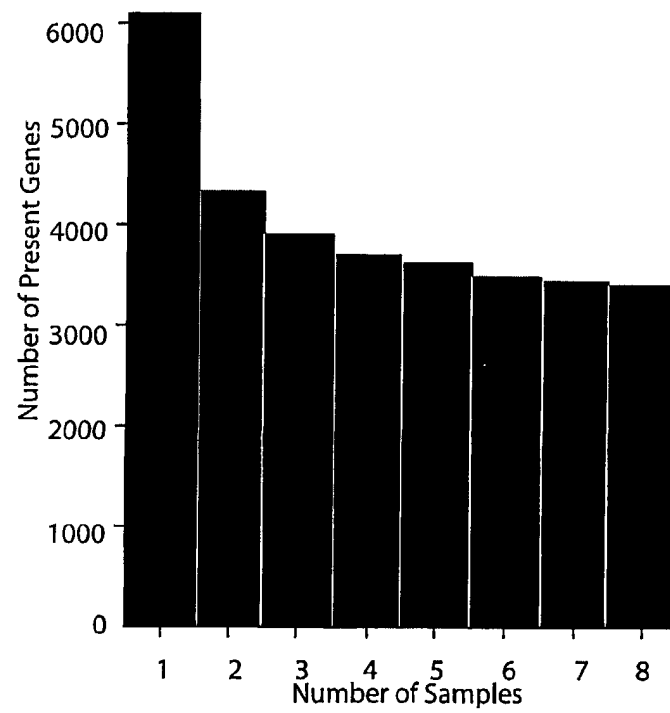
FIGURE 2A

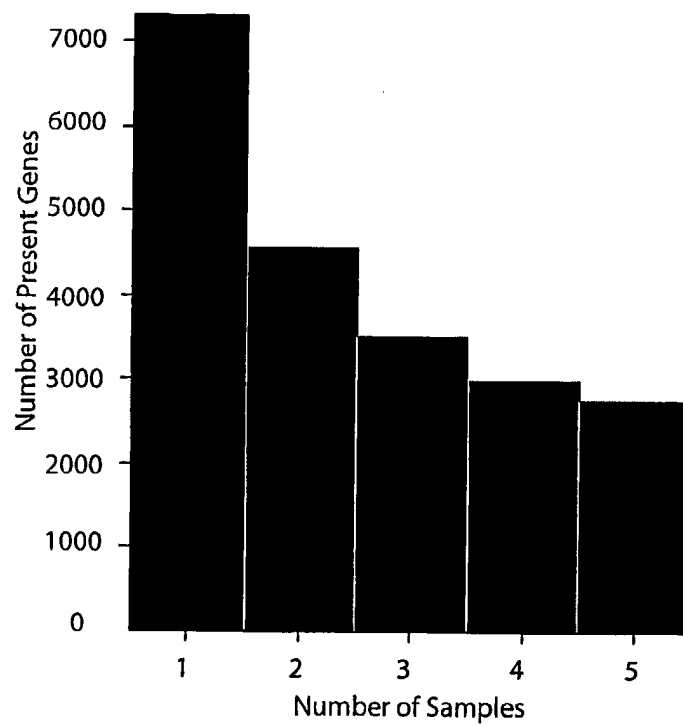
FIGURE 2B

FIGURE 2C